In Situ Hybridization (ISH) Data

SEARCHING THE IN SITU HYBRIDIZATION (ISH) DATA

Gene Search

To search for a specific gene or group of genes, type its gene name, gene symbol, NCBI Accession number, or Entrez Gene ID into the search box. Make sure the Gene radio button is selected and click the “Search” button. You will be offered suggestions to choose from while you type, but you can also search by typing the first three or more letters in its name or symbol and appending an asterisk (*) as a wildcard. You can also browse through the genes by clicking on a category.

Advanced Search

You can sort the search results or further refine your query using the Advanced Search feature.
Several additional search criteria can be used to build a query using "Advanced Search."

The following search criteria can be specified in the text box to the right of the categories. If you copy + paste in a list of terms delimited by tabs or carriage returns they will automatically be converted into a list of search criteria separated by the OR operator (|).

- Gene symbol
- Gene name
- Gene aliases
- Entrez gene ID

**Boolean Syntax**

The following special operators can be used to build queries:

<table>
<thead>
<tr>
<th>Operator</th>
<th>Example Search Type</th>
<th>Example Query</th>
</tr>
</thead>
<tbody>
<tr>
<td>AND operator: &amp;</td>
<td>Gene</td>
<td>dopamine &amp; receptor</td>
</tr>
<tr>
<td>OR operator:</td>
<td>Gene</td>
<td>ABAT</td>
</tr>
<tr>
<td>NOT operator: !</td>
<td>Gene</td>
<td>&quot;dopamine receptor“ !DRD3</td>
</tr>
</tbody>
</table>

- AND, OR and NOT may be used in place of their corresponding operators. They must be upper case.
- The AND operator (&) is implicit, so spaces between words that are not separated by an operator will be treated like an &.
- OR (!) has higher operator precedence than AND (&).
- Parenthesis can be used to group criteria, but nested parenthesis are not supported at this time.
- The NOT operator (!) is not supported within parenthesis.
- Enclose search terms in quotation marks to avoid confusion with boolean operators. For example, hyphenated words should be enclosed in quotation marks (i.e. "ATP-binding").

**Search Results**

Based on your search criteria, a list of experiments will be returned as described in the table below. Search results can be sorted by up to three categories indicated by the drop down menus. Search categories are prioritized from left to right and include all searchable columns. The checkbox labeled "asc" (ascending order) indicates the sorting direction for each column, so when checked, the sort progresses from a to z, or 1 to n, depending on whether the column is alphabetic or numeric. Leaving the box unchecked sorts the column in descending order, that is z to a, or n to 1.
ISH - Image Viewing

The Zoom and Pan (ZAP) Image Viewer window allows you to view the images from one or more experiments once they have been selected from the search returns list (by clicking the checkbox(es) and clicking "View Selections"). Each ZAP viewer consists of a filmstrip of thumbnails - which when selected will bring up the image in the main viewer, tools to navigate the image in the main viewer and a scale bar to determine the approximate size of the area in the main viewer.

To alter your workspace, click on the selections wheel at the top left hand corner of the ZAP Viewer window to select the number of columns (i.e. the number of experiments you can fit across the page).

The size of your viewers will automatically adjust to fit your screen real estate. Selecting one of the references from the Atlas drop down menu will allow you to see an annotated reference atlas along side your experiments. Drag viewers to other positions to rearrange them.

The gene symbol or treatment type is displayed in the title bar along with the Allen Institute image series ID. Additional details are displayed across the top of the viewing area, including the donor age, tissue index, and tissue location.

Thumbnails for the entire image series are displayed across the bottom of the viewer in section order. Click a thumbnail to select it for viewing, or use the keyboard to navigate through the set. The current selection is outlined in black.

### Toolbar

<table>
<thead>
<tr>
<th>Icon</th>
<th>Description</th>
</tr>
</thead>
</table>
Move the slider bar to the left to intensify the contrast or color

Show current image in a full-screen viewer with side by side Nissl comparison

See the images series in contact sheet format

Select ISH, Nissl, or Expression image type

Open a new window to view the image series' details

Close the current viewer

**Scale Bar**

Shows the current viewing resolution of the image, in microns. This value dynamically changes as you zoom in/out of the image. You can position the scale bar anywhere on the main image by dragging the scale bar by its ruler.

You can toggle the orientation of the scale bar from horizontal to vertical by clicking on the scale bar text. When you download an image, the scale bar is not included with the image.

