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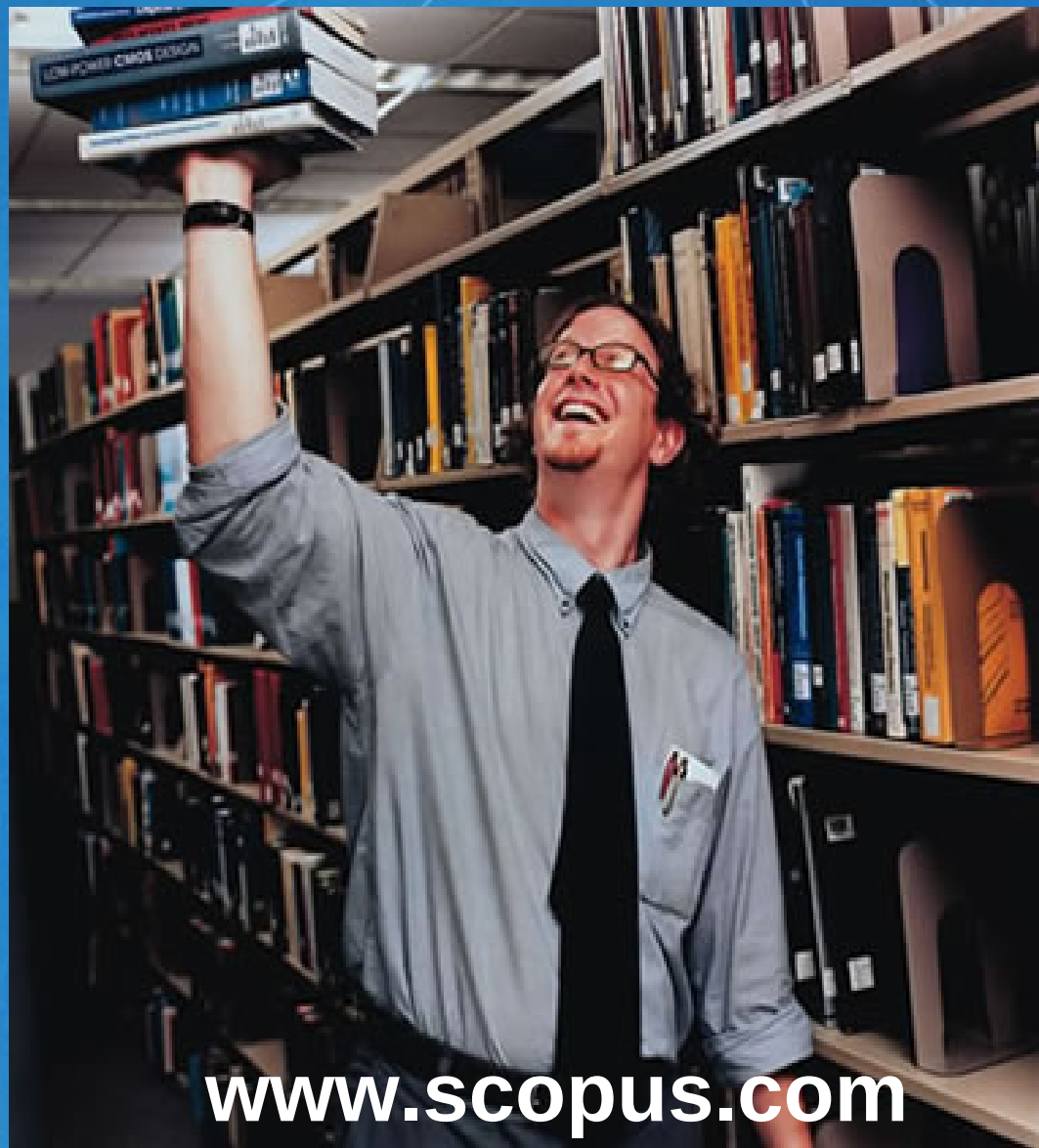

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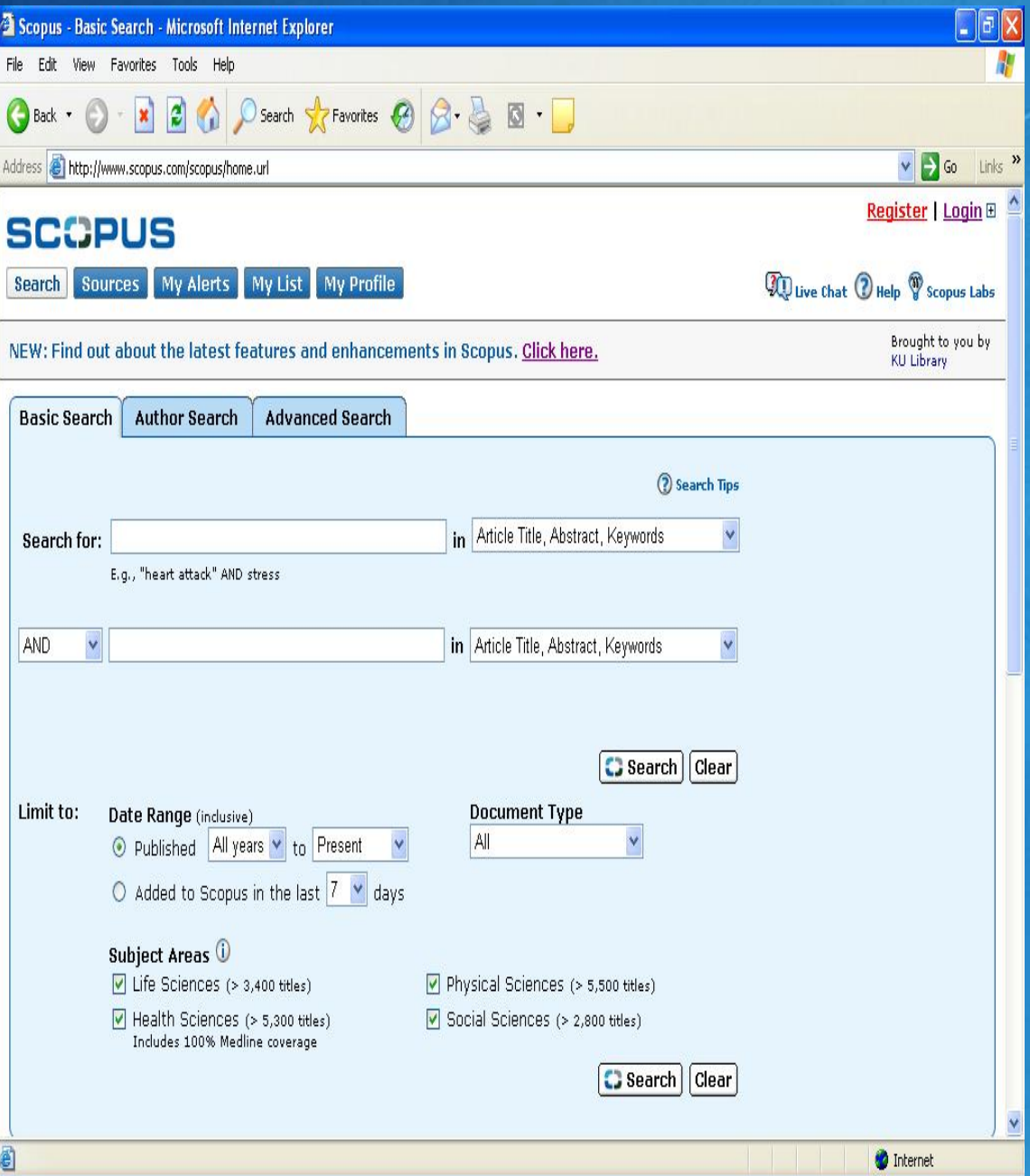

