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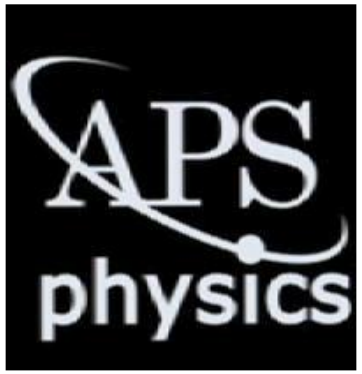

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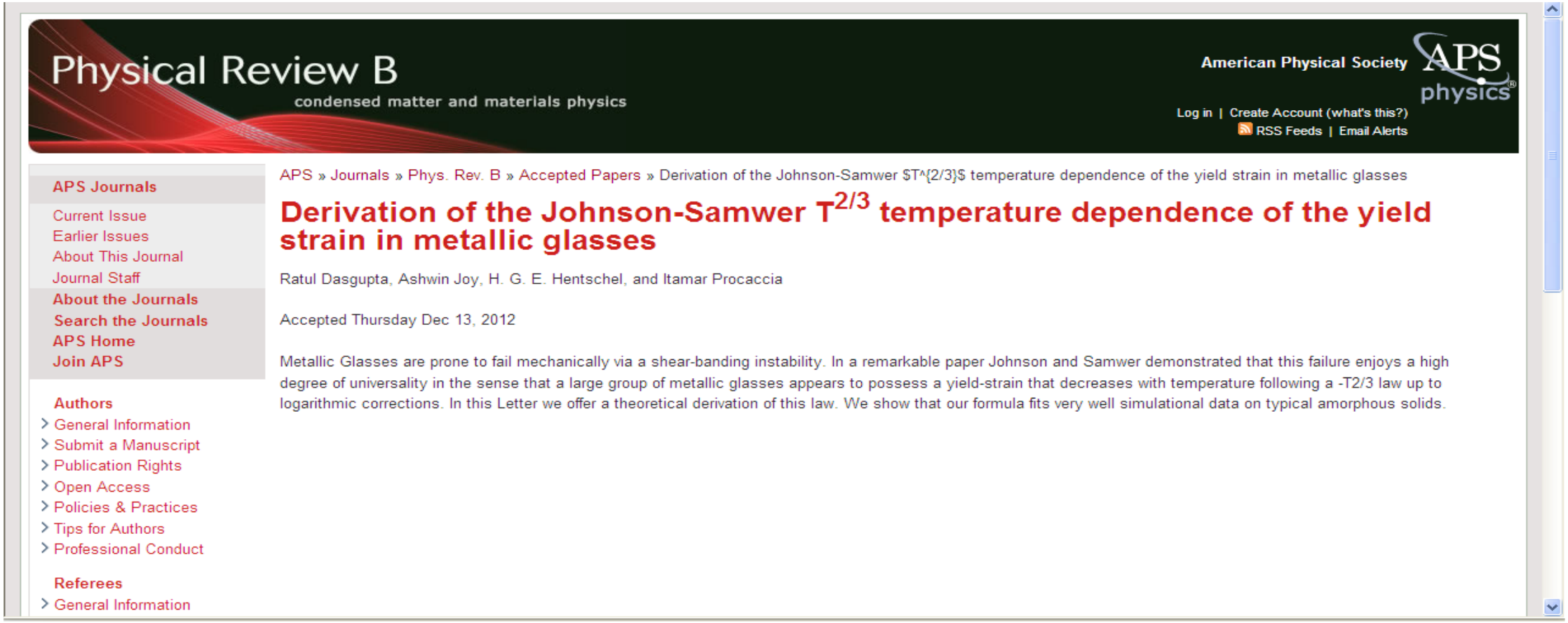

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Derivation of the Johnson-Samwer $T^{2/3}$ temperature dependence of the yield strain in metallic glasses

Ratul Dasgupta, Ashwin Joy, H. G. E. Hentschel, and Itamar Procaccia

Accepted Thursday Dec 13, 2012

Metallic Glasses are prone to fail mechanically via a shear-banding instability. In a remarkable paper Johnson and Samwer demonstrated that this failure enjoys a high degree of universality in the sense that a large group of metallic glasses appears to possess a yield-strain that decreases with temperature following a -T2/3 law up to logarithmic corrections. In this Letter we offer a theoretical derivation of this law. We show that our formula fits very well simulational data on typical amorphous solids.

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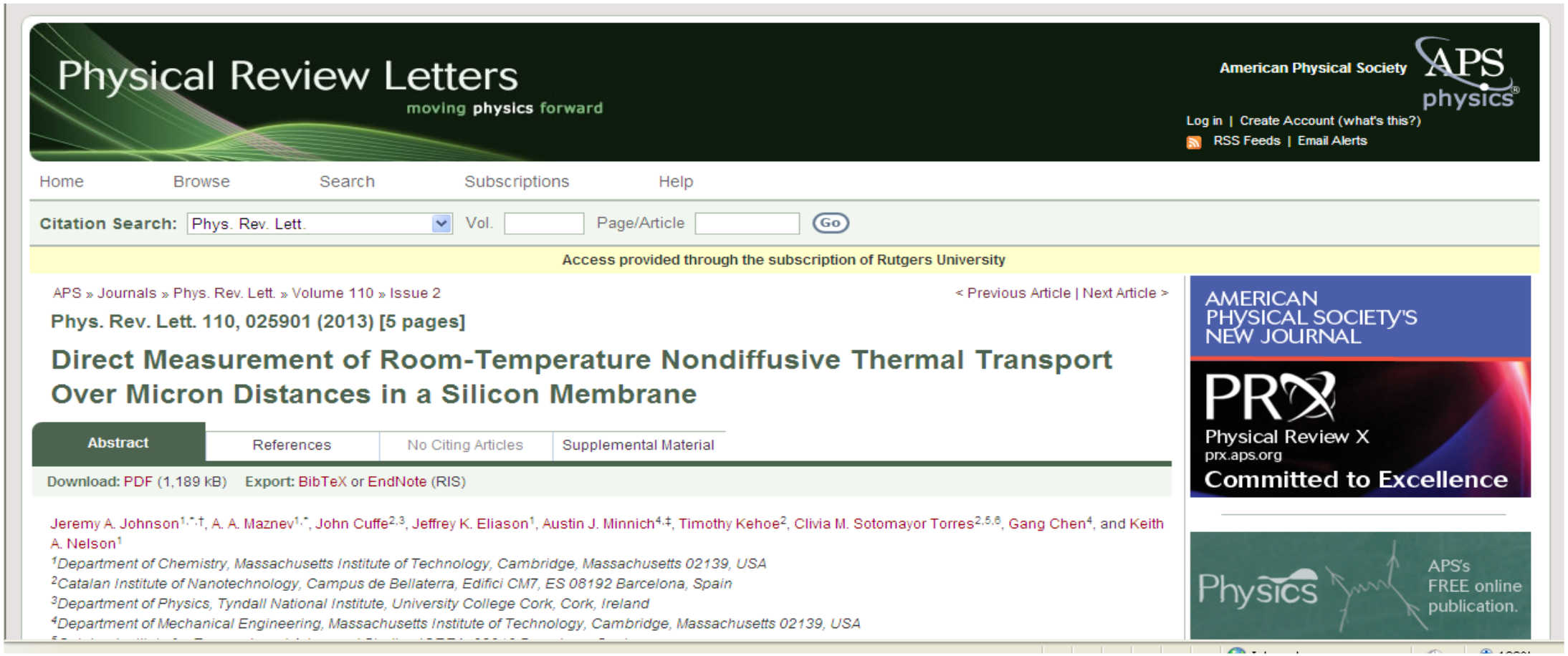

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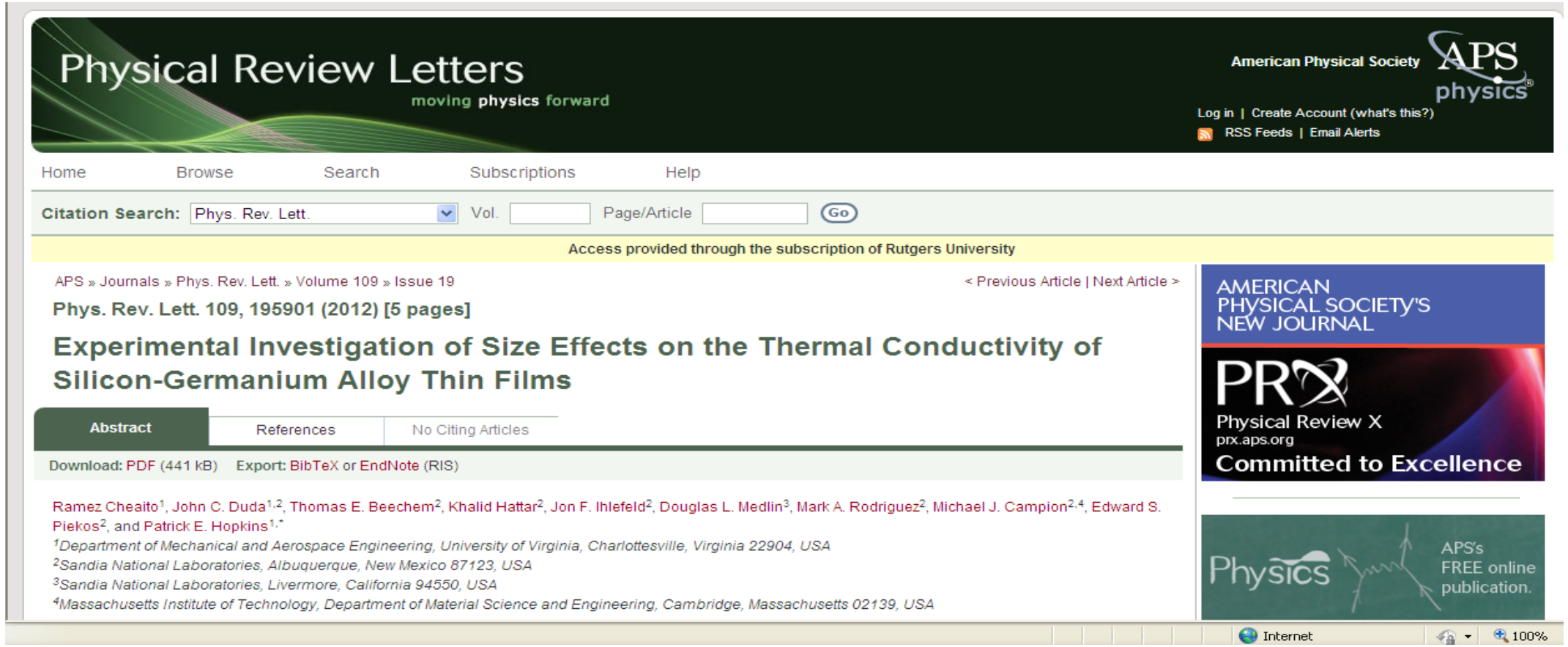

