

# SITECON

*SITECON* — is a program package for recognition of potential transcription factor binding sites basing on the data about conservative conformational and physicochemical properties revealed on the basis of the binding sites sets analysis.

To cite SITECON use the following article:

“Oshchepkov D.Y., Vityaev E.E., Grigorovich D.A., Ignatieva E.V., Khlebodarova T.M. SITECON: a tool for detecting conservative conformational and physicochemical properties in transcription factor binding site alignments and for siterecognition. //Nucleic Acids Res. 2004 Jul 1;32(Web Server issue): W208-12.”

UGENE version of SITECON provides a tool for recognition of potential binding sites for over [90 types](#) of transcription factors. Also UGENE version of SITECON provides a tool for recognition of potential binding sites basing site alignment proposed by user. For the detailed method description see the [original SITECON site](#).

Data about used context-dependent conformational and physicochemical properties are available in the [PROPERTY Database](#).

- [SITECON Searching Transcription Factors Binding Sites](#)
- [Types of SITECON Models](#)
  - [Eukaryotic](#)
  - [Prokaryotic](#)
- [Building SITECON Model](#)