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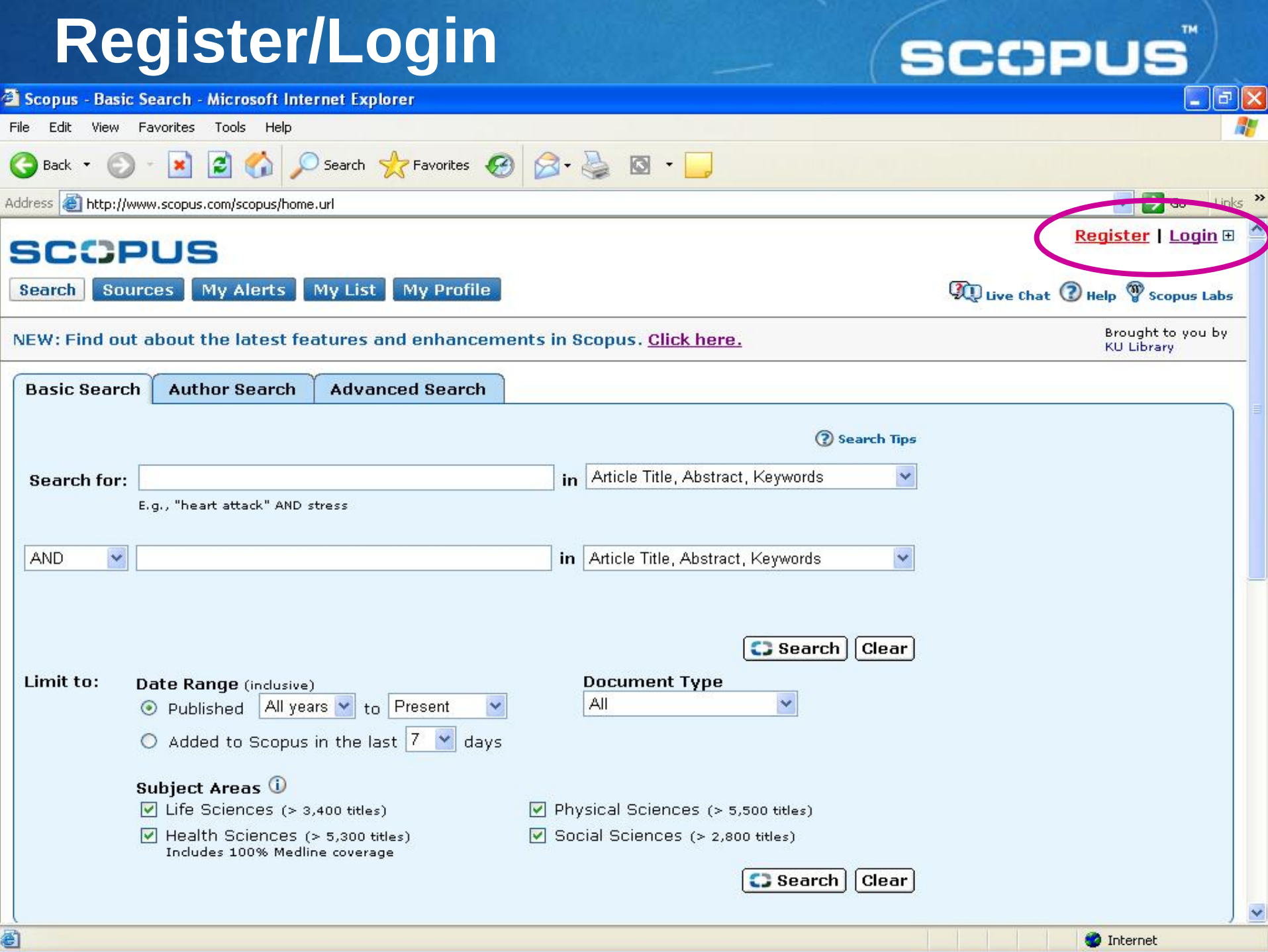