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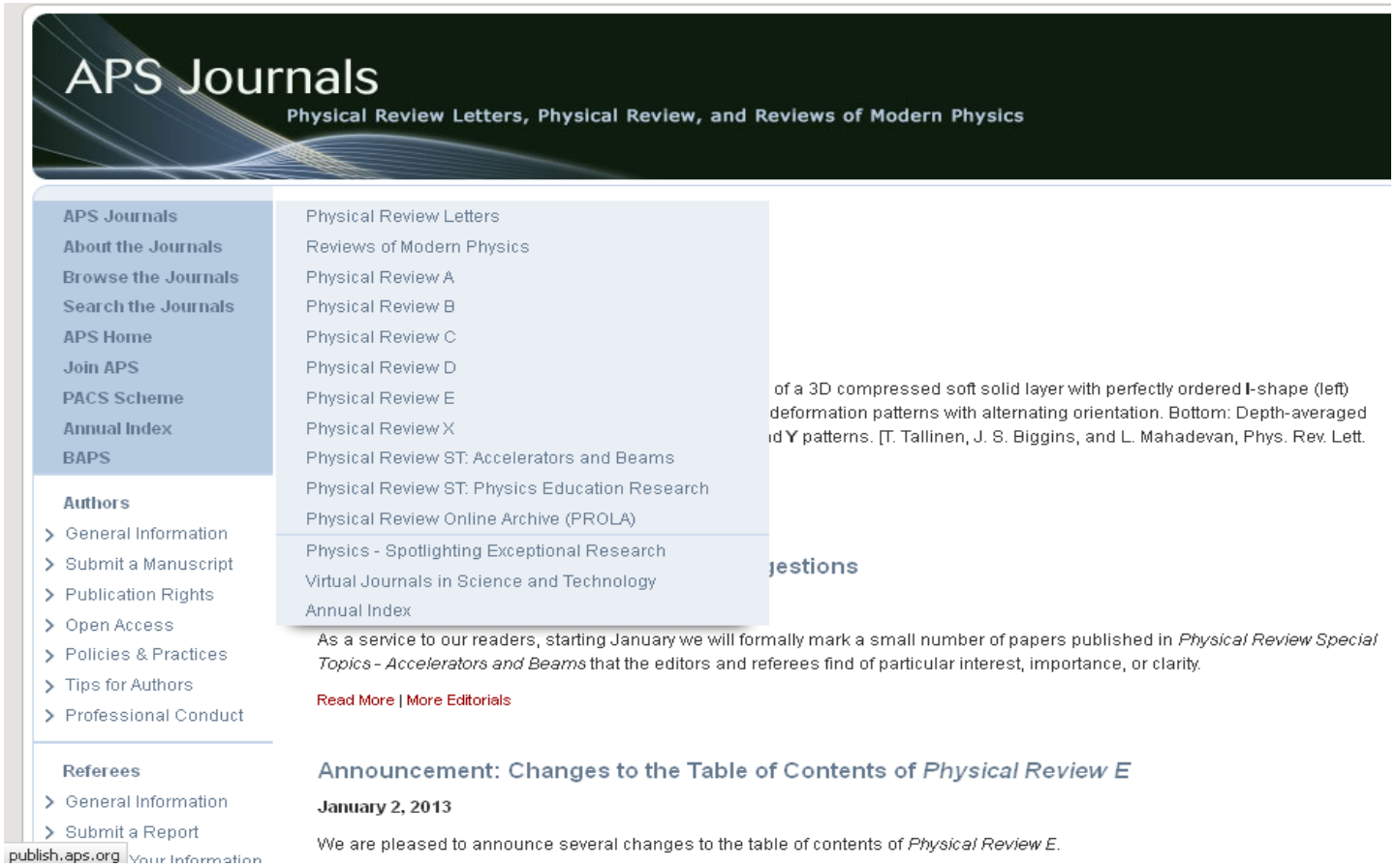

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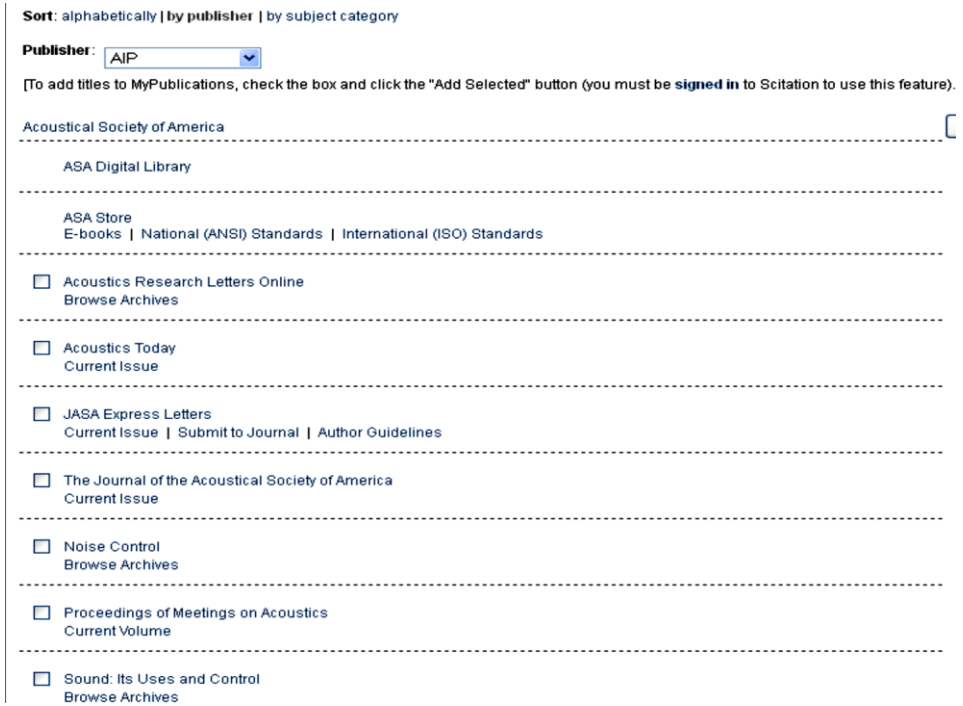

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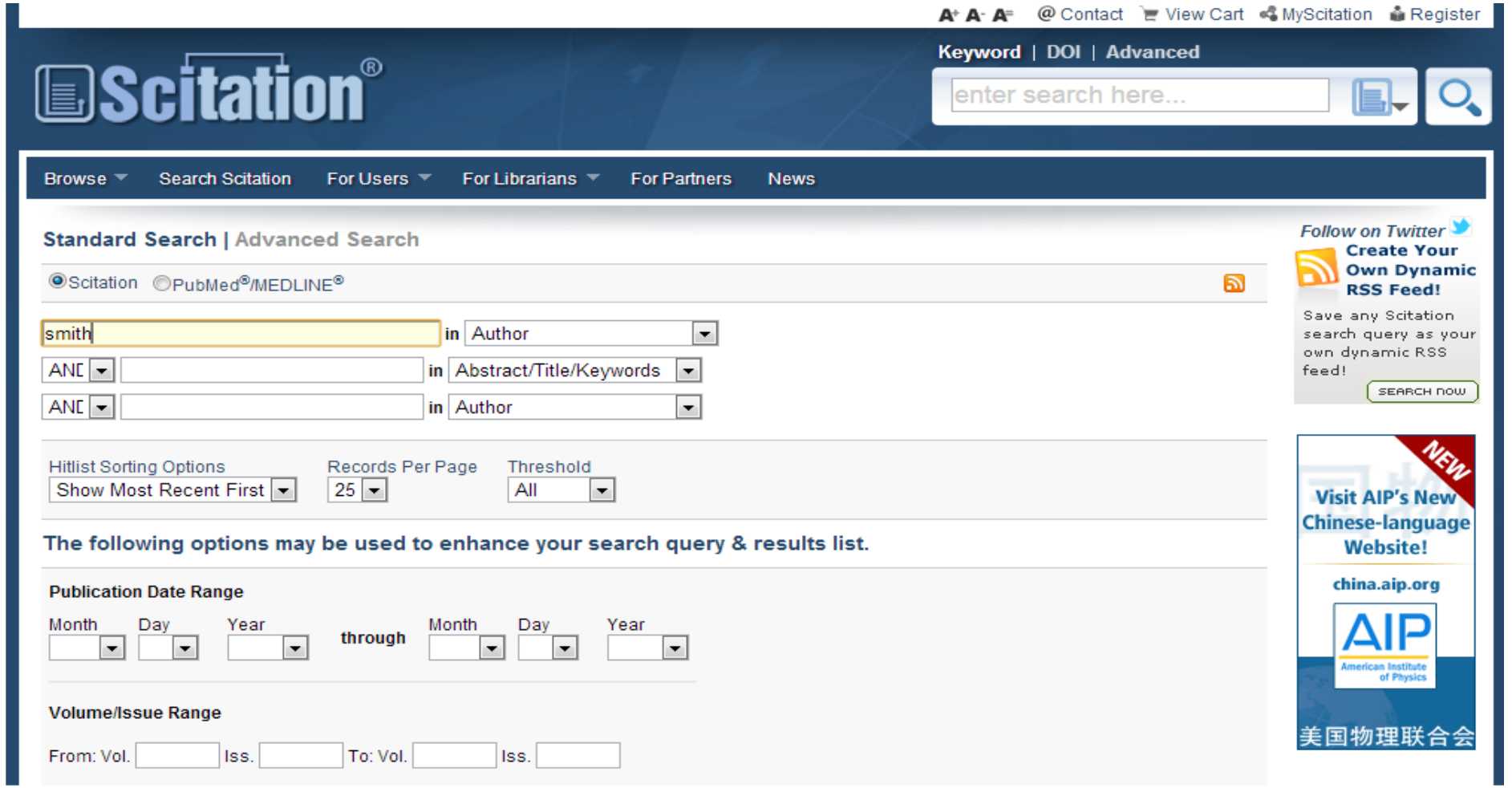

