

A quick guide to finding screen data on the Mitocheck web site

- General navigation:

Links appear in dark red (in the general case) or green (for genes, transcripts, proteins, dsRNAs or videos IDs) and turn blue and orange respectively when they have been visited. In a list of protein interactors, entries with phenotypes appear in pink (light pink when already visited).

- How to find data for a gene:

The main point of access to screen data is the gene page where phenotype information pertaining to the gene are summarized. To find a gene, enter an identifier in the search box at the top of the page and click the find button next to it. Identifiers that work best are Ensembl gene IDs or HGNC gene symbols. Gene names can generally be used but they can be ambiguous or not recognized.

- How to find movies/images:

To access videos and images for a given gene, click on the 'Movies/images' button on the right side of the gene page. This leads to a page where videos and images are grouped by dsRNA used to generate them. The phenotype column indicates whether the dsRNA gives a phenotype. Clicking on the movie/image ID leads to the movie/image page. Clicking on the dsRNA ID leads to the dsRNA page.

- How to view movies:

Movies have been compressed using the XviD codec, which is compliant with the MPEG4 standard, and packaged using the AVI format. To view them, you need to use an MPEG4-compliant video player that can read AVI files. Some players that can be used are: MPlayer, VLC, xine, QuickTime 7.x, Windows Media Player 10 and 11.

If you're having problems, here are some options:

- Install MPlayer (<http://www.mplayerhq.hu/design7/dload.html>) or VLC (<http://www.videolan.org/vlc/>).

- on Mac OS X: Upgrade to Quicktime 7.x and install the DivX codec from <http://www.divx.com/divx/mac/download/>

- on Windows with Windows Media Player: see <http://www.microsoft.com/windows/windowsmedia/player/faq/codec.msp>

- How to get all the genes with a given phenotype:

The 'Browse' button on the left side of the page gives access to 'hit lists' by phenotype. After selecting a screen and a phenotype, a list of all genes annotated with the selected phenotype in the selected screen is returned.

- How to view the phenotypes of several genes at once:

To access phenotypic profiles for several genes across all screens, use the 'Compare genes' button on the left side of the page. After entering a list of gene identifiers (Ensembl IDs or HGNC gene symbols, but not gene names) in the box, an image map of the different annotations for the input genes is generated. Clicking on the gene symbol leads to the gene page, clicking on a column returns a list of all genes sharing the corresponding phenotype.

- How to find genes with phenotypes similar to a given gene:

On the right side of the gene page, the 'similar genes' button returns a list of genes with phenotypes most similar to the gene that was shown on the previous page.