# TGx Benchmark Dose Response Guided Search Help

**Page Navigation (Quick Links)**



## Introduction

The TGx Benchmark Dose Response Guided Search allows users to view benchmark dose (BMD) data for genes included in DTT toxicogenomics studies. Data for most affected genes and Gene Ontology (GO) biological processes are displayed in accumulation plots.

## Search

From the CEBS Homepage select "TGx Benchmark Dose Response" under 'DTT Guided Searches' to open the application. The option "Select Test Article" is displayed on the opening page along with the <SHOW RESULTS> button.

- Click inside the "select a test article" text box
  - Select the test article of interest from the 23 choices displayed in the drop-down list
  - If designated, the organ studied is shown in parentheses after the test article name
- Click the green 'Show Results' button to retrieve data

## Results

The Results page is comprised of 3 elements.

- The 1st element consists of accumulation plots for:
  - Most affected genes
  - Most affected GO biological processes

  **Note:** ***The most affected genes plot can be displayed using Best BMD or maximum fold change the abscissa. To switch between these options, click the buttons in the plot header the top of the page***

- The 2nd element consists of two tables of BMD values of the data included in the corresponding accumulation plots and are displayed directly below each plot
  - The "Most Affected Genes" table includes:
    - Gene Symbols
    - BMD Median
    - BMDL Median
    - Maximum Fold Change
    - Overall Direction

  - The "Most Affected Biological Processes (Gene Ontology) table includes:
    - GO Gene Set ID
    - GO Level
    - GO Gene Set ID
    - BMD Mean
    - BMD Median
    - Maximum Fold Change

- The 3rd element at the bottom of the page provides Links to
  - BMDMedian Coordinates
  - Maxfold Coordinates
  - GO Pathway Coordinates

## Most Affected Genes

### *Interactive Accumulation Plot*

The default plot represents data for genes most affected by the test chemical ranked by BMD Medians. The Maximum Fold Change plots rank the data by the maximum fold change values of the most affected genes (**Note: *A negative fold change values show decreased expression and positive fold change values show increased expression***)

Plot interactive features:

Hover over a single data point to display the data point coordinates, rank of the Gene, Affymetrix probe number, and the gene symbol. The buttons at the top right of the plot each function independently to allow interaction with the plot. Hover over any button to display its function then the click to activate it:

From left to right the buttons are 

- **Download**: Download the plot as a high-quality image file (.png)
- **Zoom**: Click inside the plot then drag the cursor to define the zoom area
- **Pan:** Click inside the plot and hold the mouse button down while moving the mouse to pan the plot
- **Box Select**: Click and drag in the plot area to select a rectangular shaped area
- **Lasso Select**: Click and drag in the plot area to hand-draw a selection section
- **Zoom in**: Zooms into the current center of the plot
- **Zoom out**: Zooms out of the current center of the plot
- **Autoscale**: Resets the zoom of the plot to include all the available data

### *Data Table*

The data table contains more detailed information about the most affected genes in the plot

- The table contains 5 fields:
  - ***Genes Symbol***: the official gene symbol name
  - ***BMD Median***: the median Benchmark dose calculated from the data distribution
  - ***BMDL Median***: the median Lowest Confidence Limit of the BMD confidence interval
  - ***Maximum Fold Change***: the largest gene expression fold change at any dose
  - ***Overall direction***: indication of whether the gene was UP or DOWN regulated

- The table can be sorted by any of the 5 columns by clicking on the column header
- The table defaults to displaying 10 entries; to change the display number use the drop-down menu on the top left corner on the table to 25, 50, 100, or 500 entries
- Use the page numbers in the bottom right corner to scroll through the table pages

## Most Affected Biological Processes

### *Interactive Accumulation Plot*

The Most Affected Biological Process plot represents data for biological process, as defined by Gene Ontology (GO), that are most affected by the test chemical ranked by BMD Medians. The interactive plot features function the same as those described above for the Most Affected Genes plot.

### *Data Table*

The data table has six columns of data which are described below:

- Data table fields:
  - ***GO Gene Set ID***: the official Gene Ontology ID of the Biological Process
  - ***GO Level***: the number of separation levels between the specific Biological Process and the beginning of the ontology tree
  - ***GO Gene Set Name***: the name of the Biological Process
  - ***BMD Mean***: the mean BMD for the genes in this Process
  - ***BMD Median***: the median BMD for the genes in this Process
  - ***Max Fold Change***: the largest gene expression fold change for the Process at any dose

# Additional Resources

## Accumulation Plot Coordinate Files

This is the last element of the page and it contains links to download files that have the coordinates for data plotted or displayed in the data tables.

The Accumulation Plot Coordinate Files include:

- ***BMDMedian Coordinates***: the coordinate file used to generate the Accumulation Plot with the Most Affected Genes ordered by BMD Median
- ***Maxfold Coordinates***: the coordinate file used to generate the Accumulation Plot with the Most Affected Genes ordered by Maximum Fold Change
- ***GO Pathway Coordinates***: the coordinate file used to generate the Accumulation Plot with the Most Affected Biological Processes ordered by BMD Median

**Note: All Input Data files for the 'TGx Benchmark Dose Guided Search' are the output of BMDExpress3 software. For a detailed description of the data files refer to the BMDExpress user manual** (https://github.com/auerbachs/BMDExpress-2/wiki).