

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

A Home screen: Shows the Osteosarcoma Database logo and a navigation menu. A red arrow (1) points to the 'Search' link in the menu.

B Search for genes: A search box with the text 'Search for Entrez genes, gene symbols, or keywords.' A red arrow (2) points to the search input field. Below the search box, 'CDKN1A' is entered, and a red arrow (3) points to the search button.

C Browse osteosarcoma associated genes: A table of genes associated with osteosarcoma. A red arrow (3) points to the 'BROWSE GENES' link in the left sidebar. A red arrow (4) points to the pagination controls at the bottom of the table. A red arrow (5) points to the search input field in the table header. A red arrow (6) points to the '#pmid' column header. A red arrow (7) points to the number '43' in the '#pmid' column for the CDKN1A row.

D Frequency of osteosarcoma genes: A tag cloud of genes frequently mentioned in abstracts. A red arrow (7) points to the 'TOP GENES' link in the left sidebar. A red arrow (8) points to the 'CDKN1A' tag in the cloud.

- A** 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.
- B** 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.
- C** 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.
- D** 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

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Osteosarcoma Database

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Results for CDKN1A

General Information

Gene ID: 3228
Gene Symbol: CDKN1A
Gene Name: cyclin-dependent kinase inhibitor 1A (p21, Cip1)
Gene Type: protein-coding
Cytoband: 12p21.2
Ensembl ID: ENST00000124792
miRNA regulators: 32 (6)
Ovism ID: 15899

PubMed abstracts associated with CDKN1A

| PMID | Title | Tumor | Value |
|----------|---|-------|-------|
| 7565200 | Retroviral vector-mediated gene transfer of antisense cyclin D1 (CYC1D1) inhibits proliferation of human osteogenic sarcoma cells. | no | no |
| 8915638 | Apoptotic response to oncogenic signal: cooperative and antagonistic interactions between c-myc and the growth suppressor p53. | no | no |
| 8154817 | Gluocorticoid receptor-mediated cell cycle arrest is achieved through distinct cell-specific transcriptional regulatory mechanisms. | no | no |
| 10339697 | Expression of G1 phase regulators in MG-63 osteosarcoma cell line. | no | no |
| 16658722 | Resveratrol induces senescence-like growth inhibition of U2-OS cells associated with the instability of telomeric DNA and upregulation of BICCA1. | no | no |

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B

MicroRNA regulators of target gene CDKN1A

The graph below represents the microRNA regulators of CDKN1A determined by TargetScan6. The gene is represented in red color and its respective microRNA regulators in green. You can drag and drop the network's nodes to take a closer look. Below the graph you can find a table of context scores illustrating the strength of each microRNA target gene regulation.

Detailed prediction results of TargetScan 6 for CDKN1A

| Accession | Name | Site type | Context score |
|-------------|--------------|-----------|---------------|
| MMAT0000020 | hsa-miR-17 | 7mer-m8 | -0.107 |
| MMAT0000012 | hsa-miR-20a | 7mer-m8 | -0.107 |
| MMAT0000093 | hsa-miR-93 | 7mer-m8 | -0.107 |
| MMAT0000103 | hsa-miR-100a | 7mer-m8 | -0.107 |
| MMAT0000425 | hsa-miR-120a | 7mer-m8 | -0.141 |
| MMAT0000426 | hsa-miR-122 | 7mer-m8 | -0.132 |
| MMAT0000680 | hsa-miR-100b | 7mer-m8 | -0.107 |
| MMAT0000681 | hsa-miR-130b | 7mer-m8 | -0.160 |
| MMAT0000413 | hsa-miR-20b | 7mer-m8 | -0.107 |
| MMAT0004568 | hsa-miR-301b | 7mer-m8 | -0.141 |

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- 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

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Osteosarcoma Database

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Browse osteosarcoma associated abstracts

Show 25 entries Search:

| PMID | Title | Tumor | Value | #Genes |
|----------|---|-------|-------|--------|
| 24009496 | How MicroRNA and Transcription Factor Co-regulatory Networks Affect Osteosarcoma Cell Proliferation | no | no | 13 |
| 23879172 | FIM-A, a phosphorus-containing scotinus, inhibits the angiogenesis and proliferation of osteosarcomas. | no | no | 6 |
| 23872151 | MicroRNA-340 suppresses osteosarcoma tumor growth and metastasis by directly targeting ROCK1. | no | no | 2 |
| 23831057 | Sprouty2 but not Sprouty4 is a potent inhibitor of cell proliferation and migration of osteosarcoma cells. | no | no | 1 |
| 23827457 | MicroRNA expression profiling of human bone marrow mesenchymal stem cells during osteogenic differentiation reveals Osterix regulation by miR-31. | no | no | 2 |
| 23507142 | miR-16 inhibits cell proliferation by targeting IGF1R and the Raf1-MEK1/2-ERK1/2 pathway in osteosarcoma. | yes | no | 2 |
| 23470834 | Melatonin inhibits the proliferation of human osteosarcoma cell line MQ-63. | no | no | 4 |
| 23462806 | Y-box binding protein-1 regulates cell proliferation and is associated with clinical outcomes of osteosarcoma. | no | no | 3 |
| 23461061 | C-Myc overexpression promotes osteosarcoma cell invasion via activation of MEK/ERK pathway | no | no | 3 |

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- A** 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

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Osteosarcoma Database

Contact

If you find any errors or inconsistencies or you have comments or suggestions please contact us. We appreciate any kind of feedback.

Your name

Your email

Your comment

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- A** 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.