Osteosarcoma Database

Performing a gene search

This guide through the Osteosarcoma Database provides a step-by-step tutorial on how to run a gene search using the example of CDKN1A.
Multiple routes to CDKN1A

The Osteosarcoma Database home screen introduces the osteosarcoma topic and the aims of our database. Therefrom, users can enter the search (1) for genes of interest.

The gene search can be performed using the geneids from NCBI’s Entrez gene Database, by official gene symbols from the Human Gene Nomenclature Committee, or by keywords. After submitting (2) the query, all genes within the database matching the specific query are proposed (not shown). Further, clicking on a specific number in the “#pmid” column directs the user to the main results page of the respective gene.

Alternatively, users can browse the collection of genes by clicking on the (3) “Browse Genes” menu. A table is generated holding the collection of genes implicated in osteosarcoma biology. (4) Users are able to browse by pagination buttons below the table or (5) by searching for keywords within the “Symbol” or “Name” columns. (6) Again, clicking on a specific number in the “#pmid” column directs the user to the main results page of the respective gene.

To get an overview about frequently mentioned genes in abstracts dealing with osteosarcoma biology, (7) users need to press the “Top Genes” menu on the left. A tagcloud appears showing all genes mentioned in more than five abstracts. Dragging and dropping over the cloud allows the user to explore the genes in more detail. Genes are weighted according to the number of abstracts. (8) CDKN1A is currently mentioned in 43 abstracts. Clicking a marked gene inside the tagcloud directs the user to its main results page.
CDKN1A in osteosarcoma

A (1) The search menu enables user to search for a gene or microRNA query. (2) Submitting the query delivers the results page for the specific query that shows general information derived from external databases and abstracts associated with the query. (3) The table of abstracts can be browsed using pagination buttons and (4) filtered according to type of samples, potential prognostic and/or therapeutic value, or by text search within the titles. (5) To receive more manual annotations like experimental settings, biological context, and information about the abstracts an export button is provided. (6) Interested user can further explore microRNA target gene interactions (MTIs). Clicking the MTI-button opens a network view on MTIs predicted by TargetScan 6.

B (7) The MTI network visually illustrates the possible regulatory relationships of the user’s query. A detailed description of the prediction results is given in the table below. (8) Again, users are able to export the table and receive additional information from the TargetScan 6 predictions like UTR start and stops and microRNA target gene pairing.
Looking on osteosarcoma literature

Users can browse all abstracts included in the Osteosarcoma Database by clicking the "Browse Abstracts" menu (1) on the left. A table appears containing the PubMed identifiers (PMIDs) and the abstract titles. For each abstract, manual reviewed and annotated information about the number of mentioned genes/microRNAs, the type of samples (human tumors: yes or no), and the proposed prognostic or therapeutic impact (yes or no) is given. The table of abstracts can be browsed using pagination buttons (2) and filtered according to type of samples, potential prognostic and/or therapeutic value, or by text search within the titles (3). By pressing a specific number in the "#Genes" column (4), a new screen appears showing the genes and microRNAs mentioned in the respective abstract.
We appreciate any kind of feedback

If you have any kind of suggestions, comments, or you want to add a paper on osteosarcoma biology that we might missed, please contact us (1). You can enter a message in the comment field and submit the text (2). Only comments having a valid email address are submitted.