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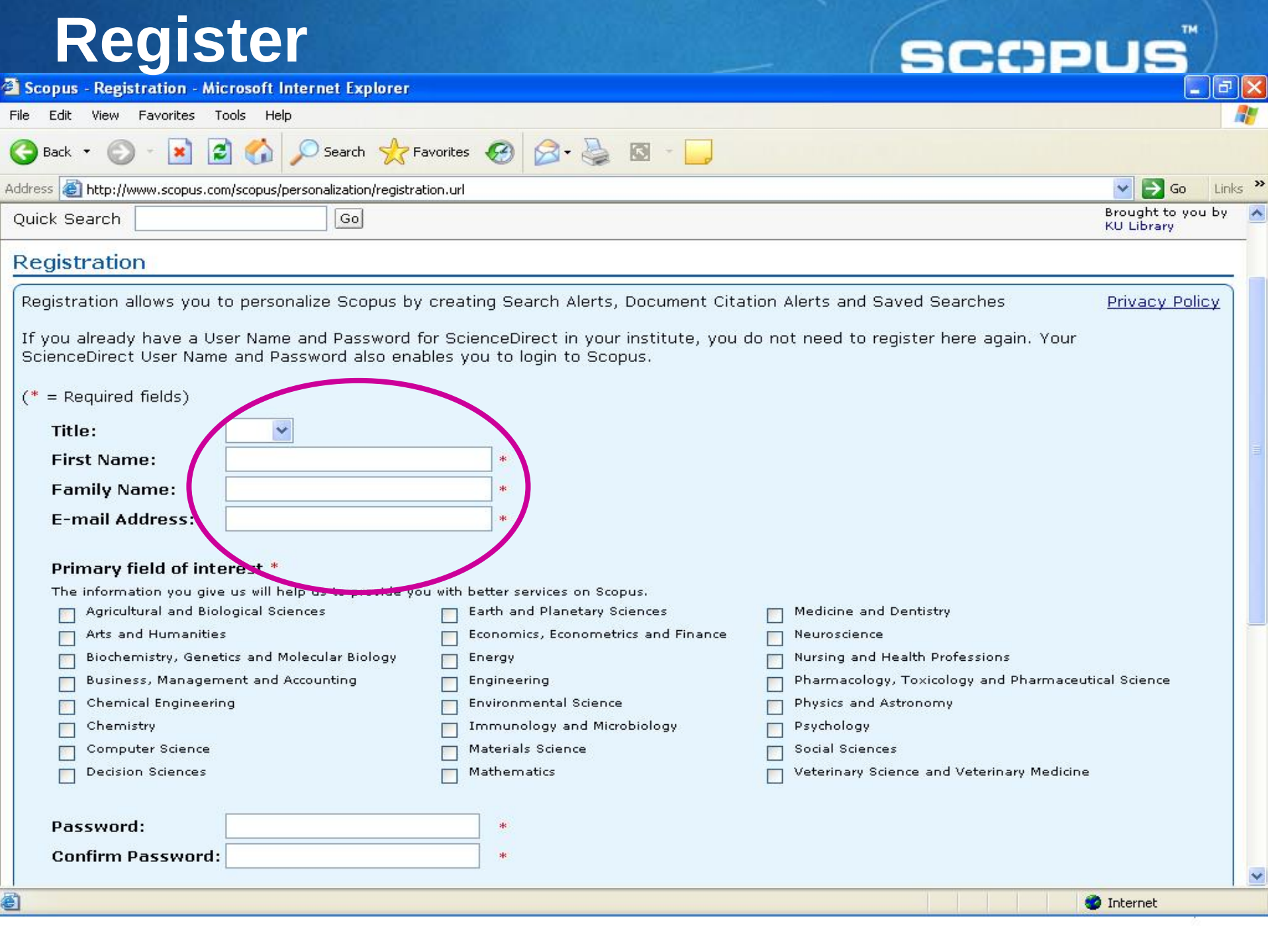
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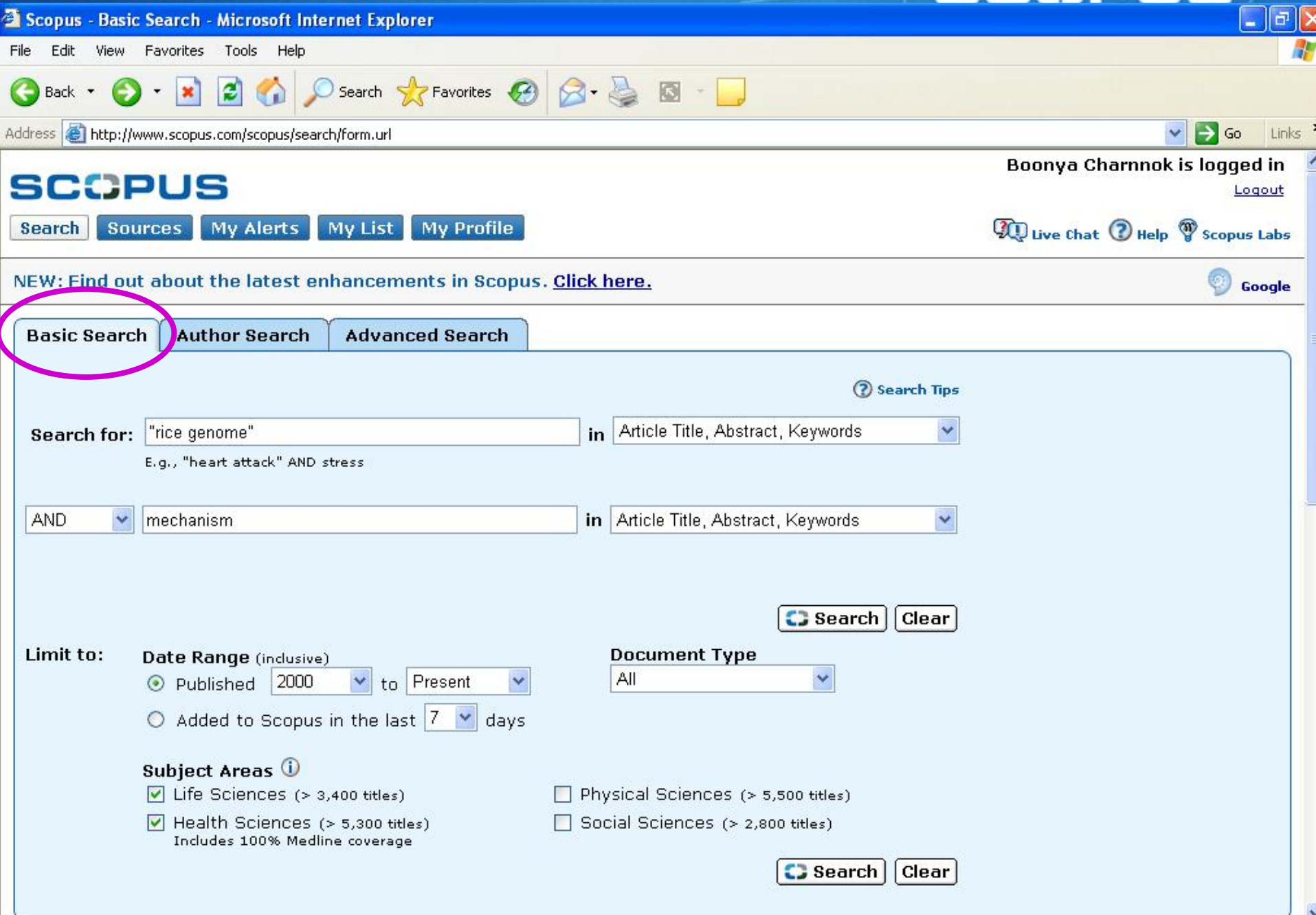