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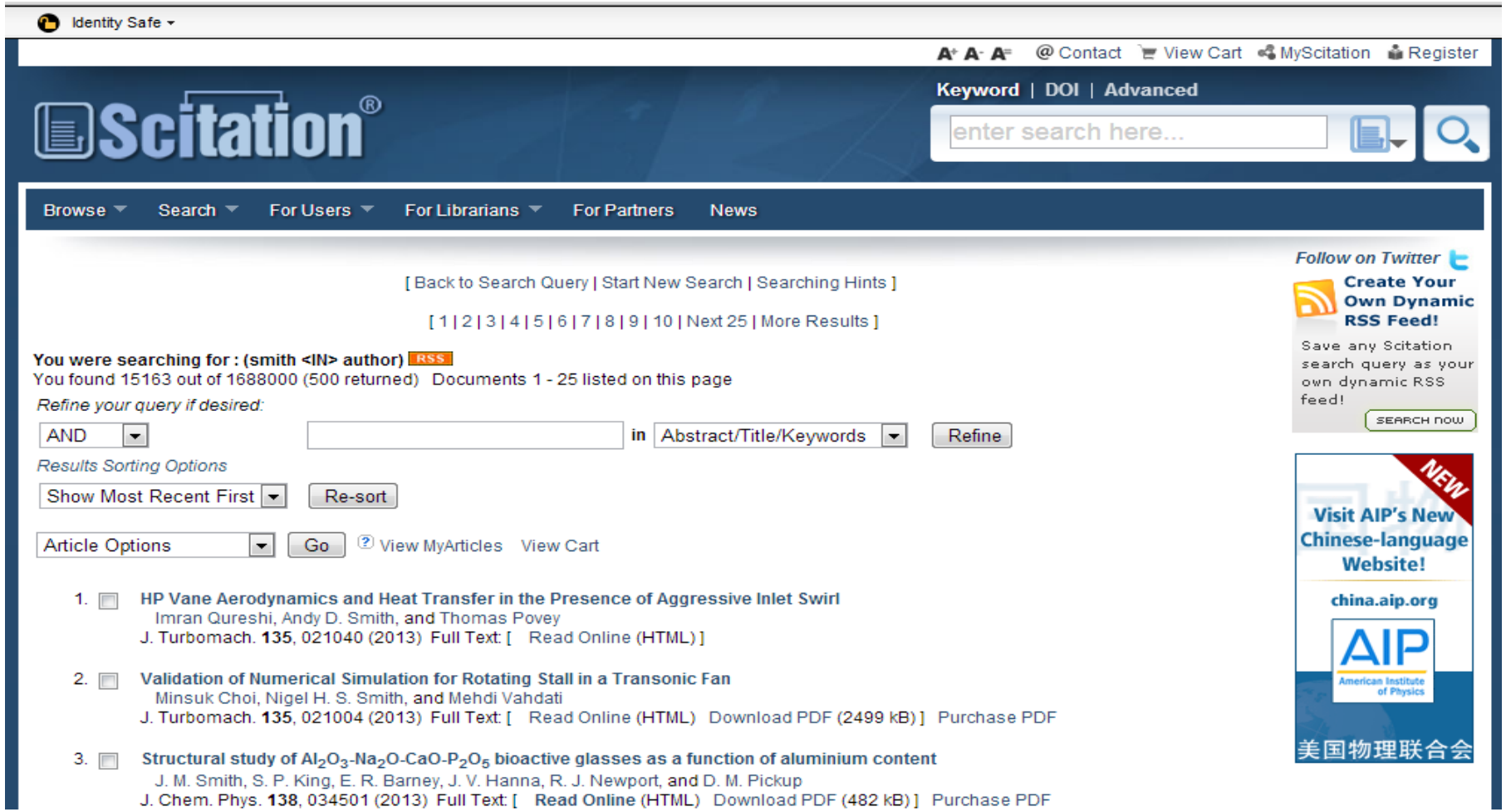

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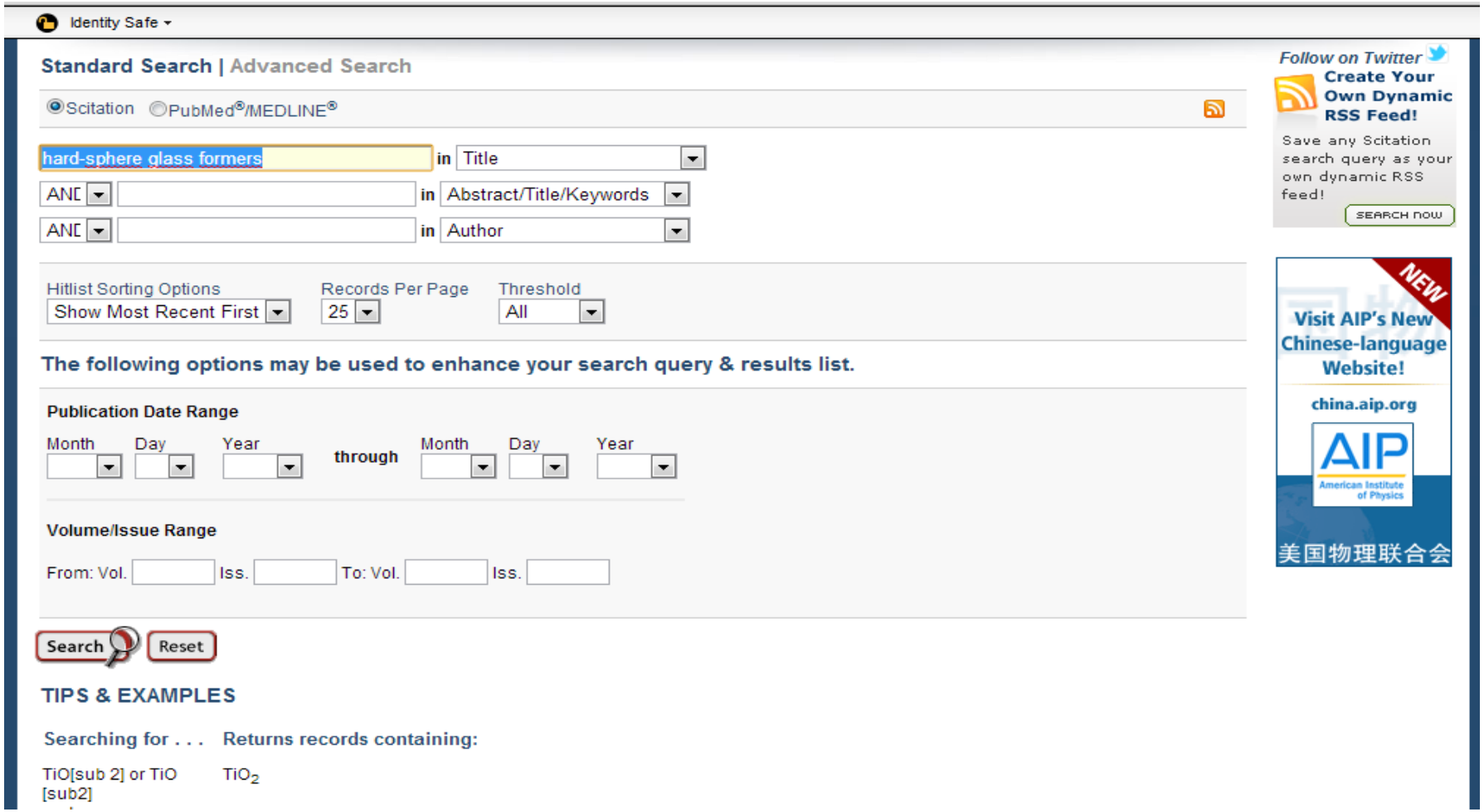

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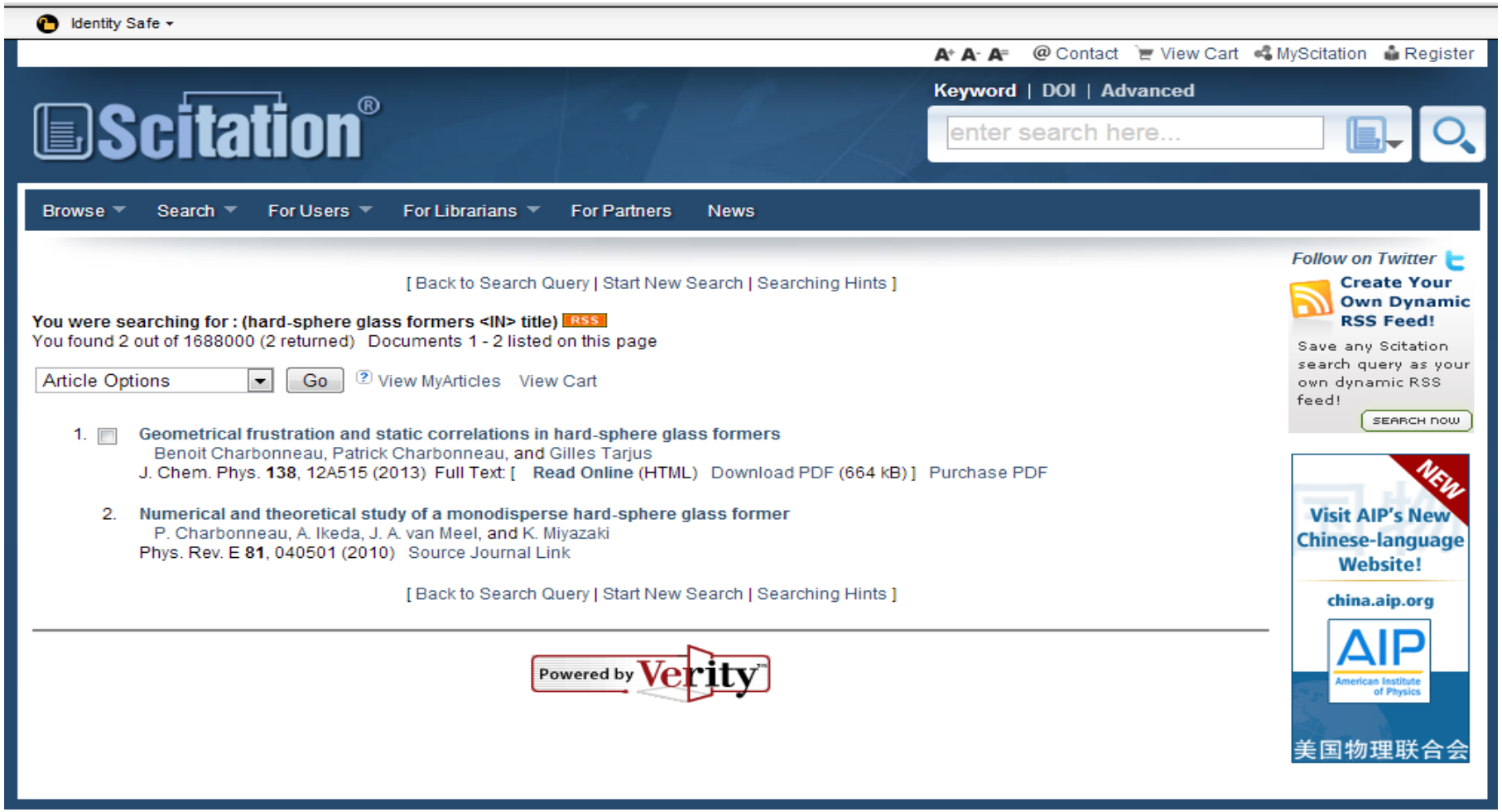

