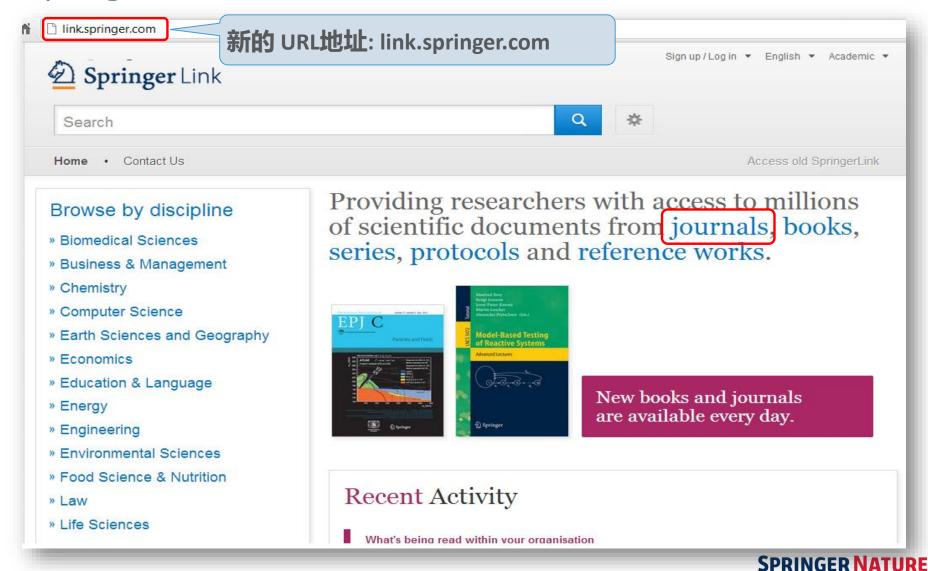
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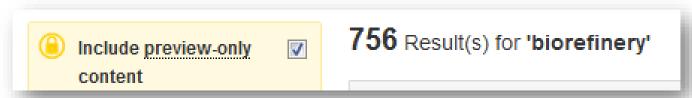
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- » Introduction
- » Patients and methods
- » Results
- » Discussion
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Results

Patient characteristics

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

Table 1 Baseline demographics and clinical char

Baseline characteristics

Patients evaluable/enrolled

Gender: Female %

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European Biophysics Journal with Biophysics Letters

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10.1007/s00249-012-0820-x

Review

Validation of macro

Michal Hammel^{1 ™}

(1) Lawrence Berkeley National Laboratory,

Michal Hammel Email: mhammel@lbl.gov

Received: 4 March 2012 Revised: 22 April

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

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Review

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

Michal Hammel 1 2

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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 (NMR), strive to determine complete and accurate states of macromole insights describing allosteric mechanisms, supramolecular complexes, and dynan 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 r 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 experiments by describing the SAXS profiles as population-weighted thermodynaming recent developments in computational techniques used for conformational sampling 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 guiding biochemical experiments. Examples of the use

