

## What is DENdb?

DENdb is a centralized on-line repository of predicted enhancers derived from multiple human cell-lines. DENdb integrates enhancers predicted by five different methods (ChromHMM, Segway, RFECS, CSI-ANN, and ENCODE integrated annotation) generating an enriched catalogue of enhancers for each of the analyzed cell-lines. It also provides means to explore genes neighboring enhancers, as well as overlapping of enhancers with DNase hypersensitive regions obtained from ENCODE and transcription factor binding sites obtained from HOCOMOCO.

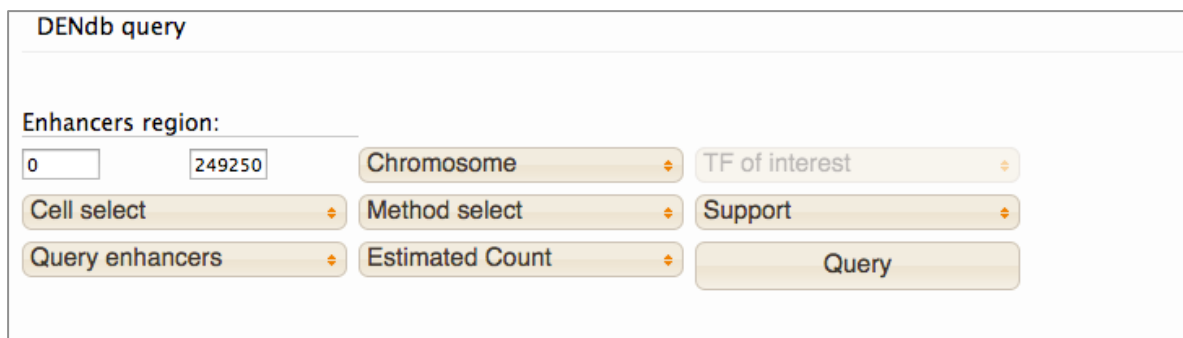
## How can I use DENdb?

DENdb provides user with four types of queries. The queries are:

- Enhancers: this query allows users to query integrated enhancers within DENdb.
- Closest gene: this query will report closest gene to DENdb enhancers, it also reports distance from enhancer to that gene.
- DNase overlap: this query will allow user to query enhancers that overlap with ENCODE DNase hypersensitive sites.
- Contains TF: this query report enhancers contain specific TF(s), it also report the TF hit location within enhancer and the hit q-value.

## Customizing DENdb search:

On DENdb [query page](#), user can find few options that can be used to make DENdb query more specific.





The screenshot shows the DENdb query interface. At the top, it says "DENdb query". Below that, there are several input fields and dropdown menus. The "Enhancers region:" section has two input boxes, one containing "0" and the other "249250". To the right of these are dropdown menus for "Chromosome" and "TF of interest". Below these are three more dropdown menus: "Cell select", "Method select", and "Support". At the bottom, there are two more dropdown menus: "Query enhancers" and "Estimated Count", followed by a "Query" button.

- Enhancer region: used to specify coordinate range in the chromosome.
- Chromosome: used to specify one or more chromosome to query the database
- Cell select: User can select from 15 different cell lines.
- Method: if user prefers specific method, user can select that to return only integrated enhancers predicted by that method.
- Support: user can set the level of confidence on his query using the support values; the higher the better.
- Query type: specify one out of 4 queries.
- Estimated count/True count: this option affects the speed of query. Estimated count uses an approximation function to count number of matched rows. While True count will do the actual counting. For a fast query estimated count is advised.
- TF of interest: a list of HOCOMOCO TFs that have at least one hit within DENdb integrated enhancers.

### **Detailed view of query results:**

For a detailed view of query results, user can click on a specific row to view its full details. In some cases detailed views are aggregated by query type; for example a detailed view of enhancer within TF query will show all TFs that has a prediction within that enhancer.

### **Downloading and visualizing results:**

Results can be downloaded in BED format by clicking on the download icon . Results also can be visualized into UCSC genome browser using visualize icon .

Downloading and visualizing results limit is up to 100 records (page max count).