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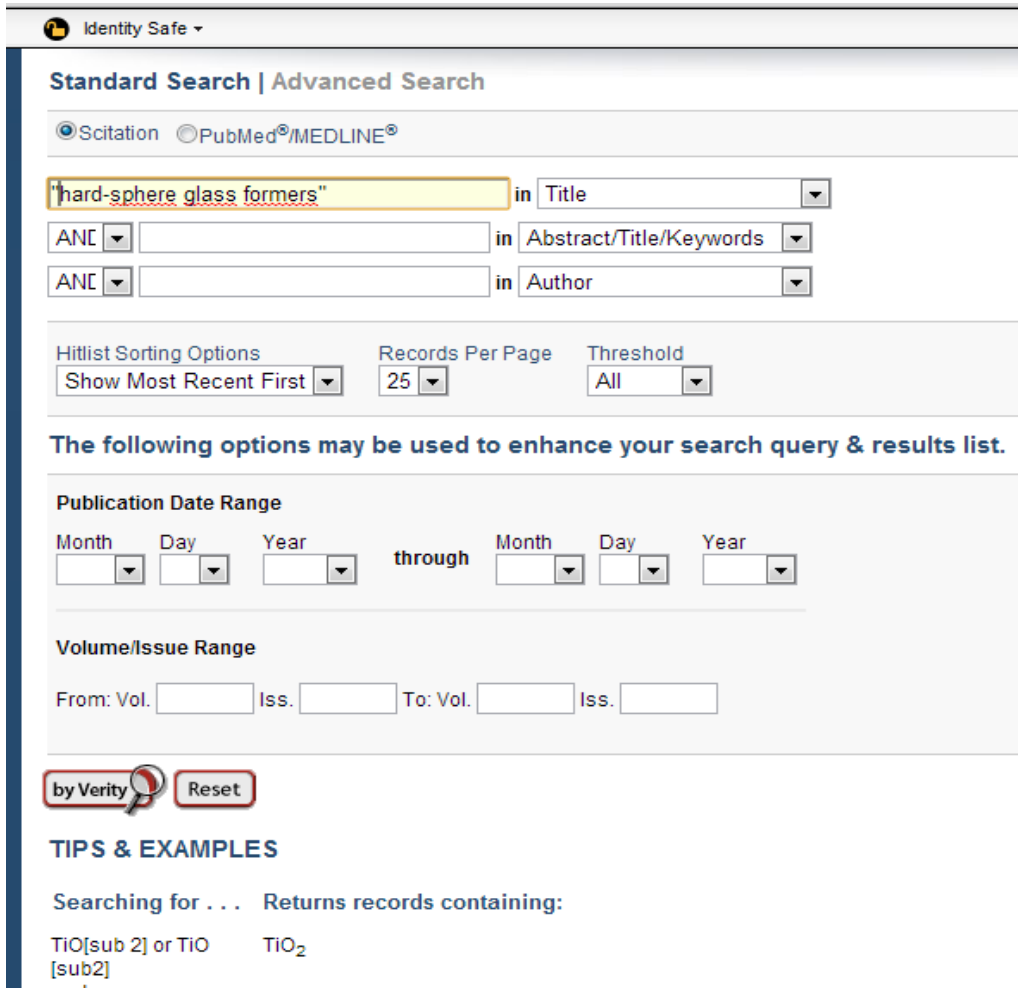

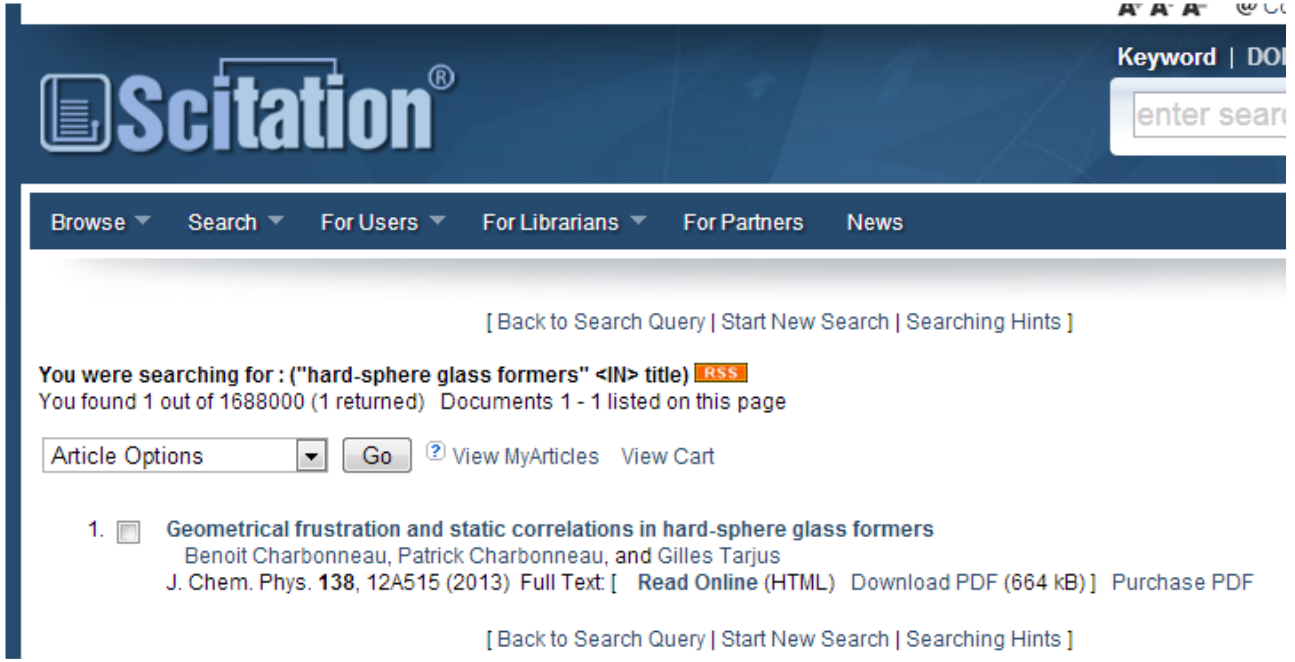

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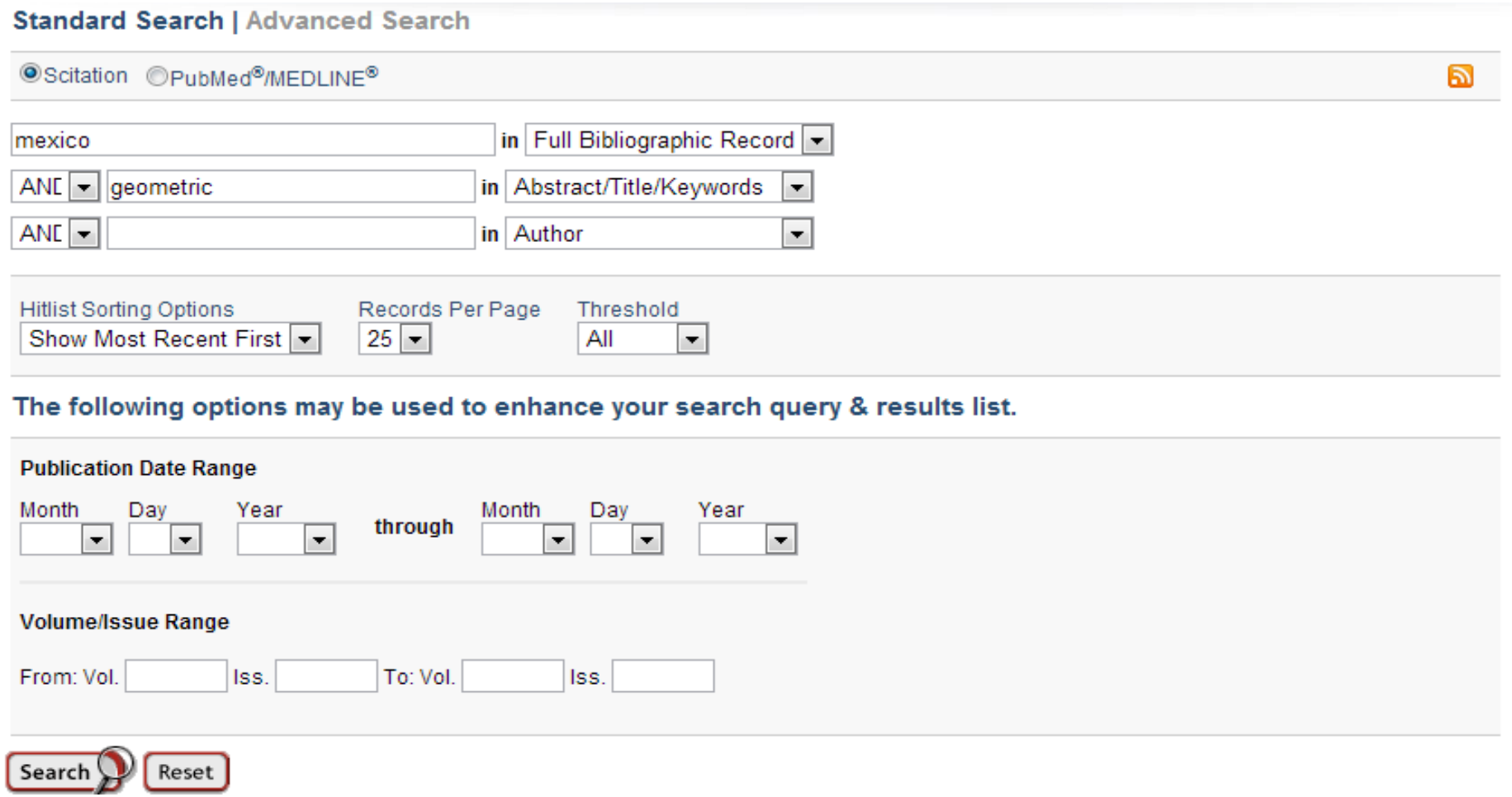