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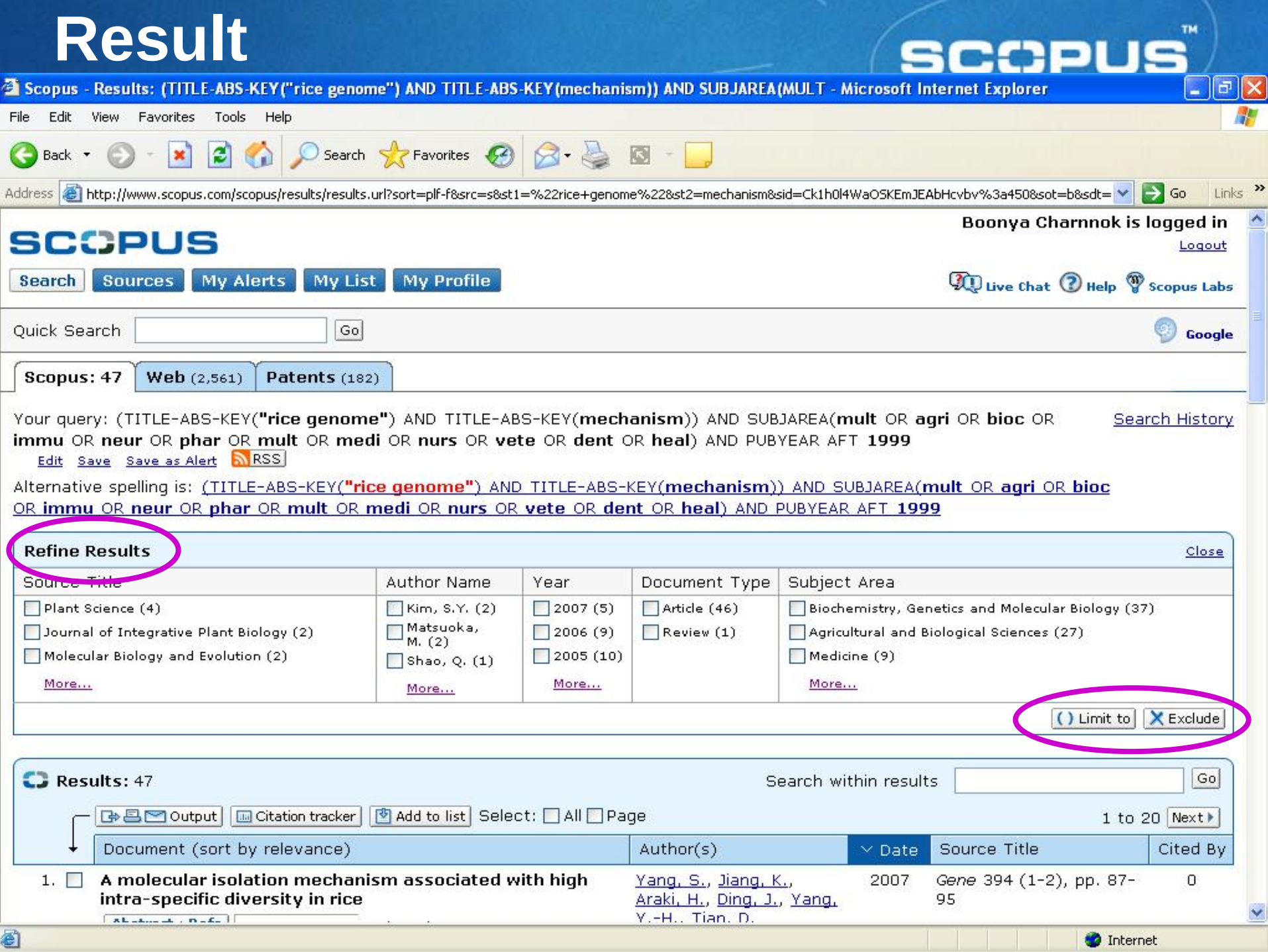
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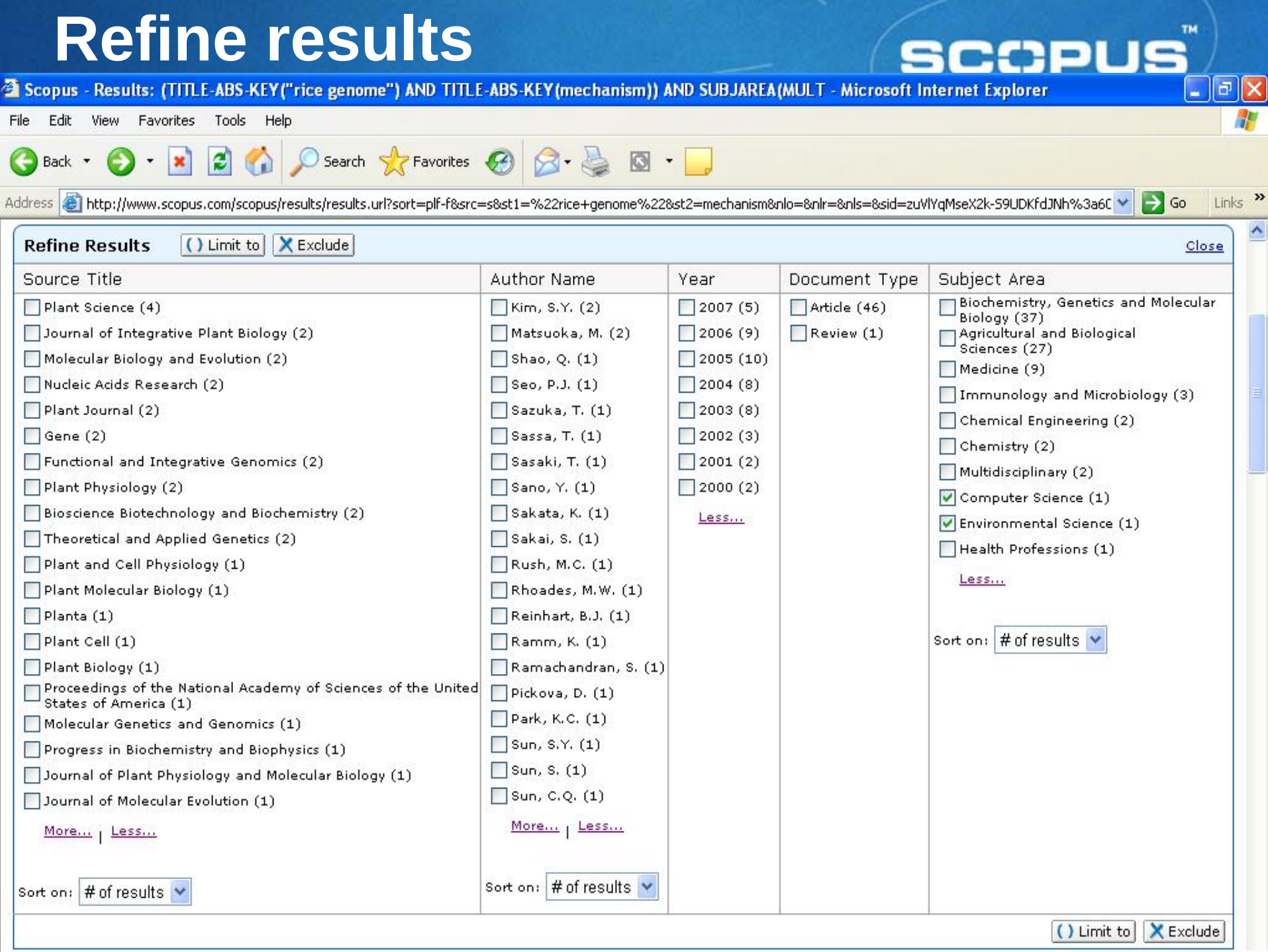

