

## Poster I-22

### BlueStar STING - A multiplatform environment for protein structure analysis



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**Short Abstract:** BlueStar STING is the latest version of the STING suite of programs and corresponding database. 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 or local files.

#### Long Abstract:

BlueStar STING is the latest version of the STING suite of programs and corresponding database. 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 or local files. Since its first appearance in 1998, STING has undergone eight major updates with ever increasing integration of data describing the protein sequence, structure, function and stability. We present in this work some of the new features available in BlueStar STING Suite and the five important aspects of this package that acquired some new characteristics, designed to add 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, we concentrate on a most interesting feature in BlueStar version of STING – 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>.

The applications cover:

- advanced STING features
- Applications: identification of active sites and folding essential residues by STING
- Sting key components: JavaProtein Dossier and STING Report
- Local file submission to STING server: generating 310 different structure/function parameters

- 3D and 2D related parameter plots for multiple structures