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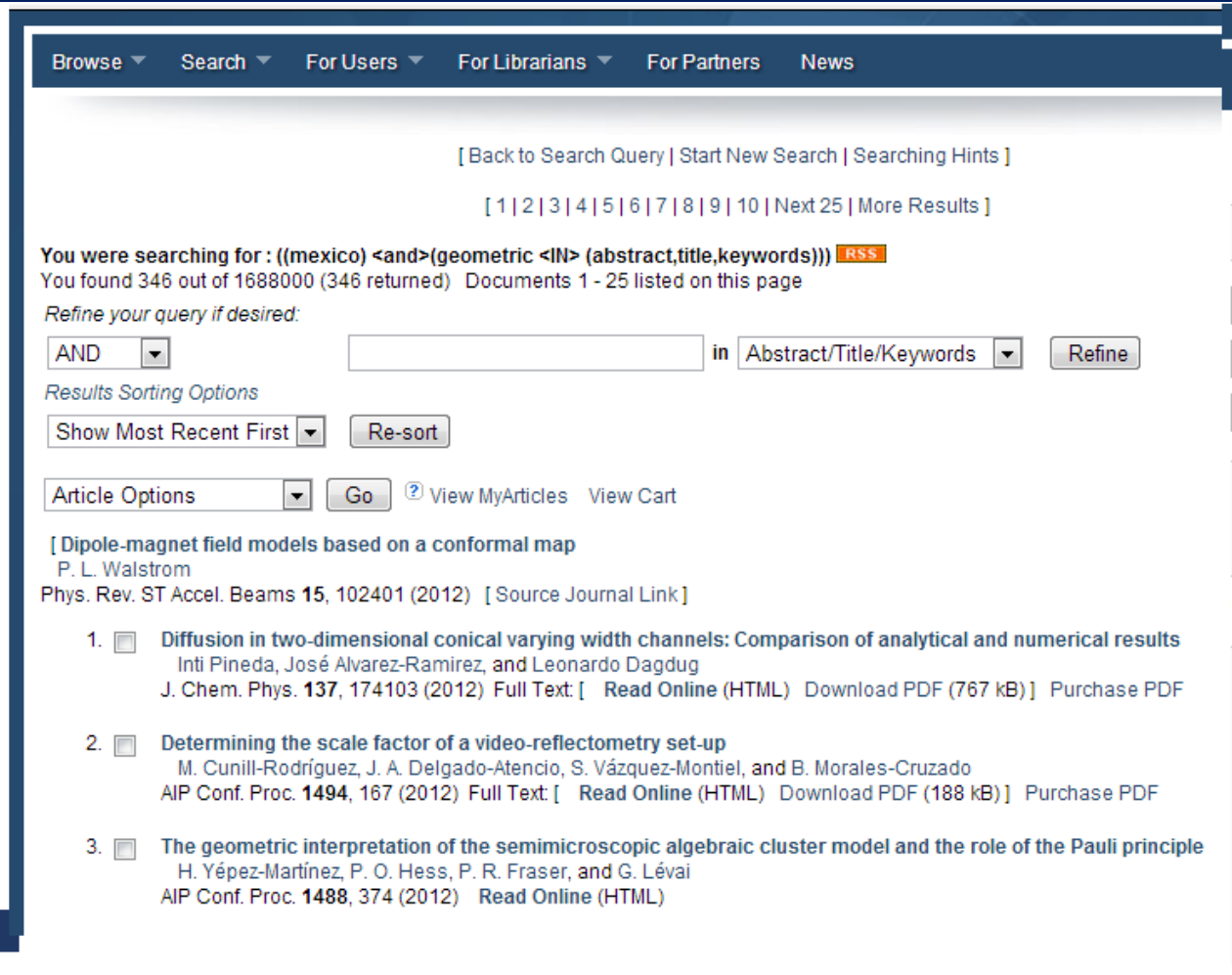

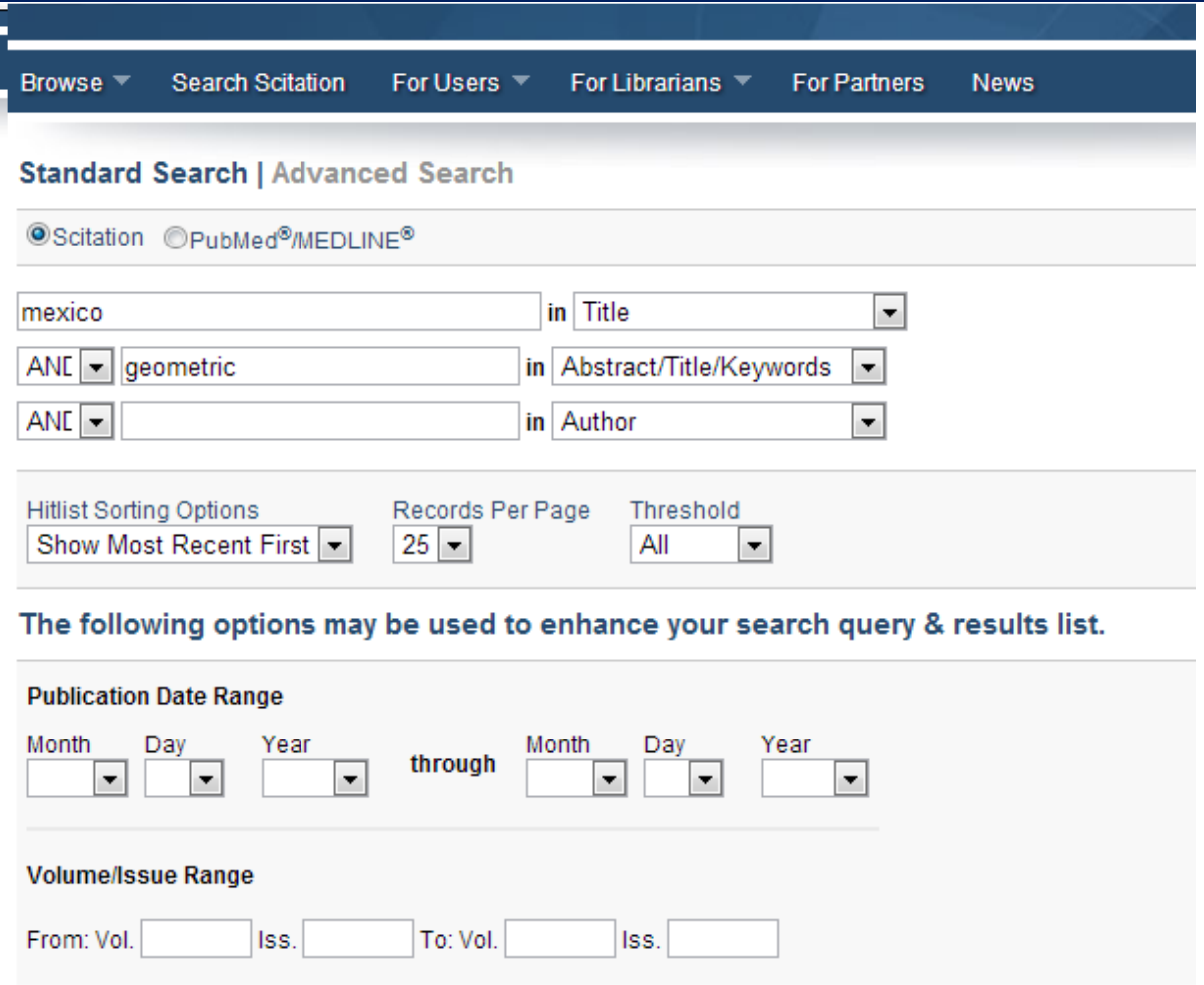

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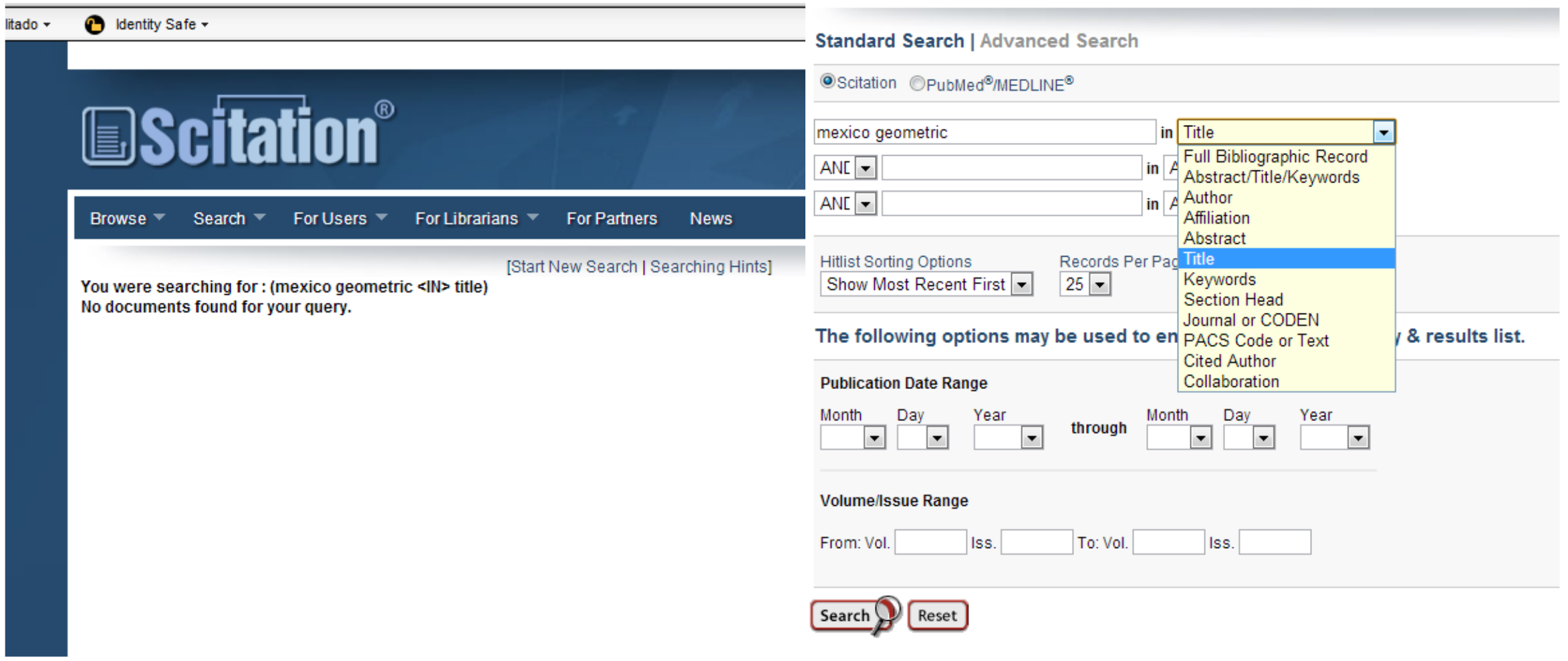