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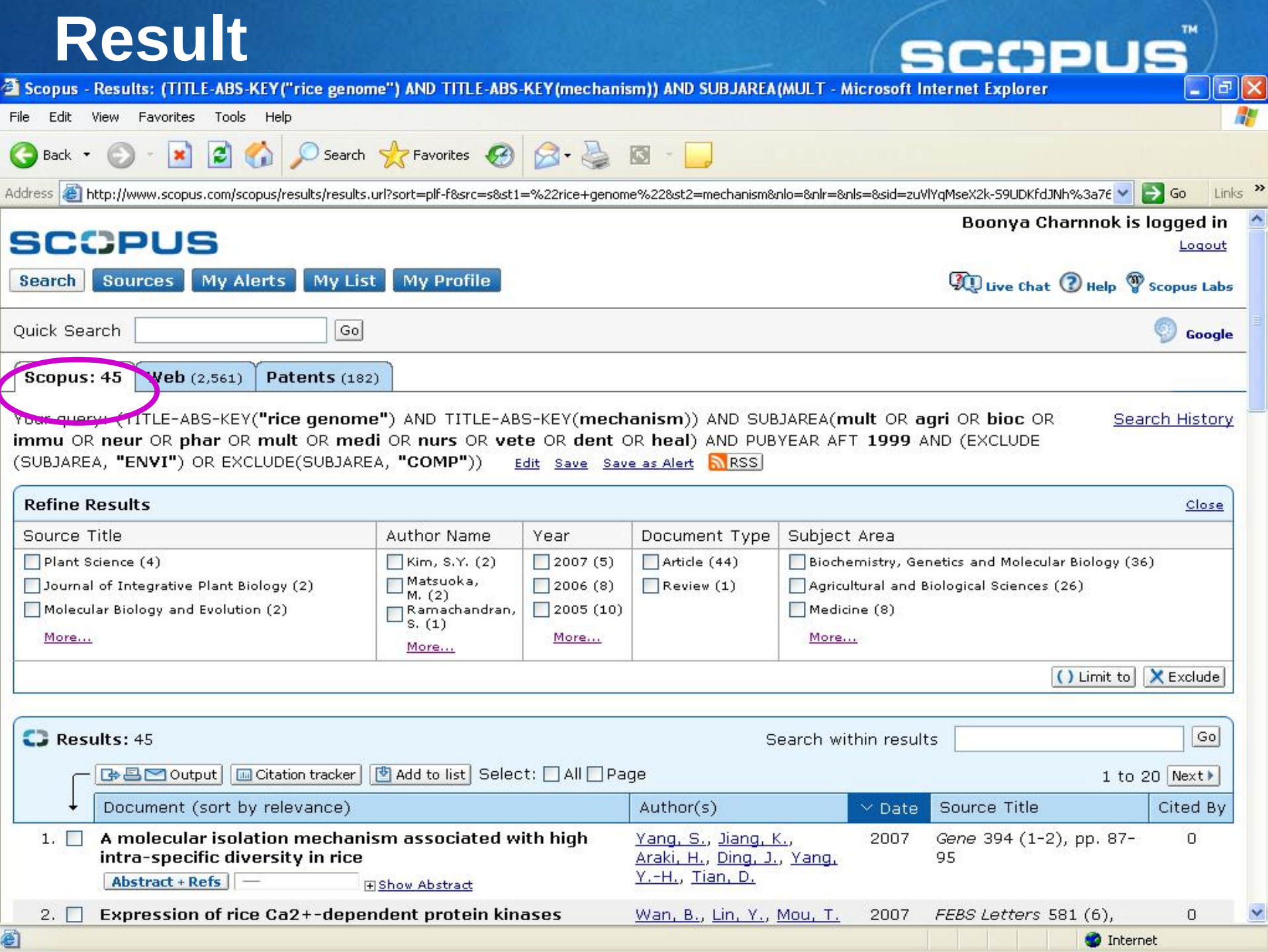
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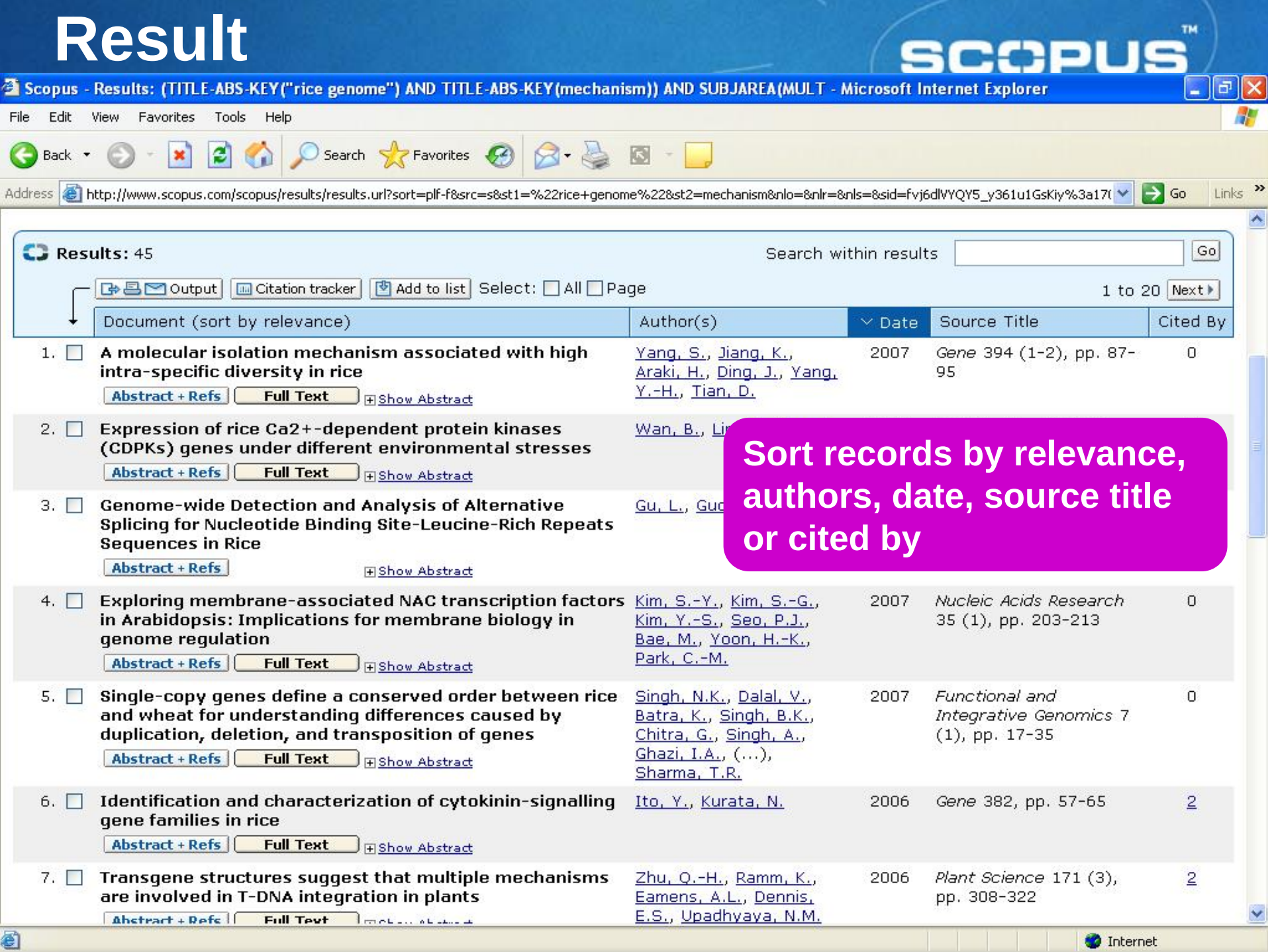

