

# Search for TFBS

This sample describes how to search for TFBS with a different methods and how to write the results into one output file.

First, the workflow reads sequences input by a user. Then, each sequence goes to searching TFBS elements. At that time two reading elements reads the matrix and model for TFBS searching and transferring this data into TFBS searching elements. After that the TFBS searching elements searches TFBS in the input sequences. After that the two data flows multiplexes into one output data flow. And finally, the multiplexed data are written into file, specified by a user.

You can configure the parameters of [Search for TFBS with Weight Matrix](#), [Search TFBS with SITECON](#) and [Multiplexer](#) elements.



## How to Use This Sample

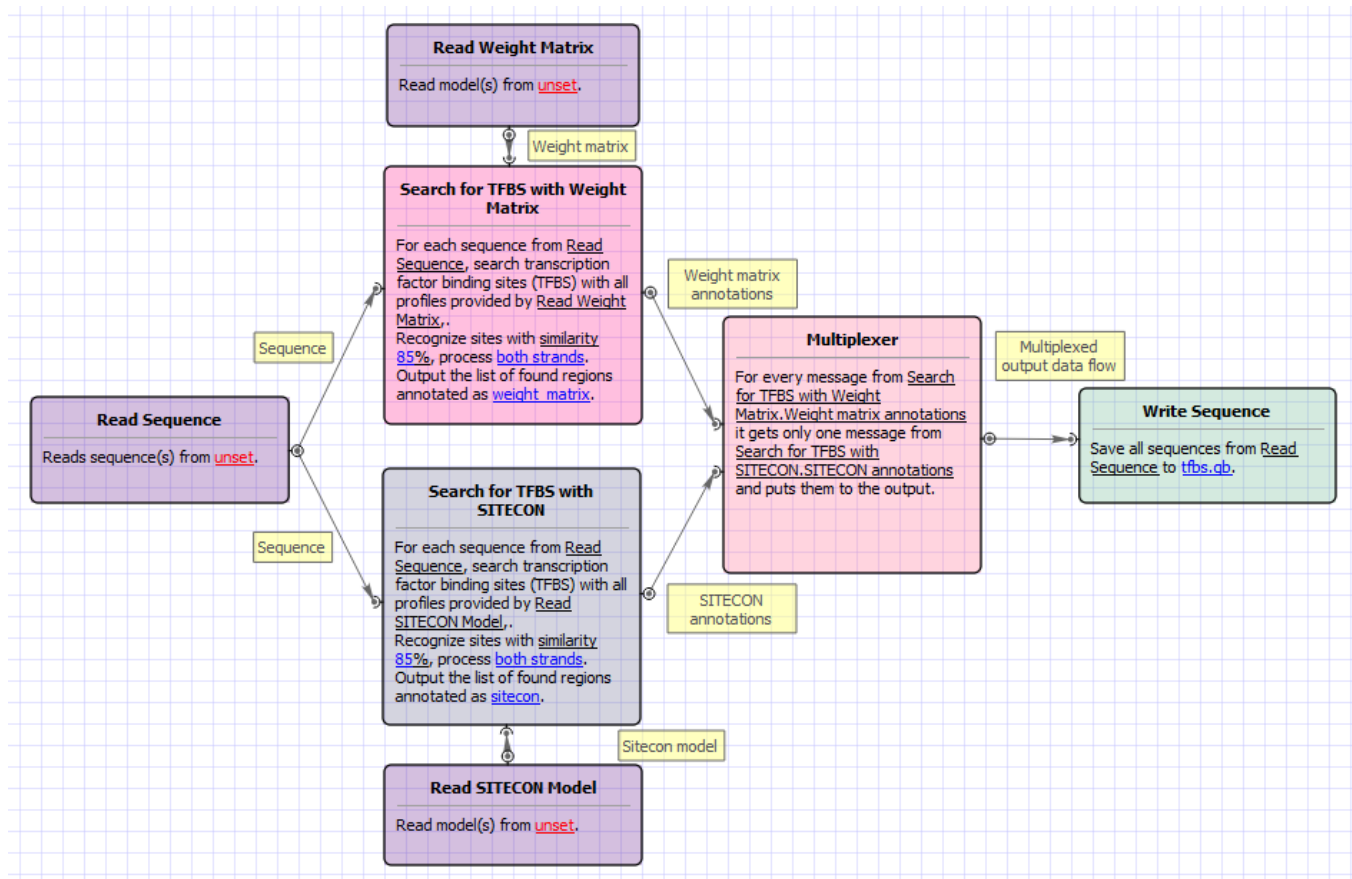
If you haven't used the workflow samples in UGENE before, look at the ["How to Use Sample Workflows"](#) section of the documentation.