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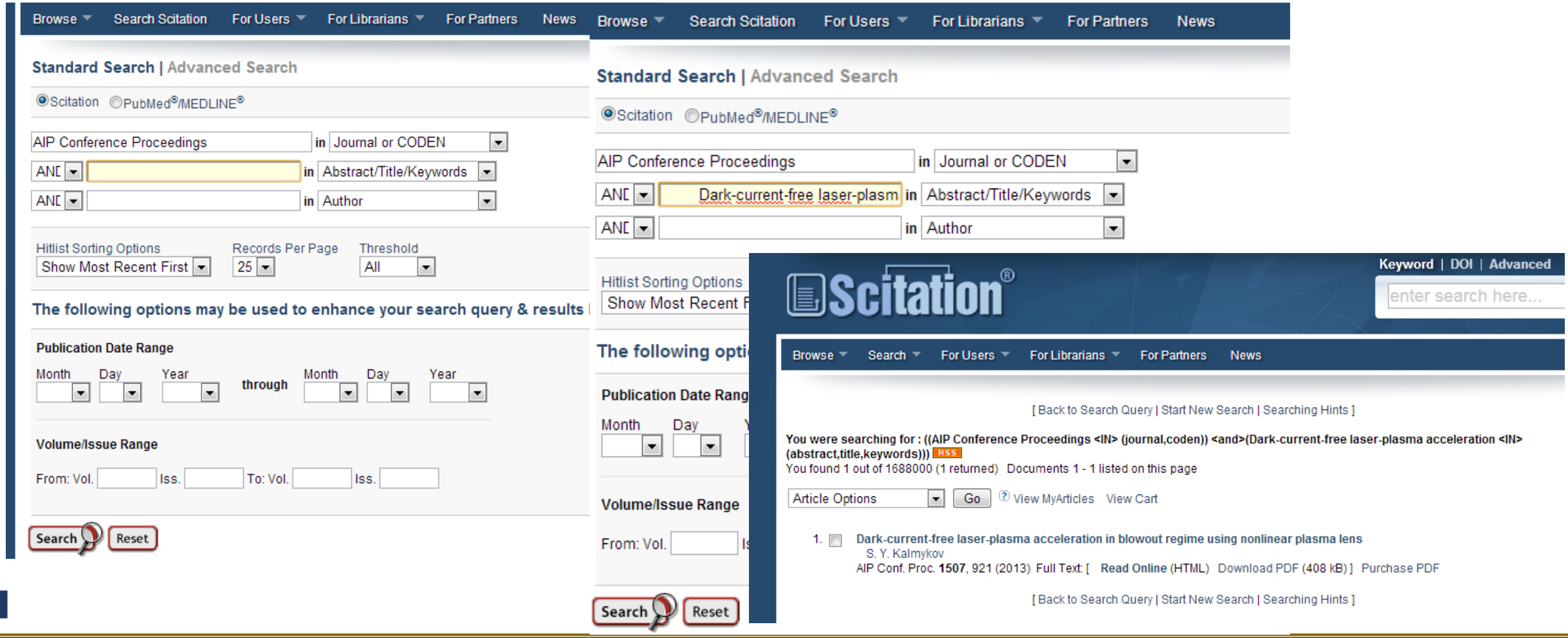

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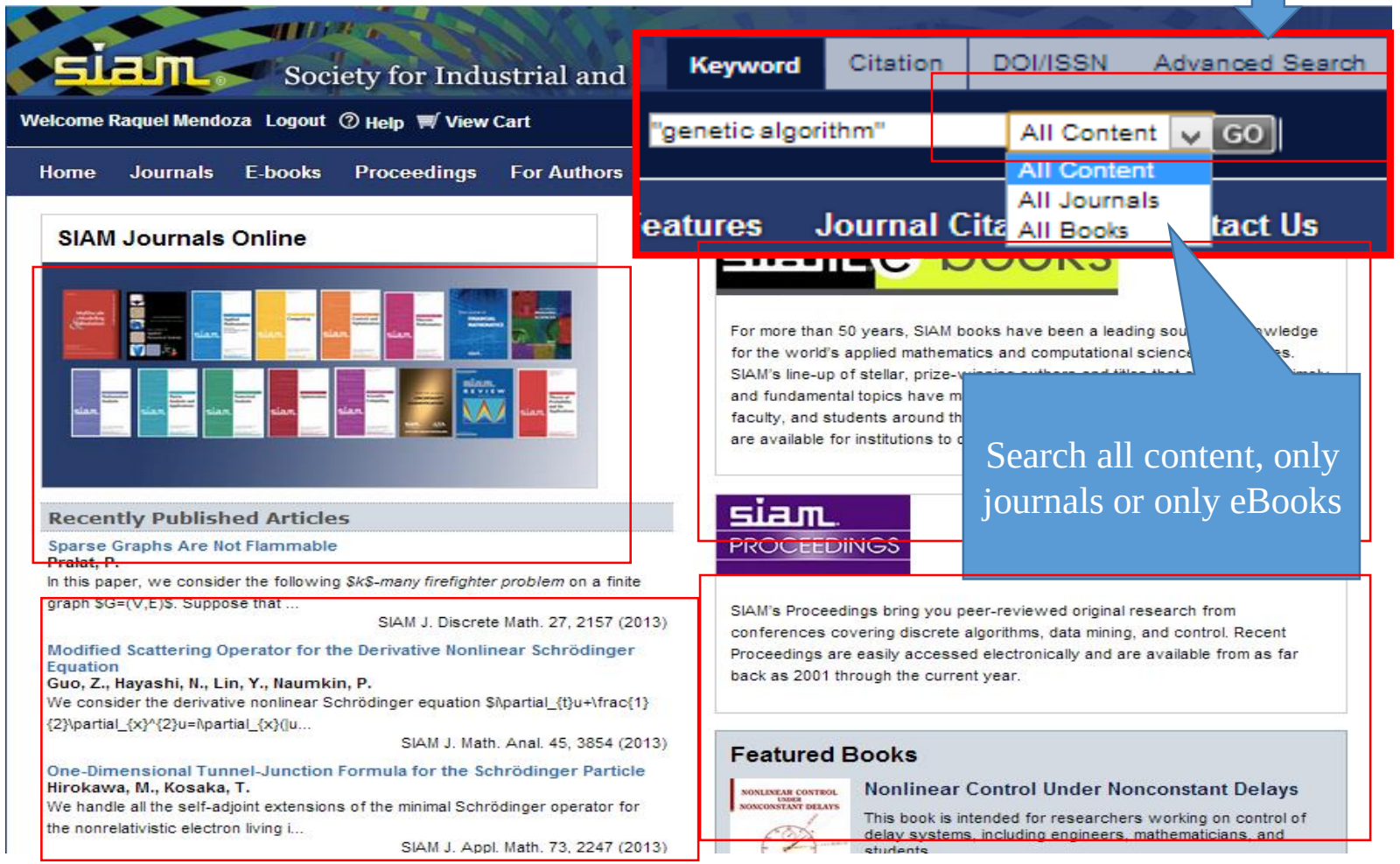

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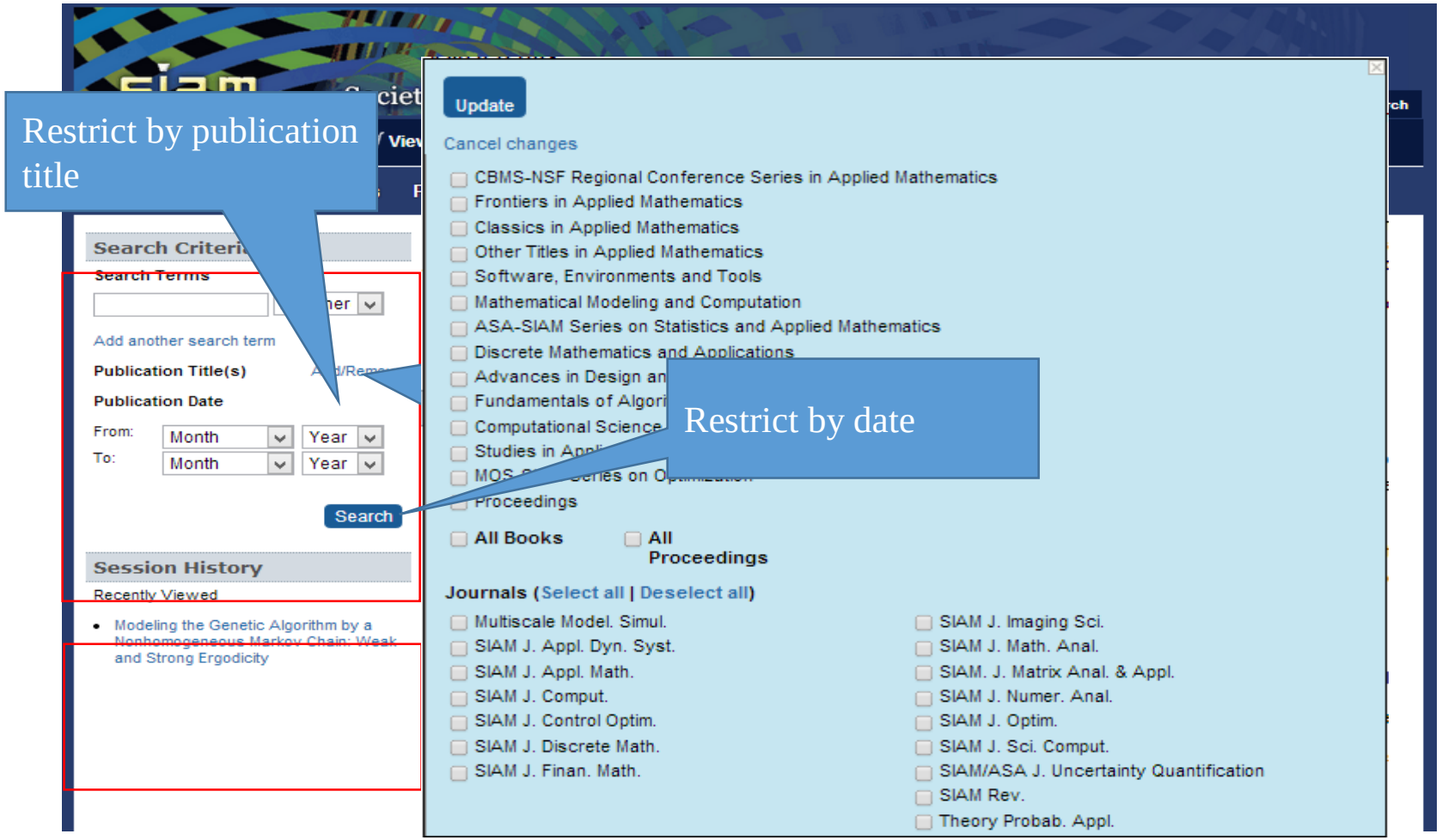

