



Interactive scatter plot viewer

This manual provides usage information for the interactive scatter plot viewer at prohits-viz.lunenfeld.ca. This tool is designed to interactively display scatter plots generated from other tools on Prohits-viz.

Browser compatibility

Optimal performance of this tool is achieved with Chrome (tested in versions 47 - 55) although it is fully compatible and supported in Firefox (tested in versions 43 - 50) and Safari (tested in versions 7 - 9). For optimal performance with very large images, close unnecessary applications and browser tabs. In some cases fonts may appear too large in Firefox due to Firefox setting a hard cap on the minimum font size. This can be disabled by following the instructions [here](#).

Any other issues should be addressed to jknight@lunenfeld.ca.

Sample input files

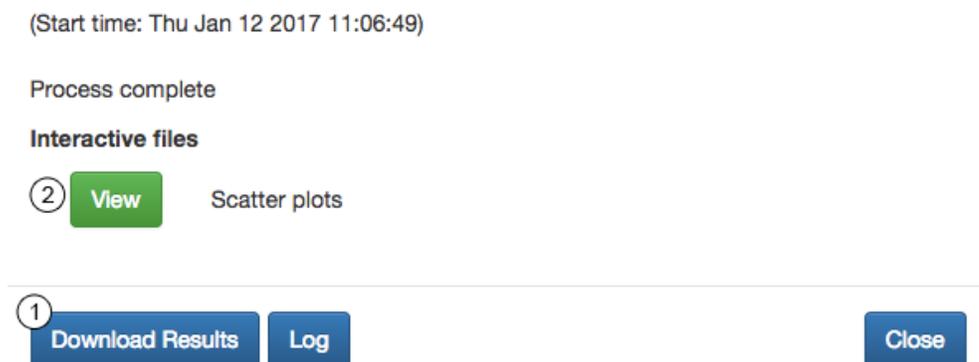
Input files are available for download from the “sample input files” hyperlink on the main page. These files were generated using the Prey Specificity and Bait-Bait Comparison tools using BioID data from the following paper:

Couzens, A.L., Knight, J.D.R., Kean, M.J., Teo, G., Weiss, A., Dunham, W.H., Lin, Z.Y., Bagshaw, R.D., Sicheri, F., Pawson, T., Wrana, J., Choi, H., Gingras, A.-C. (2013) Protein interaction network of the mammalian Hippo pathway reveals mechanisms of kinase-phosphatase interactions. *Sci Signal*, **6**: rs15. [PMID: 24255178](https://pubmed.ncbi.nlm.nih.gov/24255178/)

Inputting data

Currently, compatible output is produced from the following tools: Prey Specificity and Bait-Bait Comparison. After running these tools, results can be downloaded (1) and interactive files for this viewer will be found in the folder with the extension `_df.tsv`. Alternatively, results can be passed directly from these tools by clicking on the *Interactive files* link (2) after the task is complete.

Figure 1



The input interactive file is simply a plain tab-delimited text file with six columns as shown in **Figure 2**. The first line begins with the word “entry” to signify the start of information on a scatter plot and is followed by the plot title, the x-axis label, the y-axis label, the plot type (anything can be entered here as this is a custom parameter for generating legends specific to the tools at ProHits-vis) and the name for the score parameter in the dataset (optional). This line is followed by lines for each data point, beginning with the gene name, x and y coordinates, circle radius in pixels, circle colour (#hex value) and text information on the point that will be displayed when the point is moused-over. Multiple scatter plots can be included in a single file, with each beginning with the “entry” line as described above.

Figure 2

entry	plot title A	x-axis label	y-axis label	plot type	score name
gene A	x coordinate	y coordinate	circle radius	circle color	point information

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After loading an image the title of the current scatter plot will be displayed at (1). If more than one scatter plot is available to view, the others can be selected from this same dropdown. If the plot has been zoomed or translated, its original view can be reset with (2). Labels can be added to the plot with (3). Individual points can also be labelled selectively by clicking on them (4). The legend can be toggled with (5). By default, plots will be drawn to fill the browser window but square plots (x- and y- axis equivalent lengths) can be made by selecting (6). The image can be exported using (7) either as an SVG or PNG image. Images on ProHits-viz will only be stored temporarily. Clicking the archive (8) button will store the image in our database with a permanent URL. The input at (9) is used for gene searches. Searches are case insensitive and currently require a complete match. Matches can be removed by (10). To display information about a point, simply hover over it (11). Finally the image can be zoomed along both axes by positioning the cursor over the plot and using the scroll wheel (12), or zooming can be restricted to a single axis by placing the cursor over that axis (13).

Figure 3

