

BlockLogo: visualization of peptide and sequence motif conservation

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Abstract

BlockLogo is a web-server application for the visualization of protein and nucleotide fragments, continuous protein sequence motifs, and discontinuous sequence motifs using calculation of block entropy from multiple sequence alignments. The user input consists of a multiple sequence alignment, selection of motif positions, type of sequence, and output format definition. The output has BlockLogo along with the sequence logo, and a table of motif frequencies. We deployed BlockLogo as an online application and have demonstrated its utility through examples that show visualization of T-cell epitopes and B-cell epitopes (both continuous and discontinuous). Our additional example shows a visualization and analysis of structural motifs that determine the specificity of peptide binding to HLA-DR molecules. The BlockLogo server also employs selected experimentally validated prediction algorithms to enable on-the-fly prediction of MHC binding affinity to 15 common HLA class I and class II alleles as well as visual analysis of discontinuous epitopes from multiple sequence alignments. It enables the visualization and analysis of structural and functional motifs that are usually described as regular expressions. It provides a compact view of discontinuous motifs composed of distant positions within biological sequences. BlockLogo is available at: <http://research4.dfci.harvard.edu/cvc/blocklogo/> and <http://met-hilab.bu.edu/blocklogo/>.

Original language English

Pages (from-to) 37-44

Number of pages 8

Journal [Journal of Immunological Methods](#)

Volume 400-401

State Published - Dec 31 2013

Olsen, L. R., Kudahl, U. J., Simon, C., Sun, J., Schönbach, C., Reinherz, E. L., ... Brusic, V. (2013). BlockLogo: visualization of peptide and sequence motif conservation. *Journal of Immunological Methods*, 400-401, 37-44. DOI: [10.1016/j.jim.2013.08.014](https://doi.org/10.1016/j.jim.2013.08.014)