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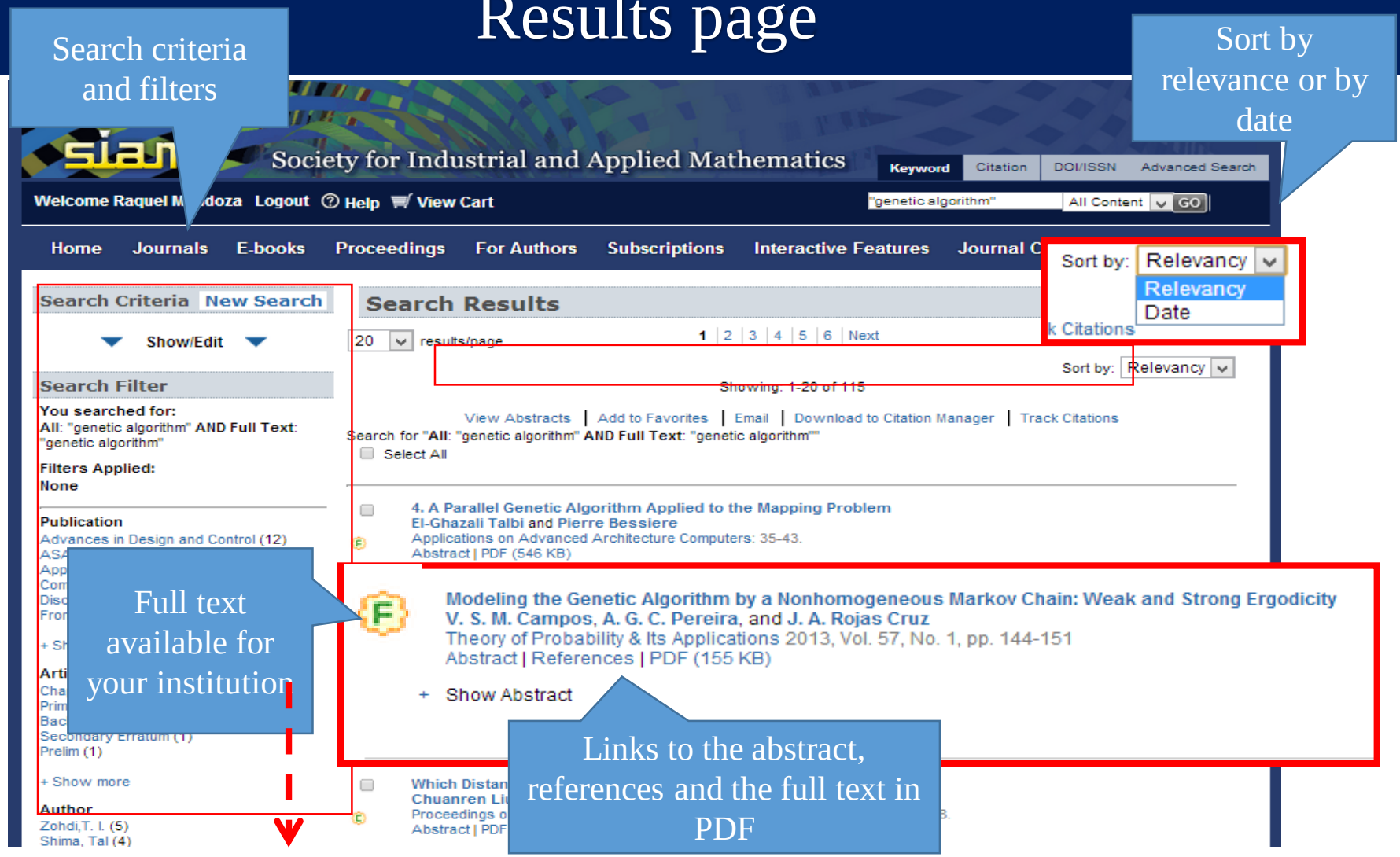

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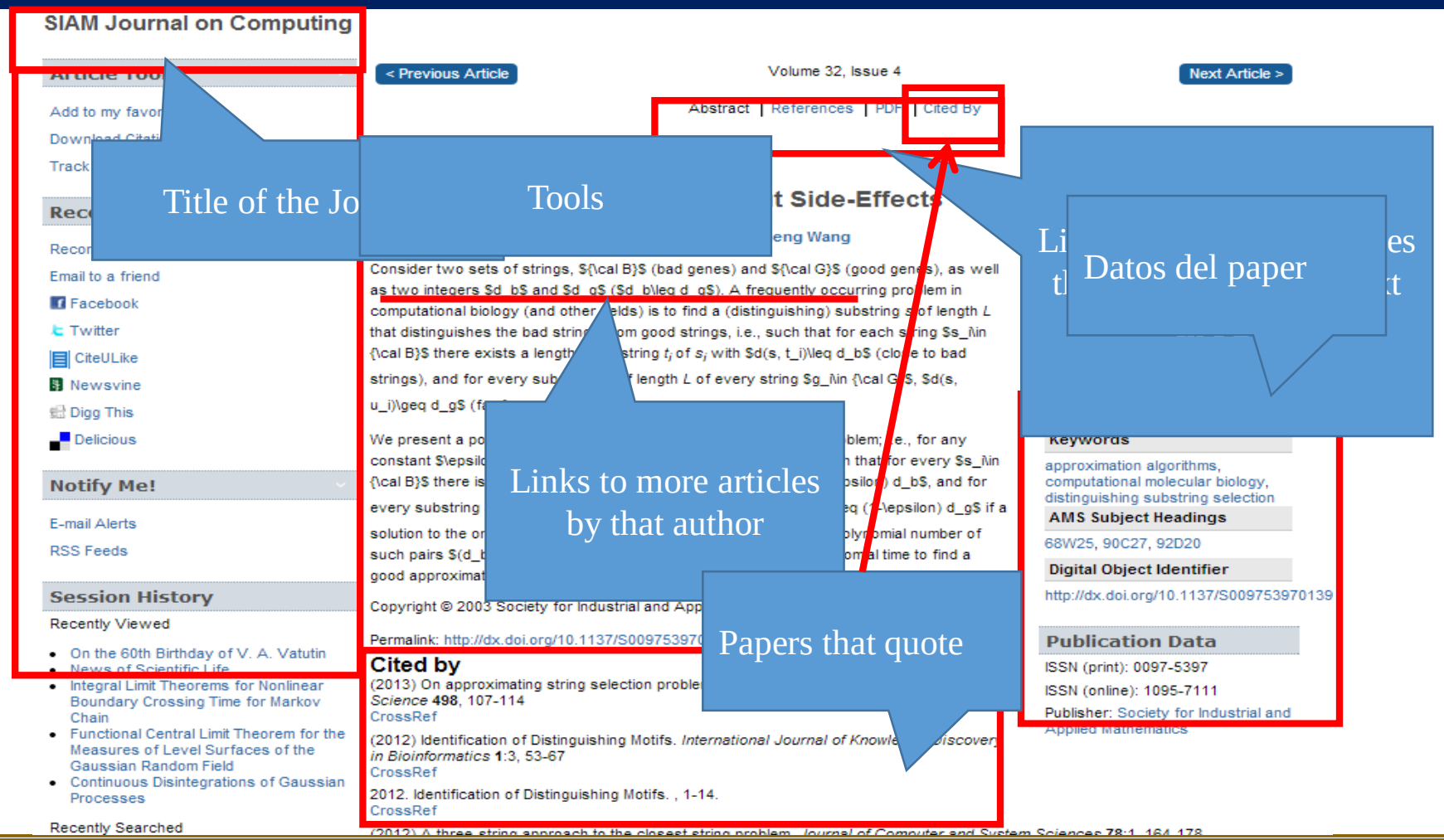

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Xiaotie Deng, Guojun Li, Zimao Li, Bin Ma, and Lushen[illegible]ang

Consider two sets of strings, ${\cal B}$ (bad genes) and ${\cal G}$ (good genes), as well as two integers d_b and d_g ($d_b\leq d_g$). A frequently occurring problem in computational biology (and other fields) is to find a (distinguishing) substring s of length L that distinguishes the bad strings from good strings, i.e., such that for each string $s_i\in {\cal B}$ there exists a length-L substring t_i of s_i with $d(s, t_i)\leq d_b$ (close to bad strings), and for every substring u_i of length L of every string $g_i\in {\cal G}$, $d(s, u_i)\geq d_g$ (far from good strings).

