MITELMAN DATABASE OF CHROMOSOME ABERRATIONS AND GENE FUSIONS IN CANCER

The database has been transferred to the Institute for Systems Biology (ISB)
https://mitelmandatabase.isb-cgc.org/

The updated web site offers some major advances:

1) FAST SEARCH. Powered by Google BigQuery, a cloud-enabled parallel query engine, each search can be executed faster than most web applications with conventional database engines.
2) USER INTERFACE ENHANCEMENTS. The user interface for the new web site has been simplified with a more responsive front-end, and is easier to use. Major changes added to the web site include the autocomplete drop-down list for Gene, Topography, and Morphology inputs.
3) CAPABILITY TO DOWNLOAD SEARCH RESULTS. Users can now download query results into a TSV text file.
4) EASIER ON-LINE NAVIGATION. Search results are simpler to navigate, through use of text filtering, paginations on the search result pages, and user-defined sorting of columns in the search results.

The last update on October 15, 2019, contains information on cytogenetic abnormalities in 69,551 cases and 22,091 unique gene fusions involving 12,044 genes.