

MouseMine Module

For these problems, please access MouseMine either from MGI (homepage>“Batch Data and Analysis Tools”>“MouseMine”, or dropdown menu Search>“MouseMine”) or direct, at:

<http://www.mousemine.org/mousemine/begin.do>

You are a researcher working on DNA repair and have generated a list of 321 mouse genes based on functional annotations. This list is pre-loaded into MouseMine – go to the “Lists” tab, “View” and click on “Mouse DNA repair genes 2013-01-06”.

Be sure to scroll down the page to find Enrichment widgets and Template queries.

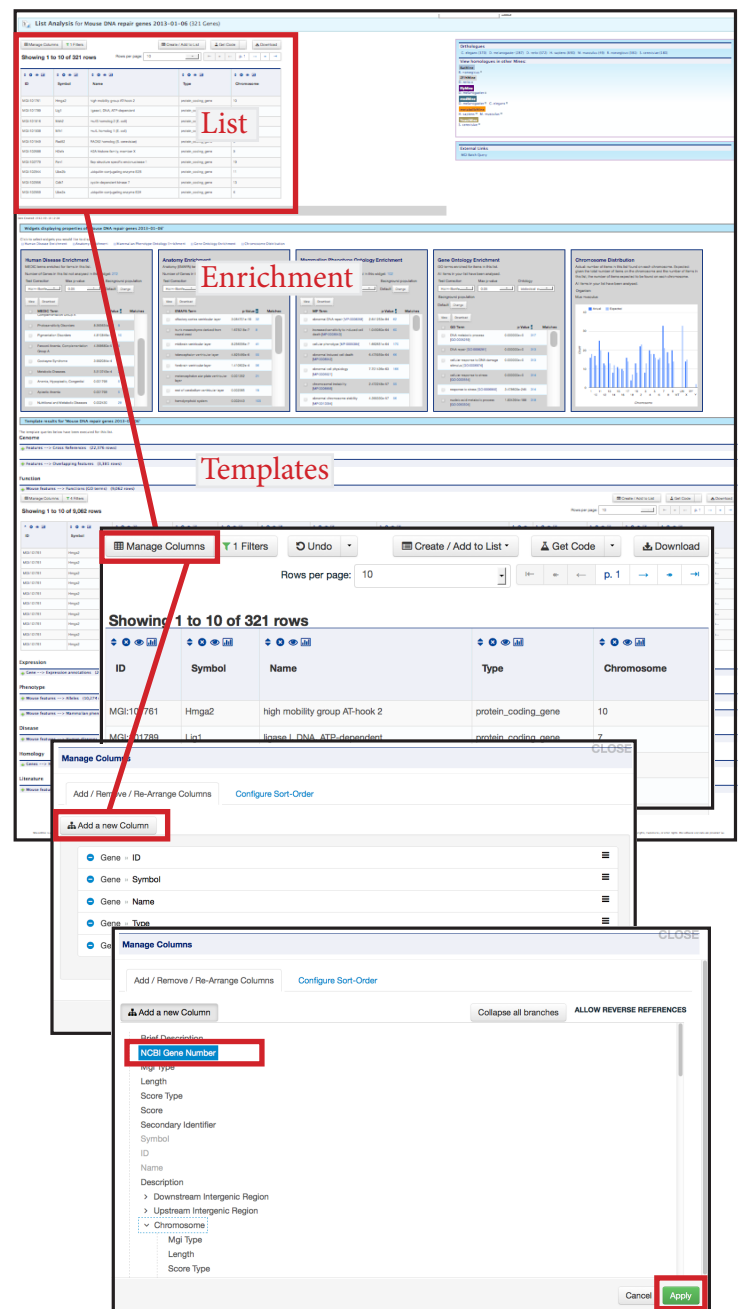
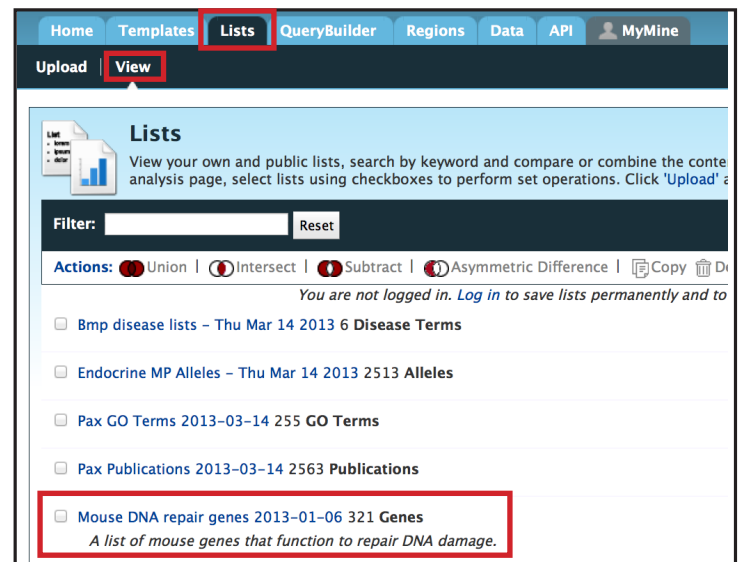
*** Please note that the content in these worksheets is accurate as of 16 May 2014. Updates to the data may cause some numbers to shift slightly. ***

19. At the top of the page where your list appears, use **Manage Columns** (may compress to “Columns” in smaller windows) to add a column for “NCBI Gene Number” to the list of 321 DNA repair genes. What is the NCBI Gene Number for Hmga2?

