BlueStar STING - A multiplatform environment for protein structure analysis

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Abstract

BlueStar STING is the latest version of the STING suite of programs and corresponding database. STING is a web based suite of programs for visualization and comprehensive analysis of macromolecular structures. STING continues to build on what is considered its major asset: a principal DB of per-residue-reported descriptors (available for display both numerically and graphically) for either the public PDB (1) or local files. Since its first appearance in 1998, STING has undergone eight major updates (2, 3, 4, 5, 6) with ever increasing integration of data describing the protein sequence, structure, function and stability. New features were embedded in the BlueStar version of STING Suite and important aspects of this package acquired some new characteristics, adding key advantages to the whole suite: 1) Availability for most popular platforms and browsers, 2) Introduction of the STING_DB quality assessment, 3) Improvement in algorithms for calculation of three STING parameters, 4) Introduction of ten new STING modules, and 5) Expansion of the existing modules. Special emphasis will be given to amino acid co-evolution module and modules related to calculation and presentation of the protein-ligand, protein-DNA and protein-protein contacts. In addition, another interesting feature in BlueStar version of STING is the presentation of the ensemble of related parameters for a single structure and the presentation of a single parameter for number of structures.

The BlueStar STING is freely accessible at:

http://sms.cbi.cnptia.embrapa.br/SMS/ and http://trantor.bioc.columbia.edu/SMS.

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