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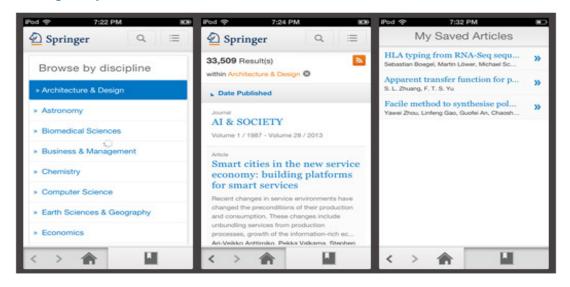
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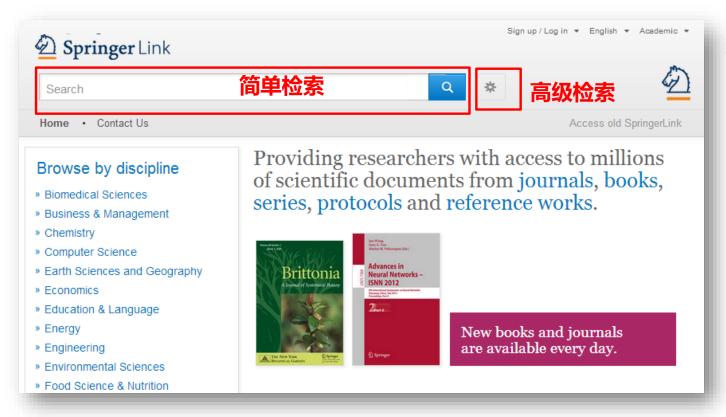
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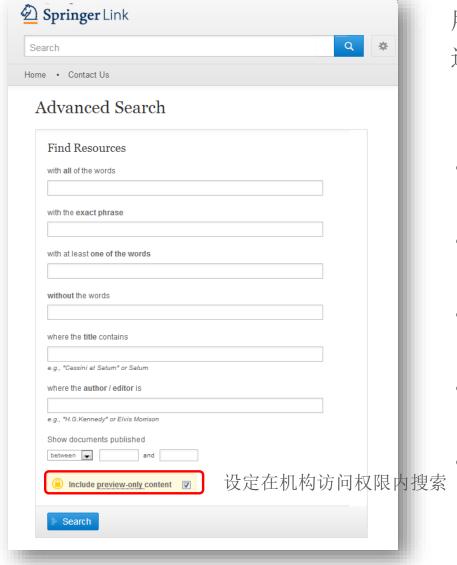
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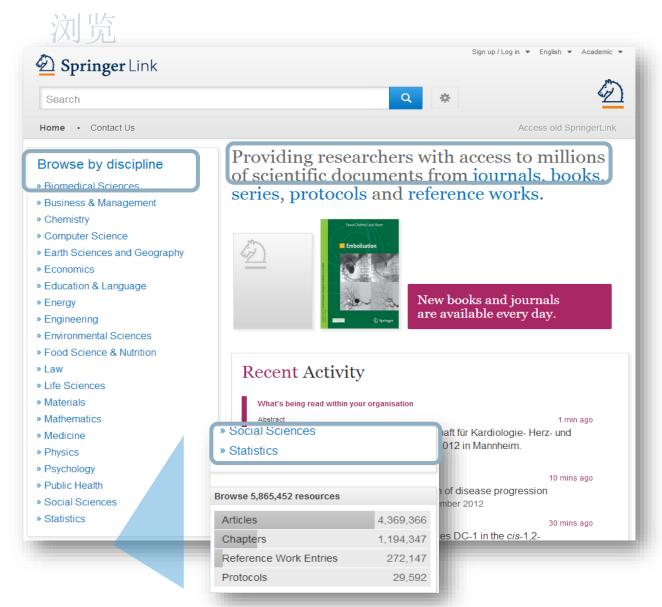