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A molecular isolation mechanism associated with high intra-specific diversity in rice

Yang, S.[a], Jiang, K.[a], Araki, H.[b], Ding, J.[a], Yang, Y.-H.[a], Tian, D.[a]

[a] State Key Laboratory of Pharmaceutical Biotechnology, Department of Biology, Nanjing University, Nanjing, 210093, China
[b] Department of Zoology, Oregon State University, Corvallis, OR 97331, United States

Abstract

High levels of inter-specific diversity are expected due to genetic isolation, the reproductive or geographical barriers, which lead to the accumulation of nucleotide variation. However, high levels of genetic variation are repeatedly observed even within species, notably at loci of the human major histocompatability complex and of plant resistance genes. Are molecular isolations responsible for the high intra-specific variation? To address this issue, we performed a genome-wide survey of the relationship between the possible factors that could cause genetic isolation, and the level of polymorphism, based on two rice genome comparisons. Here, we show that the levels of polymorphism in rice genes are positively correlated with the proportions of non-alignable flanking sequences, and

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[a]State Key Laboratory of Pharmaceutical Biotechnology, Department of Biology, Nanjing University, Nanjing 210093, China
[b]Department of Zoology, Oregon State University, Corvallis, Oregon 97331, USA
Received 18 October 2006; revised 10 February 2007; accepted 12 February 2007. Available online 24 February 2007.

Abstract

High levels of inter-specific diversity are expected due to genetic isolation, the reproductive or geographical barriers, which lead to the accumulation of nucleotide variation. However, high levels of genetic variation are repeatedly observed even within species, notably at loci of the human major histocompatability complex and of plant resistance genes. Are molecular isolations responsible for the high intra-specific variation? To address

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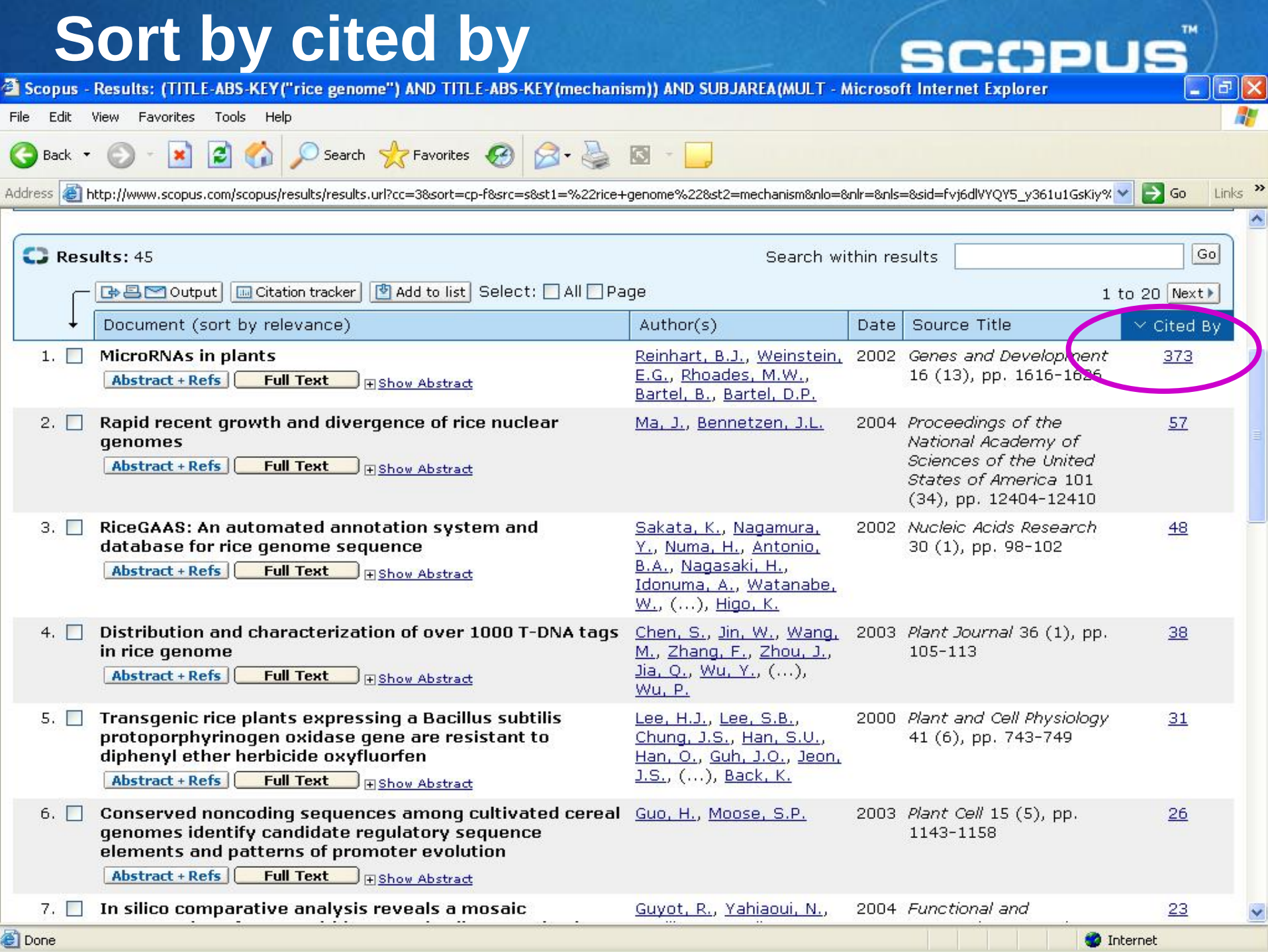