- a) 15368
b) 22210
c) 13248
d) 35510
e) 11478


On the right is a zoomed out view of the complete list analysis page, with the uploaded list situated at the top, followed by Enrichment widgets in the middle and a series of compressed template results at the bottom.

Click the **Manage Columns** button just above the list, then **Add a new Column**. Select the column that you’d like to add and apply.



20. In the Human Disease Enrichment widget, using the default of Holm-Bonferroni test correction, what is the associated p-value for the MEDIC term: “DNA Repair-Deficiency Disorders”?
- 2.641253e-84 with 62 genes matched
 - 5.148577e-27 with 23 genes matched
 - 0.001798 with 5 genes matched
 - 0.05
 - There is no significant enrichment for this term

Scroll below the list to the middle of the page where Enrichment widgets can be found.

This widget presents a downloadable table for all MEDIC terms with significant enrichment within the uploaded list, according to a hypergeometric distribution (click on the info icon ) for more details on the statistics). Genes which match each MEDIC term can be viewed by clicking on the hyperlinked number in the “Matches” column.

This list is highly enriched for **DNA Repair-Deficiency Disorders**, with 23 gene matches and a Holm-Bonferroni corrected p-value of 5.148577e-27.

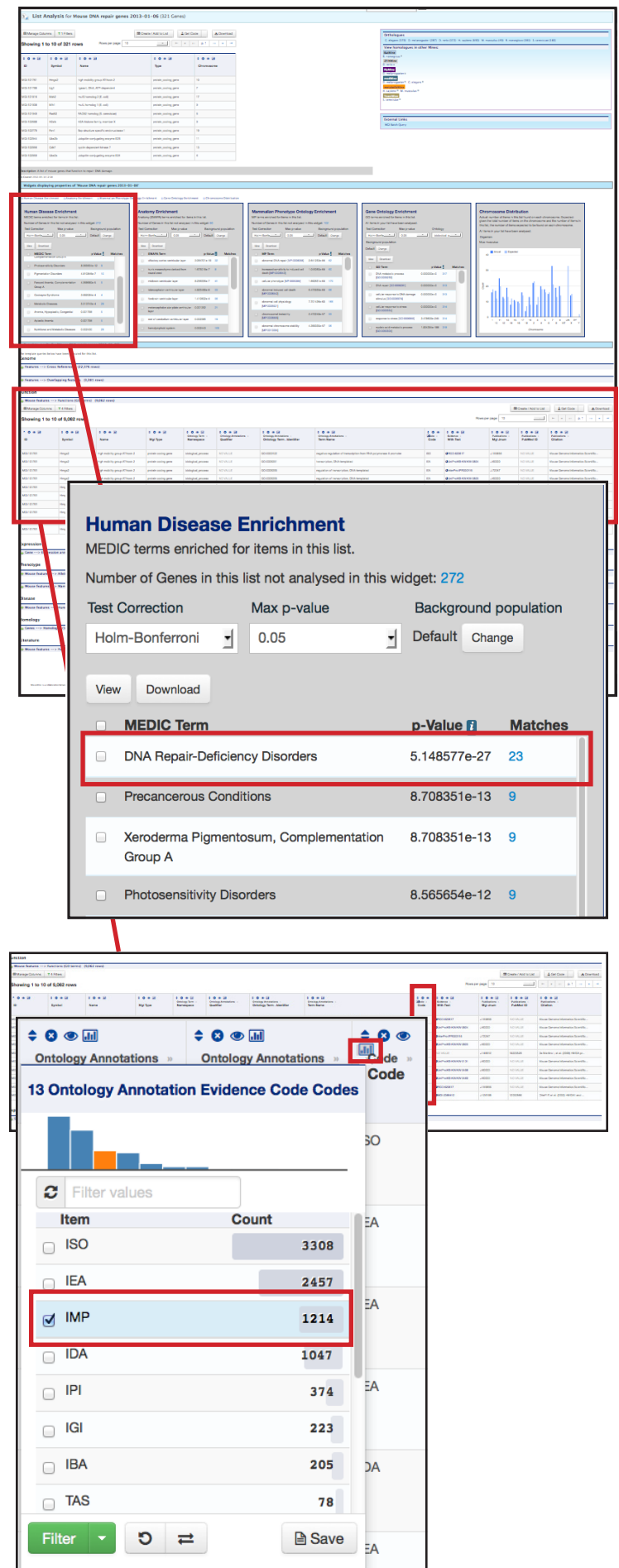
21. Scroll further down the page below the **Enrichment widgets** to the **Template results** for this list.