**Side By Side Nissl Viewing**

Once you click on the full screen viewer button, you will be taken to a screen with side by side viewers. The left hand viewer shows the ISH image series and the right hand viewer displays the closest Nissl image from the same specimen block. Clicking on another ISH image will automatically display the nearest Nissl section. Clicking on an image thumbnail in the Nissl image series will automatically take you to the nearest ISH image. While the "Sync" box is checked the Zoom and Pan functions will affect both images. Round spots on the Nissl image are "hotspots" and when hovered over will display the name of the structure. Clicking on the hotspots while viewing ISH images from an adult brain will take you to the Adult Human ISH Guide. While viewing pre-natal ISH images, clicking on the hotspot will take you to the appropriate aged prenatal Reference Atlas.
Keyboard Commands

<table>
<thead>
<tr>
<th>Key</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>F</td>
<td>Advance to the next image in the series</td>
</tr>
<tr>
<td>D</td>
<td>Go back to the previous image</td>
</tr>
<tr>
<td>R</td>
<td>Advance to the last image in the series</td>
</tr>
<tr>
<td>E</td>
<td>Go back to the first image in the series</td>
</tr>
<tr>
<td>A</td>
<td>Zoom in</td>
</tr>
<tr>
<td>Z</td>
<td>Zoom out</td>
</tr>
</tbody>
</table>

Expression Mask Colors

The Expression Mask image display highlights those cells that have the highest probability of gene expression using a heat map color scale (from low/blue to high/red).

Experiment Details Page

Clicking on the experiment ID from the search results page will return a page with metadata about the experiment including experiment details, specimen details, related Institute data, probe details and a ZAP Image Viewer.
Gene Details Page

When you click on the gene symbol from the search returns page you will be taken to a page that includes all the experiments performed in this study with this gene.

Specimen Detail Information

Clicking on the specimen link from the search results page or on the specimen link in the experiment details page will take you to detailed specimen information. Specimen detail information includes Specimen Information, Specimen Block Layout, Section Information, Gene Information and an Image Viewer.
Donor/Specimen Metadata

### Specimen ID: H00-0028.01.02

<table>
<thead>
<tr>
<th>Field</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>26 yrs</td>
</tr>
<tr>
<td>Tissue Location</td>
<td>Visual cortex</td>
</tr>
<tr>
<td>RNA Integrity</td>
<td>7.6</td>
</tr>
<tr>
<td>Race</td>
<td>White or Caucasian</td>
</tr>
<tr>
<td>Conditions</td>
<td>Smoker - no, disease categories - control</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Field</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex</td>
<td>F</td>
</tr>
<tr>
<td>Hemisphere</td>
<td>Left</td>
</tr>
<tr>
<td>pH</td>
<td>6.0</td>
</tr>
<tr>
<td>Handedness</td>
<td>Unknown</td>
</tr>
</tbody>
</table>

### Specimen Block Layout

<table>
<thead>
<tr>
<th>Specimen</th>
<th>Position (x,y,z)</th>
<th>Date</th>
</tr>
</thead>
<tbody>
<tr>
<td>80103230</td>
<td>1,1,1</td>
<td>Y</td>
</tr>
<tr>
<td>80103236</td>
<td>1,1,2</td>
<td>Y</td>
</tr>
</tbody>
</table>

### Section Information

- **Gene**: GAP43
- **Experiment**: 80499034
- **Section Number**: 1
- **Treatments**: ISH
- **Study**: Human Brain ISH Cortex Study

### Genes evaluated in this specimen

- ADORA2A
- ADORA3
- ADRA1A
- ADRA2B
- ADRB2
- AGTR1
- AGTR2
- ARLN
- ANKR1B
- CCKAR
- CCKGR

This data is also available as XML.
Specimen ID - internal ID
Age - years
Sex - male or female
Tissue Location - tissue origination in brain
Hemisphere - right or left hemisphere tissue origination
RNA Integrity Number - metric indicating RNA integrity from tissue. Ranges from 1 to 10 (degraded to intact RNA)
pH - tissue sample pH
Race - ethnicity
Handedness - right, left, or ambidextrous
Conditions - disease conditions, smoker

Specimen Block Layout

Specimens are received as variable sized blocks of frozen tissue. Before they are sectioned for ISH experiments they are divided into a number of sub-specimens. Throughout this site, when we refer to a specimen we are actually referring to one of these sub-specimens.

This list denotes the current sub-specimen (in black) and sibling sub-specimens, with their locations and whether data was collected on the sub-specimen. Sibling sub-specimen can be viewed if there is data (denoted by Y) by clicking on their links.

Section Information

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The section information box lists information from the current gene pictured in the image viewer including the gene name, the experiment ID, the section number, the treatment and which study the data came from.

Gene Information

The Gene information section lists the genes that were assayed in this specimen block.

By default, all genes from this specimen are selected for viewing. You can select fewer genes/histological stains to view in the image viewer by first clicking the "Gene" checkbox, then selecting the checkboxes next to the gene/stain(s) you would like to view.

Image Viewer
The viewer displays the image from the current gene listed in the section information box. Below the image is an indicator of the position in the specimen block of that particular section, as well as a visualization of the depth of the section into the block. You can view the sections in order (default or by clicking the button) or grouped by gene ( button). When you click on the magnifying glass in the bottom of the image viewer, a new window will open with a magnified view the area in the image viewer outlined by the red box. you can increase or decrease the magnification with the scale at the bottom.
This data can be downloaded as an XML file.