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## New Features on SpringerLink Platform

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#### Within this Article:

- » Introduction
- » Patients and methods
- » Results
- » Discussion
- » References

## Results

### **Patient characteristics**

Between 11/04/2003 and 12/13/2004, sevent seen in this initial cohort. Table <u>1</u> summarizes

Table 1 Baseline demographics and clinical char

#### **Baseline characteristics**

Patients evaluable/enrolled

Gender: Female %

## Improved HTML

European Biophysics Journal with Biophysics Letters © The Author(s) 2012 10.1007/s00249-012-0820-x

Review

#### Validation of macro

#### Michal Hammel<sup>1</sup> 🖂

(1) Lawrence Berkeley National Laboratory,

#### Michal Hammel Email: <u>mhammel@lbl.gov</u>

Received: 4 March 2012 Revised: 22 April

#### Abstract

The dynamics of macromolecular conforma nuclear magnetic resonance (NMR), strive dynamic molecular machines. This review a combine solution-scattering data with highmethods used to calculate theoretical SAX minimal ensemble search (MES), enhance computational techniques used for conform detail, the knowledge gained from ensembl X-ray crystallography, NMR, and comput

Keywords Small-angle X-ray scattering (

Special Issue: Scattering techniques in biol-

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European Biophysics Journal with Biophysics Letters © The Author(s) 2012 10.1007/s00249-012-0820-x

#### Review

#### Validation of macromolecular flexib solution by small-angle X-ray scatte (SAXS)

Michal Hammel<sup>1</sup>

(1) Lawrence Berkeley National Laboratory, Physical Biosciences Division, Berkeley,

Michal Hammel Email: mhammel@lbl.gov

> Received: 4 March 2012 Revised: 22 April 2012 Accepted: 5 May 2012 Published online: 26 May 2012

#### Abstract

The dynamics of macromolecular conformations are critical to the action of cellular scattering studies, in combination with macromolecular X-ray crystallography (MX) resonance (MMR), strive to determine complete and accurate states of macromole insights describing allosteric mechanisms, supramolecular complexes, and dynam This review addresses theoretical and practical concepts, concerns, and considera techniques in conjunction with computational methods to productively combine sol high-resolution structures. I discuss the principal means of direct identification of n from SAXS data followed by critical concerns about the methods used to calculate from high-resolution structures. The SAXS profile is a direct interrogation of the the and techniques such as, for example, minimal ensemble search (MES), enhance i experiments by describing the SAXS profiles as population-weighted thermodynam recent developments in computational techniques used for conformational asampline techniques provide a basis for assessing the level of the flexibility within a sample. approaches sacrifice atomic detail, the knowledge gained from ensemble analysis developing hypotheses and quiding biochemical experiments. Examples of the use

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- Search Results Display & Authorization Recognition
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- Most users find content through a simple search box
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		products (e.g. biofuel biochemicals etc	<ul> <li>via multiple conversion pat</li> </ul>	thways and technologies		

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