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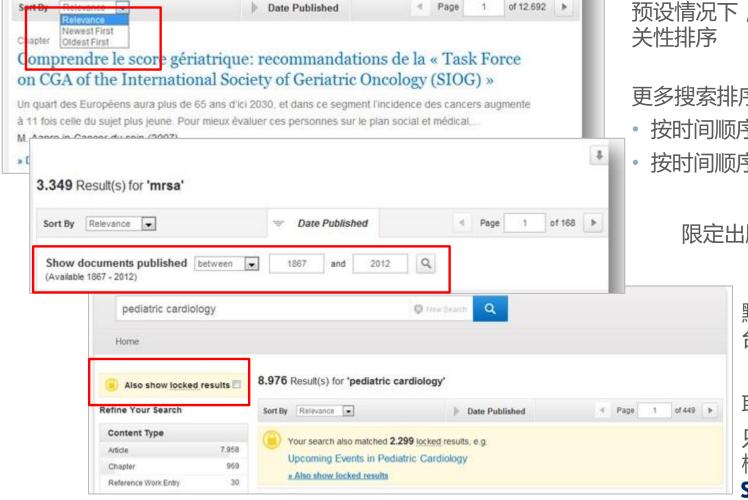
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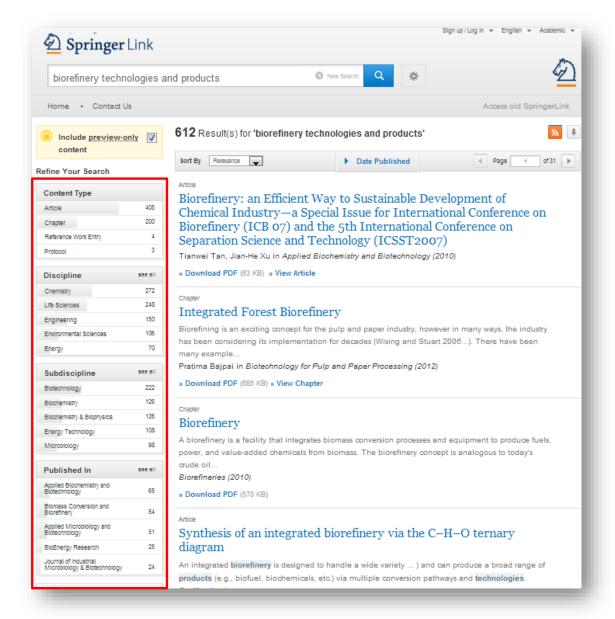
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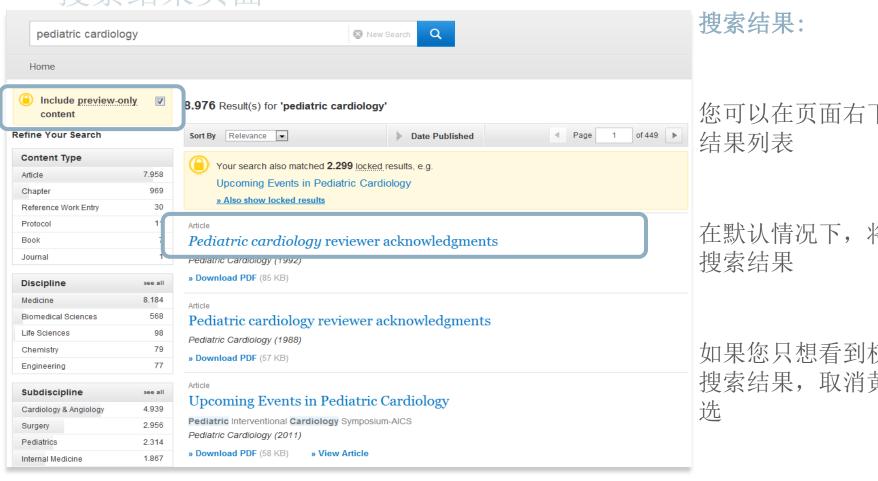
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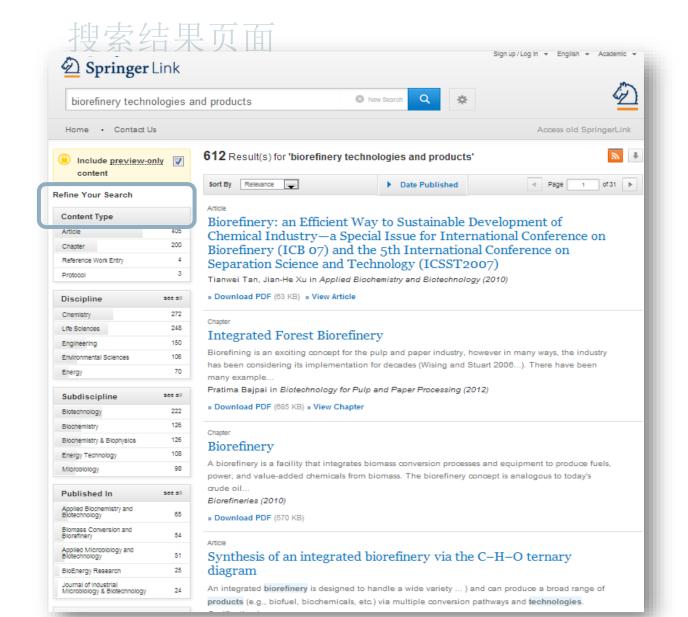
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