

SITECON Searching Transcription Factors Binding Sites

To search transcription factor binding sites in a DNA sequence select the *Analyze Search TFBS with SITECON...* context menu item.

In the appeared search dialog you must select a file with TFBS profile. The profiles supplied with UGENE are placed in the \$UGENE/data/sitecon_models folder.

After the profile is loaded the threshold-filter is populated with values read from profile. You can use the filter to remove low-scoring regions from the result.

The screenshot shows the SITECON Search application interface. At the top is a title bar with the application name and standard window controls. Below the title bar are input fields for "File with model" and "Threshold". A large white area is reserved for search results. To the left of this area are radio button options for "Strands": "Both strands" (selected), "Direct strand", and "Complement strand". To the right are "Region" settings, including a dropdown menu set to "Whole sequence" and a range selector showing "1 - 199950". Below these settings is a table with five columns: "Range", "Strand", "PSUM", "First type error", and "Second type error". The table body is currently empty. At the bottom left are two buttons: "Clear results" and "Save as annotations". In the center bottom is the text "0 results found". At the bottom right are three buttons: "Search", "Close", and "Help".

The regions found by SITECON algorithm can be saved as annotations to the DNA sequence in the Genbank format.

Every *SITECON* profile supplied with UGENE contains complete information about calibration settings provided to UGENE team by the author of *SITECON*.

The original TFBS alignments used to calculate profiles can be requested directly from the author of *SITECON*.