

# [Sr and protein binding sites in dna.](https://assignbuster.com/sr-and-protein-binding-sites-in-dna/)

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Sr no. Tool Description References 1. CLUSTAL Omega Multiple sequence alignment of biological sequences using algorithms. 2 2.

MEGA Reconstruct or rebuild evolutionary relatedness among organisms. 3 3. MEME To find motifs in biomolecules, domains in proteins and protein binding sites in DNA. 4 4. JALVIEW To edit, analyze and visualize the multiple sequence alignment in biological sequences, predict secondary structures in protein molecules. 5 5.

MUSCLE Alignment of protein sequences by multiple sequence alignment, phylogenetic analysis and predict protein structures. 6 6. Taverna Comforts bioinformaticians who are not skillful in web services and programming by providing interface between different tools and databases. 7 7. GENSCAN Find whole genome structures of human, predict exons, introns, transcriptional, translational signals and intergenic regions, find gene or multiple genes in DNA. 8   It is such a tool used to find and search whole structurespresent in genomic DNA of humans. GENSCAN used to predict exons, introns, transcriptional, translational signals and intergenic regions in the DNA.

Geneor multiple genes present in DNA can also be predicted by using this tool. Thistool proved to be accurate as it predicted 75 to 80 % exons precisely. (Chris Burge, Samuel Karlin, 1997) 8. 7.    GENSCANTaverna has number of uses in constructing and performinga sequence of activities that comforts bioinformaticians who are not skillfulin web services and programming languages. It provides interface betweenbioinformaticians and web services that helps to communicate between differenttools and databases for sequence analyses.

Taverna has many services and one ofthem provided by INSDC (http://www. insdc. org/ ). (Duncan Hull et. al, 2006) 7. 6.    TavernaIt is a protein sequence alignment tool used to buildalignments of protein sequences by multiple sequence alignment with greataccuracy.

It is reported to be the fastest sequence alignment tool comparedwith other alignment tools e. g., T-Coffee, CLUSTALW etc. It has wide range ofuses including phylogenetic analysis, to predict protein structure etc. Themost important thing of this tool is to show the evolution of sequences bygraphs. (Robert C. Edgar, 2004) 6. 5.

MUSCLEIt a tool used to edit, analyze and visualize themultiple sequence alignment of biological sequences and refine the sequences. Itis used to align the sequences and predict the secondary structures of theprotein molecules. It shows the alignment results by showing figures andconstruct phylogenetic trees of sequences. JALVIEW 1. 0 is not able to analyzethe huge and detailed tasks, so JALVIEW 2 is constructed by bioinformaticiansto perform greater tasks. (Andrew M. Waterhouse et.

al, 2009) 5. 4.    JALVIEWIt is a bioinformatics tool used to find out motifs inbiological sequences of biomolecules e. g., proteins and DNA. It is also used todiscover domains in proteins and protein binding sites in DNA. It can also beused to find out repeated sequences in proteins and DNA when query sequencesare submitted into it.

(Timothy L. Bailey et. al, 2006) 4. 3.

MEME (Multiple EM For Motif Elicitation)Itis a bioinformatics tool used to reconstruct or rebuild evolutionaryrelatedness among the species or organisms. MEGA’s important feature is the useof graphical user interface (GUI), that shows the graphical representation ofthe given data, phylogenetic trees and results. (Sudhir Kumar et. al, 2012) 3. 2.

MEGA(Molecular Evolutionary Genetics Analysis)CLUSTAL Omega is a latest version of theCLUSTAL programs for multiple sequence alignment of biological sequences. Ituses algorithms for construction of guide trees. The software has proved to bebetter than earlier CLUSTAL series and it has great precision. The larger alignmentscan be done using this tool even on home computers.

(SieversF., Higgins D. G., 2014) 2. 1.    CLUSTALOmegaBioinformatics tools for biologicalsequence analysesThesequences are the information stored in DNA and proteins in the form of letters. These letters are instructions and have specific arrangements given by thenature to our DNA and from DNA to proteins. The nucleotides in DNA areinstructions that pass from generation to generation.

The proteins aremacromolecules made of amino acid sequences and perform many functions of thebody. The sequences came into existence due to molecular attractions ofdifferent molecules. Sequence analysesis the comprehension of novel arrangement and characteristics of codes in abiomolecule like nucleic acid and protein, that are responsible for theiroperation and function. (Mehmood MAet. al, 2014) 1.

For carrying out sequence analyses, the sequences after retrieval from differentdatabases are refined and submitted to various tools that speculate theirfeatures important for their function, structure and evolutionary history withextreme precision. (Mehmood MA et. al, 2014) 1. The objective of this review is to encompass all the tools beingused for biological sequence analyses. Introduction