

# Visualization tool for comparison of amino acids in protein simulations

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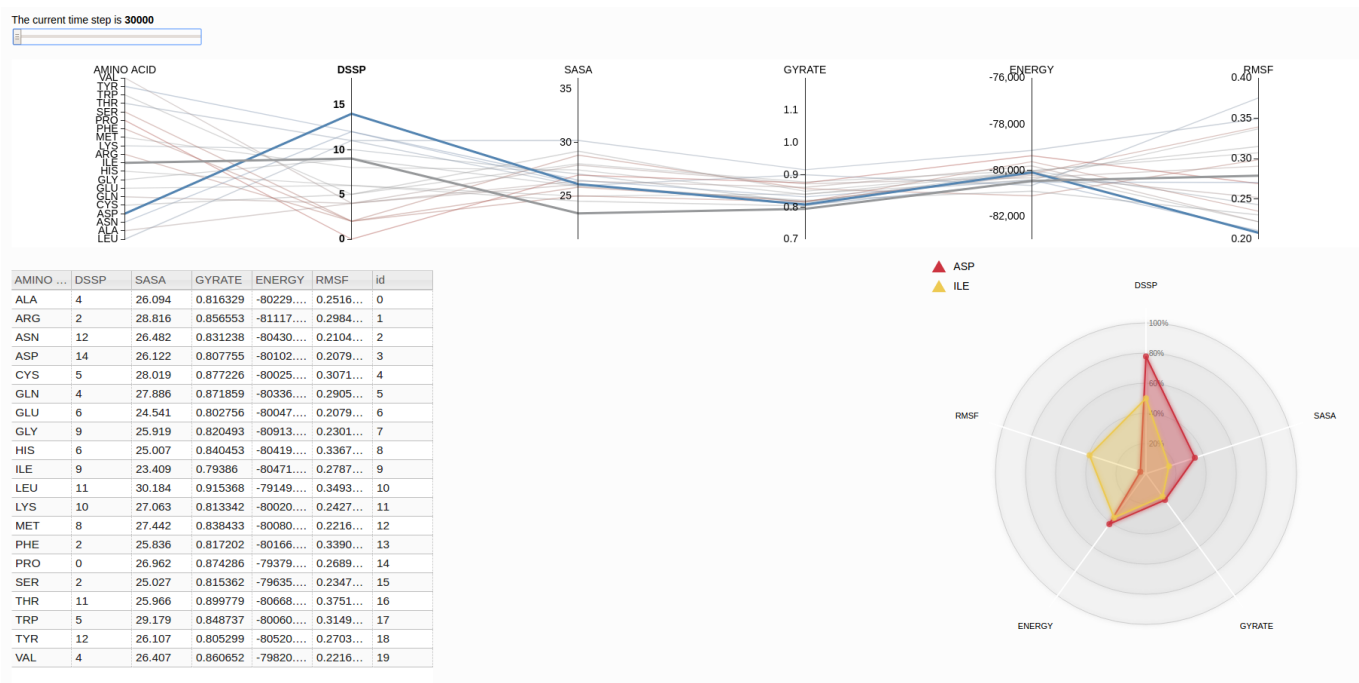


Fig. 1. Image of the tool with all elements presented.

## Abstract—

**Keywords**—one or two words; separated by semicolon; from specific; to generic fields;

**GYRATE:**  
**ENERGY:**  
**RMSF:**

## I. INTRODUCTION

### A. Related work

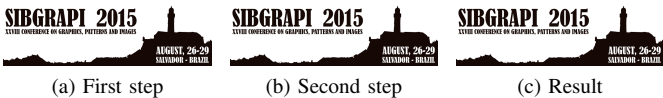


Fig. 2. Technique overview

## II. DATA CHARACTERIZATION

### A. Data dimensions

**DSSP:**  
**SASA:**

## III. TECHNICAL BACKGROUND

In this section, we detail this classical technique. The reader can find a more complete exposition in the work of Paul [?].

## IV. TECHNIQUE OVERVIEW

In order to produce this application, we start with this processing, followed by this technique. In order to cope with this challenge, we introduce this formulation to produce this intermediate result. The formulation leads to this type of system, which is efficiently solved by adapting this technique. The final result is produced by this transform. The whole process is schematized in Fig. 2.

### A. Grid

*Item highlighting:*

*Item selection:*

*B. Parallel Coordinates*

*Axis brushing:*

*Axis sorting:*

*Axis reordering:*

*Recoloring by axis selection:*

*C. Radar Plot*

*Item highlighting:*

*D. Slider*

V. EXPERIMENTS

VI. RESULTS AND DISCUSSION

*A. Future work*

VII. CONCLUSION

ACKNOWLEDGMENT

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REFERENCES