We present a polynomial time approximation scheme to settle the problem; i.e., for any constant $\epsilon >0$, the algorithm finds a string s of length L such that for every $s_i\in {\cal B}$ there is a length-L substring t_i of s_i with $d(t_i, s)\leq (1+\epsilon) d_b$, and for every substring u_i of length L of every $g_i\in {\cal G}$, $d(u_i, s)\geq (1-\epsilon) d_g$ if a solution to the original pair ($d_b\leq d_g$) exists. Since there is a polynomial number of such pairs (d_b,d_g), we can exhaust all the possibilities in polynomial time to find a good approximation required by the corresponding application problems.

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(2013) On approximating string selection problems with outliers. *Theoretical Computer Science* **498**, 107-114
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Genetic Design of Drugs Without Side-Effects

Xiaotie Deng, Guojun Li, Zimao Li, Bin Ma, and Lusheng Wang

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Keywords

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GENETIC DESIGN OF DRUGS WITHOUT SIDE-EFFECTS*

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Abstract. Consider two sets of strings, $\mathcal{B}$ (bad genes) and $\mathcal{G}$ (good genes), as well as two integers d_b and d_g ($d_b \leq d_g$). A frequently occurring problem in computational biology (and other fields) is to find a (distinguishing) substring s of length L that distinguishes the bad strings from good strings, i.e., such that for each string $s_i \in \mathcal{B}$ there exists a length-L substring t_i of s_i with $d(s, t_i) \leq d_b$ (close to bad strings), and for every substring u_i of length L of every string $g_i \in \mathcal{G}$, $d(s, u_i) \geq d_g$ (far from good strings).

We present a polynomial time approximation scheme to settle the problem; i.e., for any constant $\epsilon > 0$, the algorithm finds a string s of length L such that for every $s_i \in \mathcal{B}$ there is a length-L substring t_i of s_i with $d(t_i, s) \leq (1 + \epsilon)d_b$, and for every substring u_i of length L of every $g_i \in \mathcal{G}$, $d(u_i, s) \geq (1 - \epsilon)d_g$ if a solution to the original pair ($d_b \leq d_g$) exists. Since there is a polynomial number of such pairs (d_b, d_g), we can exhaust all the possibilities in polynomial time to find a good approximation required by the corresponding application problems.

Key words. approximation algorithms, computational molecular biology, distinguishing substring selection

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1. Introduction. Research effort in molecular biology, such as the human genome project, has been revealing the secret of our genetic composition, the long DNA sequences that can determine many aspects of life. Applications that use this information have posed new challenges to the design and analysis of efficient computational methods.

A frequently recurring problem in biological applications is to find one substring of length L that appears (with a few substitutions) at least once in each of a set of bad strings (such as bacterial sequences) and is not "close" to any substring of length

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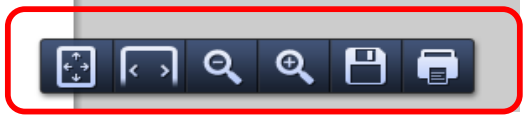

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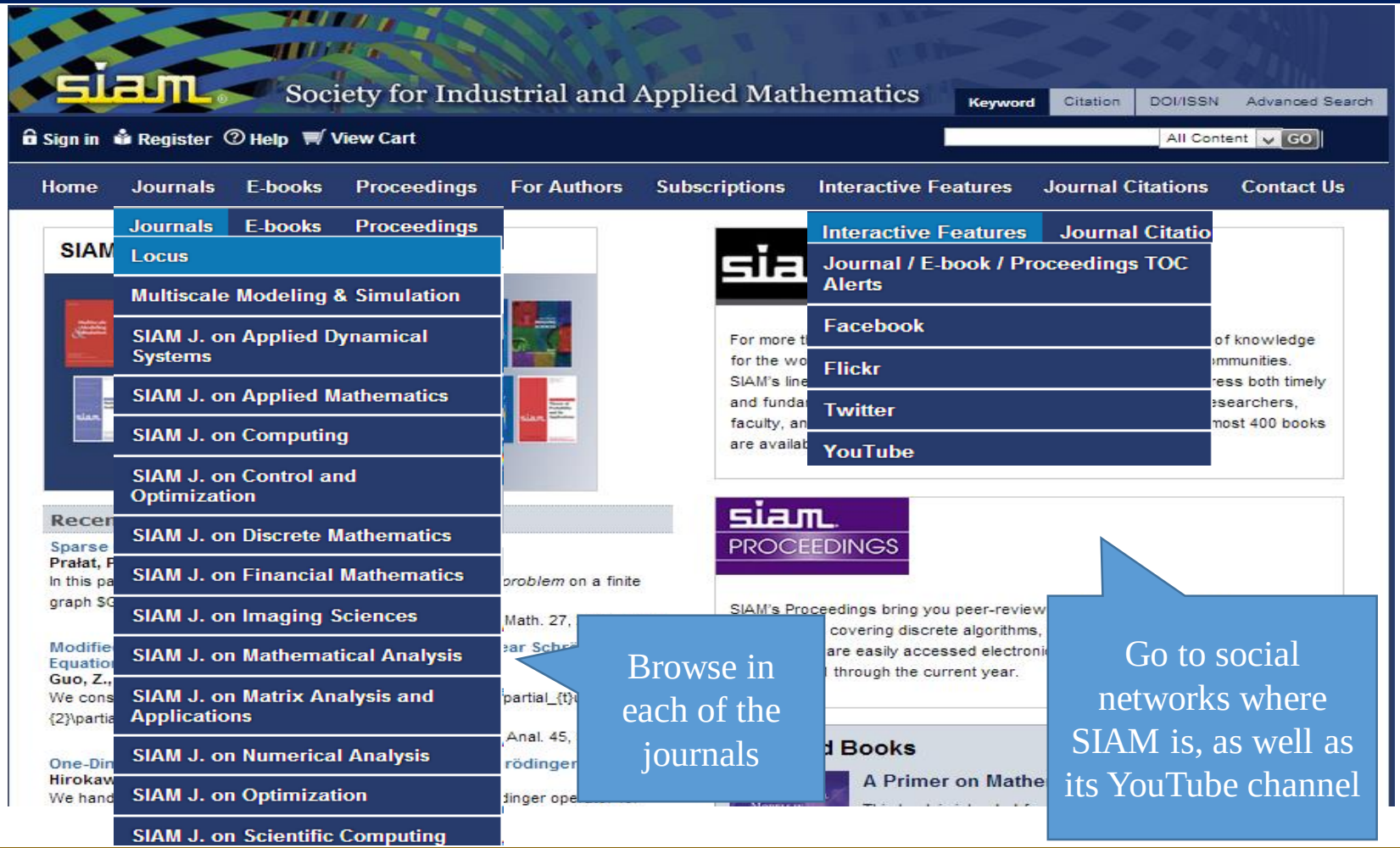

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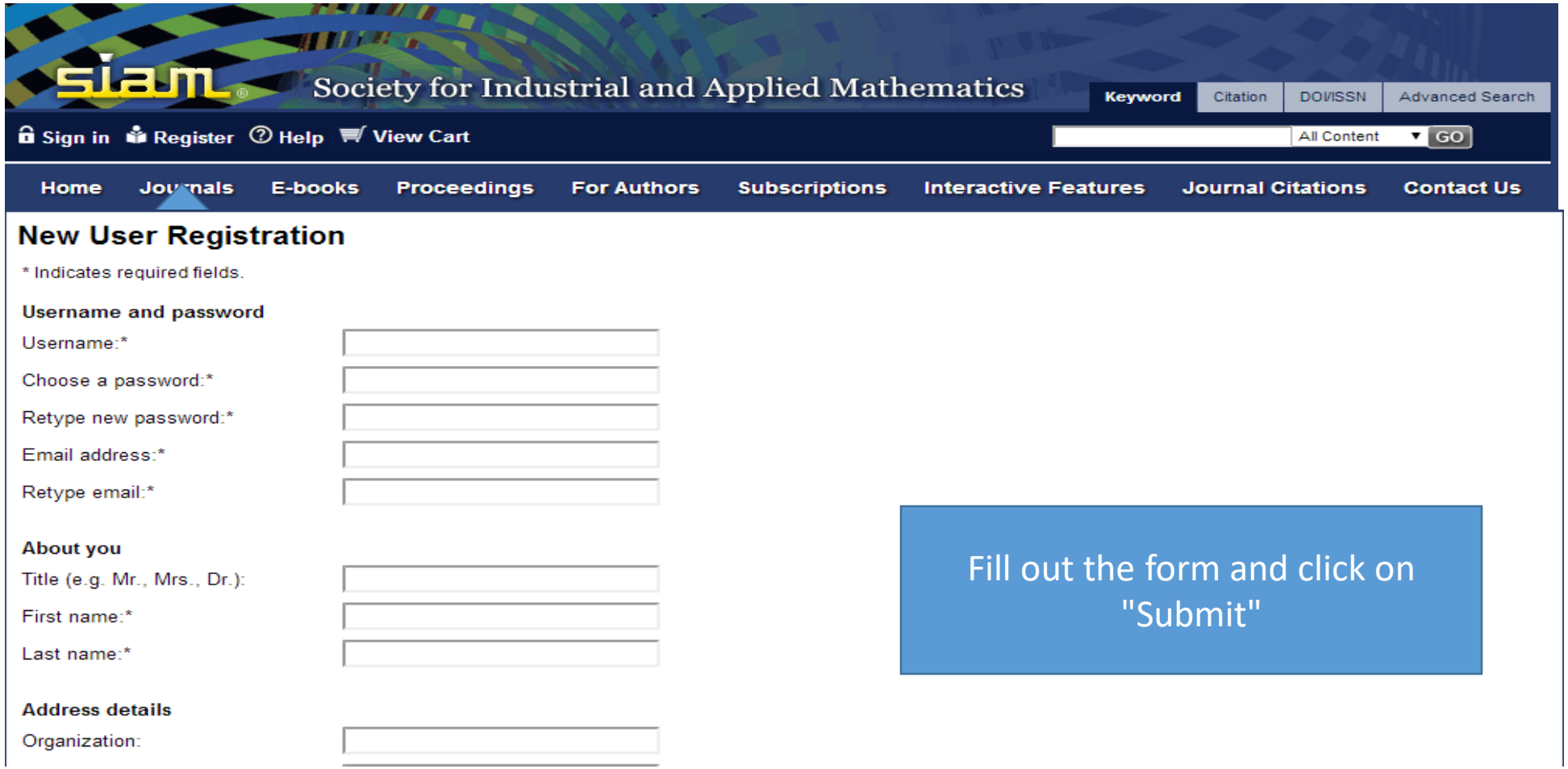

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Thank You Very Much

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