## Workflow Sample Location

The workflow sample "Search for TFBS" can be found in the "Data Merging" section of the Workflow Designer samples.

## Workflow Image

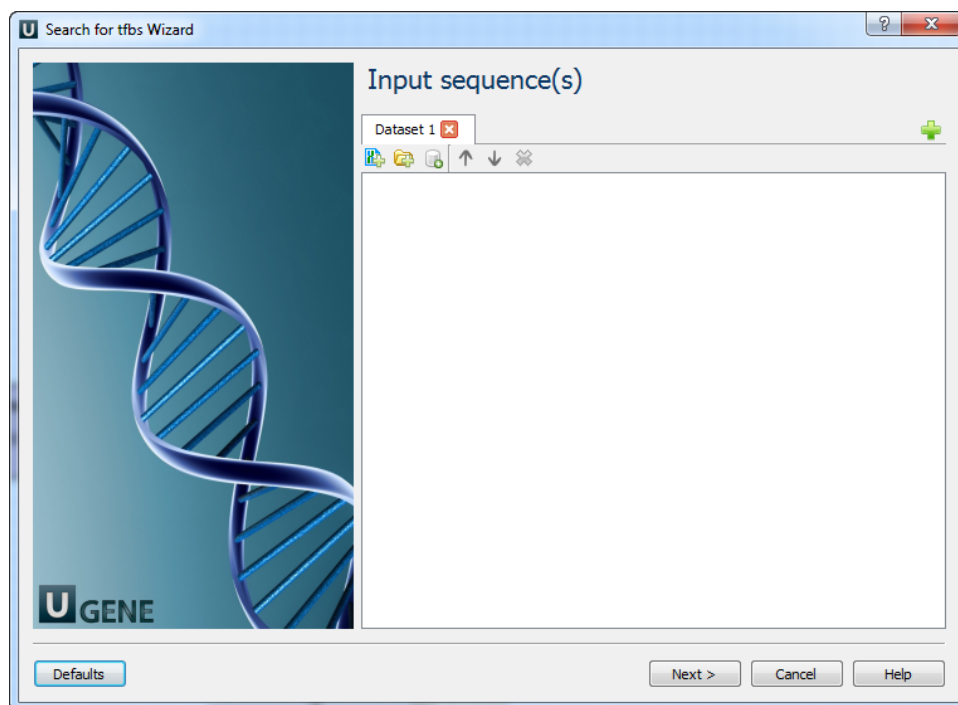
The workflow looks as follows:



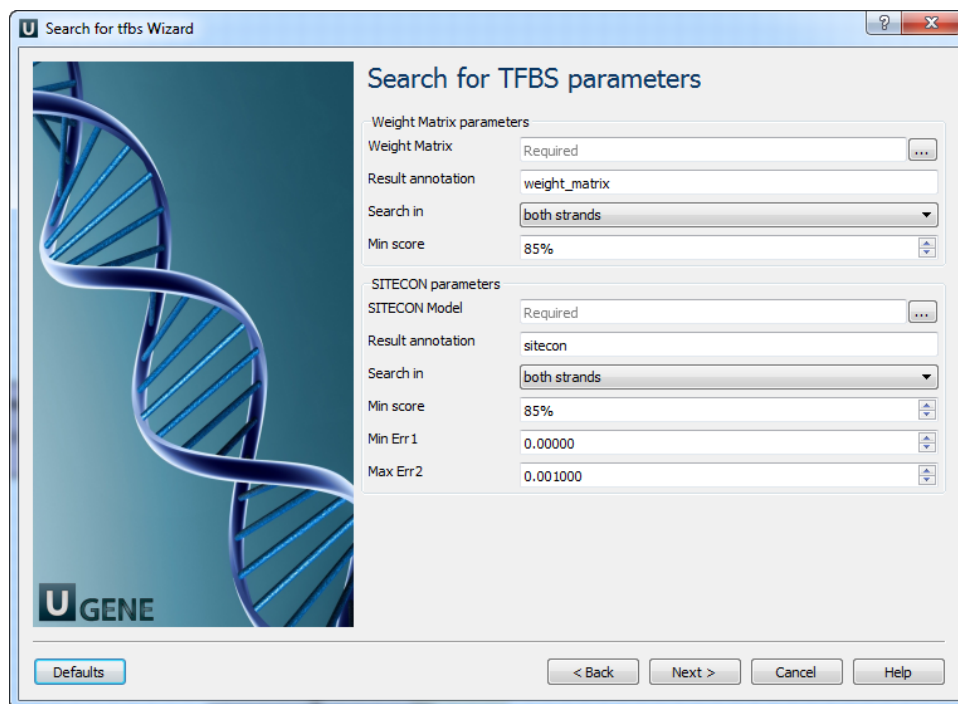
## Workflow Wizard

The wizard has 3 pages.

1. Input sequence(s): On this page you must input sequence(s).



2. Search for TFBS parameters: On this page you can modify search for TFBS parameters.

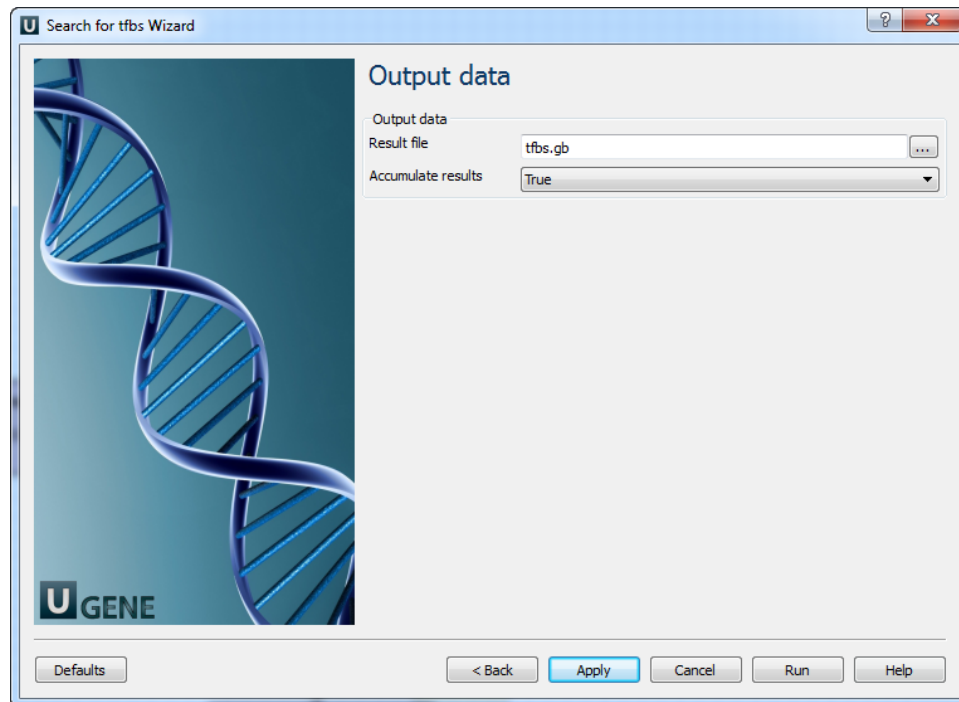


The following parameters are available:

Weight Matrix	Semicolon-separated list of paths to the input files.
Result annotation	Annotation name for marking found regions.
Search in	Which strands should be searched: direct, complement or both.
Min score	Minimum score to detect transcription factor binding site
SITECON model	Semicolon-separated list of paths to the input files.

Result annotation	Annotation name for marking found regions.
Search in	Which strands should be searched: direct, complement or both.
Min score	Minimum score to detect transcription factor binding site
Min err1	Alternative setting for filtering results, minimal value of Error type I. Note that all thresholds (by score, by err1 and by err2) are applied when filtering results.
Max err2	Alternative setting for filtering results, max value of Error type II. Note that all thresholds (by score, by err1 and by err2) are applied when filtering results.

3. **Output data:** On this page you can modify output parameters.



The following parameters are available:

Result file	Location of output data file. If this attribute is set, slot "Location" in port will not be used.
Accumulate results	Accumulate all incoming data in one file or create separate files for each input. In the latter case, an incremental numerical suffix is added to the file name.