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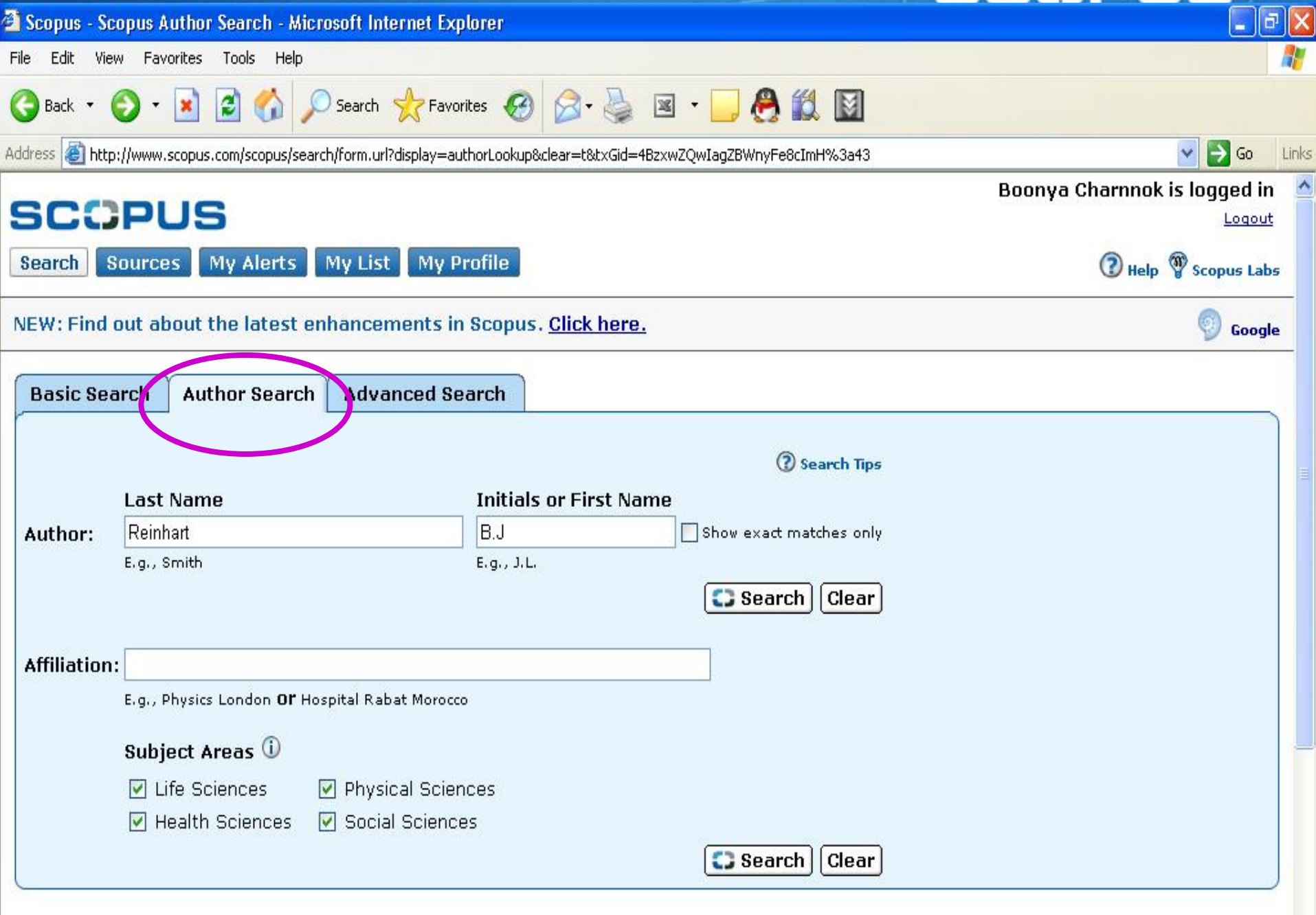