Locate the table for **Function: “Mouse Features → Functions (GO terms)”**. Expand, if necessary, by clicking on the name of the template. According to the column summary for **“Code”** (bar graph icon in column header), how many functional annotations have the evidence code **“IMP”**, which corresponds to “Inferred from Mutant Phenotype”?

- 9062
- 1214
- 3308
- 13
- none

Locate the Code column in the results table that corresponds to the **Mouse Features → Functions (GO terms)** template. This should be the 3rd template in the section, and, in brackets, indicate that the table is comprised of 9062 total rows.

Find the column for **Code**, which follows the ontology details and precedes the references columns. Click the bar graph icon in the header to reveal column summary statistics. IMP was used as the evidence code for 1214 GO annotations to the genes in this list.



22. Exit the list analysis tools and return to MouseMine Home. Find the template for **Homology: “Genes → Homologs”** and enter “pxn” for the Paxilin gene into the search box, leaving the Organism dropdown menu at the default *M. musculus*.

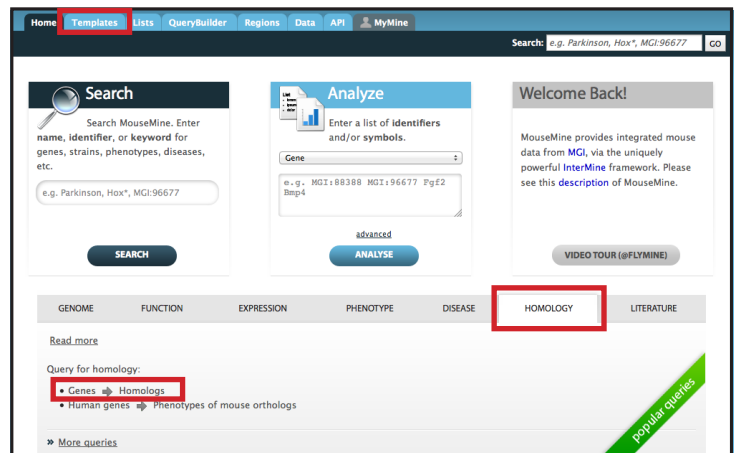
What is the **Homolog symbol** corresponding to the **Homolog Organism: *Saccharomyces cerevisiae***?

- a) PXN
- b) Pax
- c) PXL1
- d) pxna
- e) there is no homolog in *S. cerevisiae*

On the homepage, select the **Homology** tab from the **Popular templates** or browse the list of all templates by using the **Templates** tab along the top of the page. Click on the **Genes → Homologs** to select.

Enter “pxn” into the **LOOKUP** search box, then click **Show Results** to return all cross-species homologs of *Pxn* in the MouseMine data sets. These are provided by HomoloGene (as are vertebrate homologs presented in MGI) and/or by Panther.

Locate *S. cerevisiae* in the **Homolog.Organism.Name** column, where it appears one time. Use the column **Homolog.Symbol** to retrieve the official gene symbol for the homolog in this species.



Trail: Query
Genes → Homologs
Returns homologs of specified genes.

Showing 1 to 16 of 16 rows

| ID | Symbol | Organism | Homologs - Homologue - Primary Identifier | Homologs - Homologue - Symbol | Homologs - Homologue - Organism - Name | Homologs - Type | Data Sets - Name |
|------------|--------|--------------|---|-------------------------------|--|---------------------------|---------------------|
| MGI:108295 | Pxn | Mus musculus | 5829 | PXN | Homo sapiens | orthologue | HomoloGene data set |
| MGI:108295 | Pxn | Mus musculus | ENSG000000089159 | NO VALUE | Homo sapiens | least diverged orthologue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | FBgn0041789 | Pax | Drosophila melanogaster | orthologue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | FBgn0050176 | CG30178 | Drosophila melanogaster | orthologue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | FBgn0051988 | CG31988 | Drosophila melanogaster | orthologue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | FBgn008354 | CG34325 | Drosophila melanogaster | orthologue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | MGI:102784 | Tgfb11 | Mus musculus | paralogue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | MGI:2147677 | Lpin | Mus musculus | paralogue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | RGD:1305759 | Pxn | Rattus norvegicus | least diverged orthologue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | RGD:1305759 | Pxn | Rattus norvegicus | orthologue | HomoloGene data set |
| MGI:108295 | Pxn | Mus musculus | S000001798 | PXL1 | Saccharomyces cerevisiae | orthologue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | WBGen00012379 | None | Caenorhabditis elegans | orthologue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | WBGen00016197 | pef-1 | Caenorhabditis elegans | orthologue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | WBGen00016386 | None | Caenorhabditis elegans | orthologue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | WBGen00018000 | None | Caenorhabditis elegans | orthologue | Panther data set |
| MGI:108295 | Pxn | Mus musculus | ZDB-GENE-040105-1 | pepa | Danio rerio | orthologue | Panther data set |

For any questions, please contact:

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MouseMine questions can also be addressed directly to the developers by using the **Contact Us** link at the top right corner of MouseMine pages.