

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.

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“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