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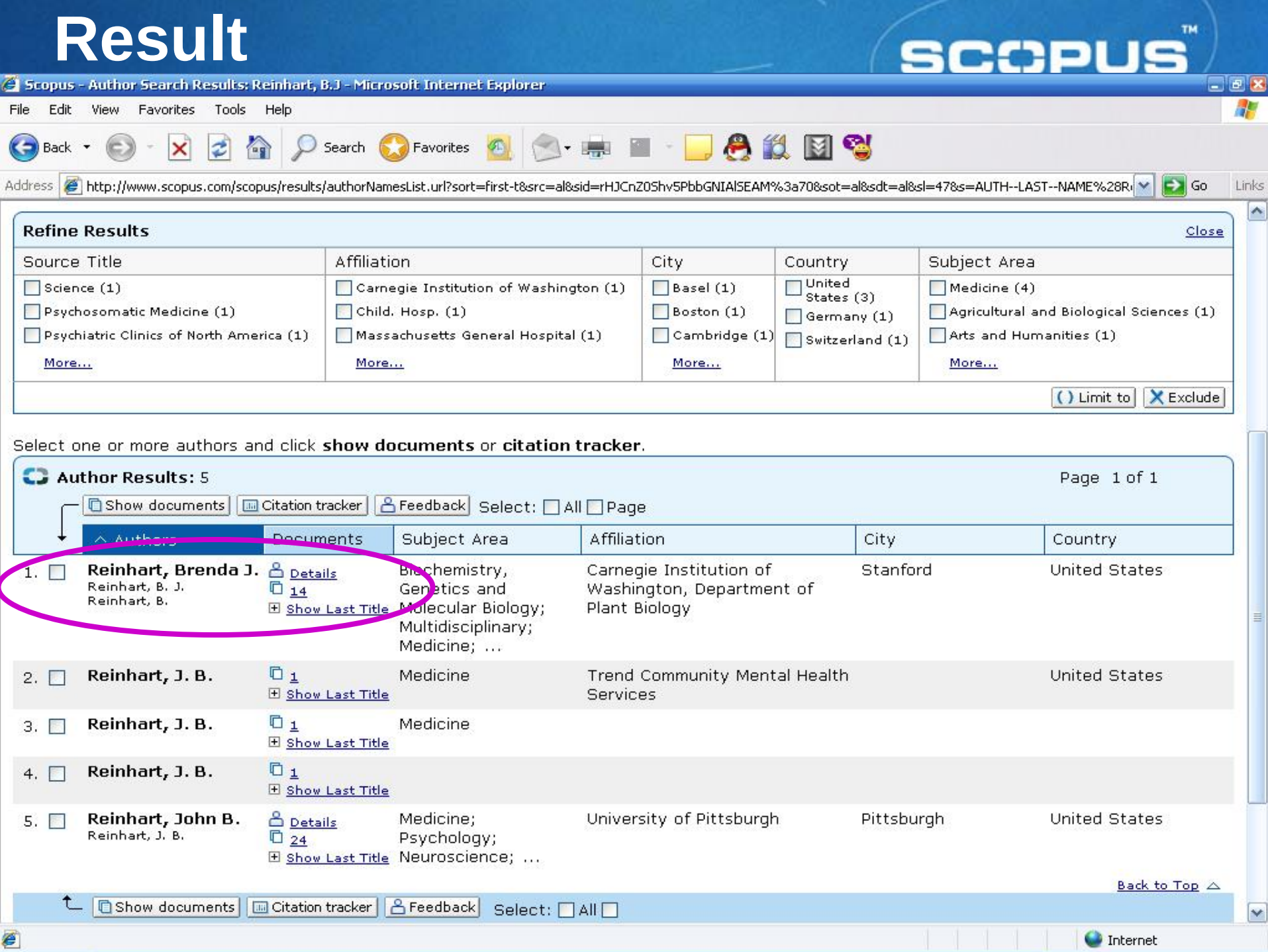
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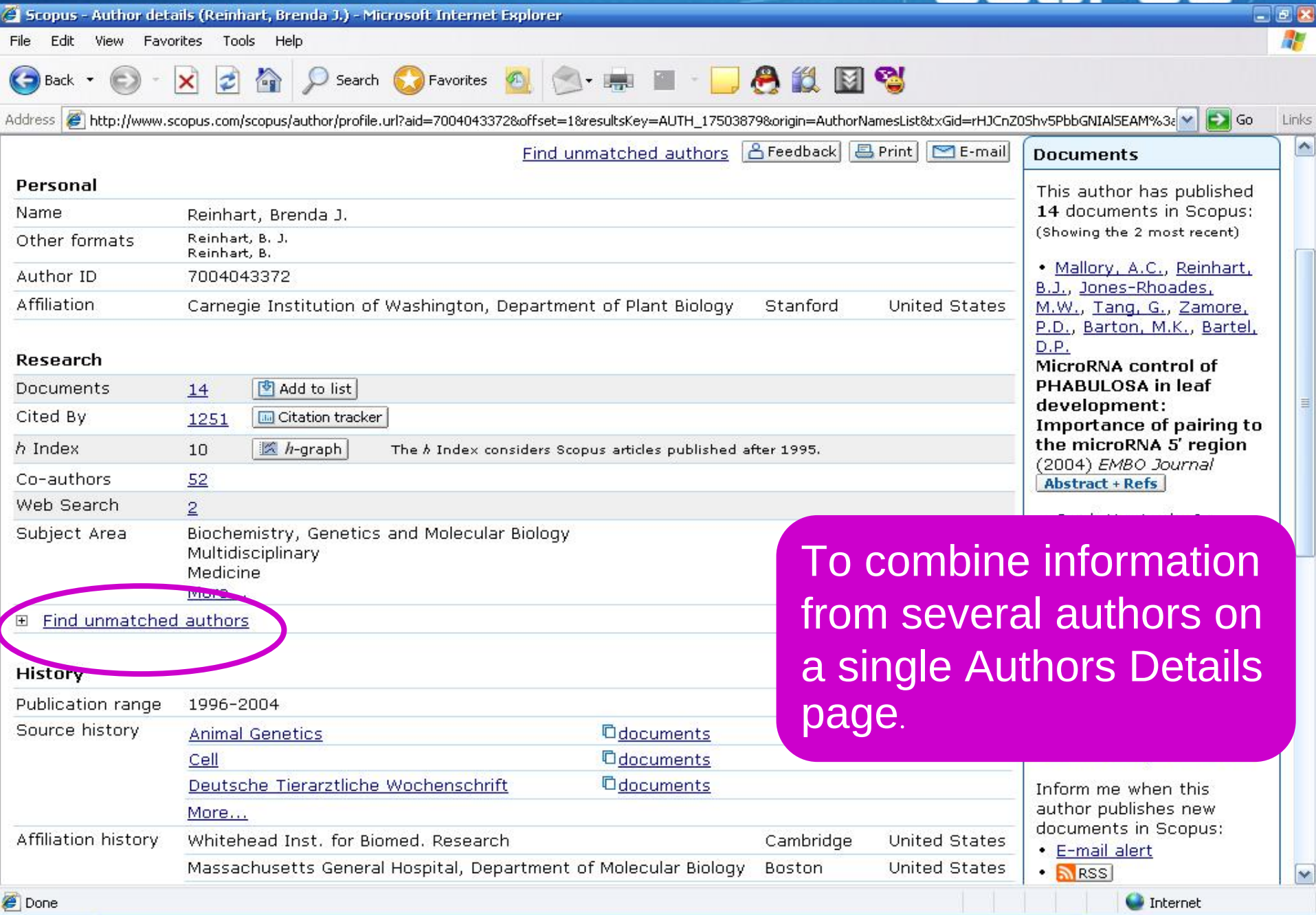

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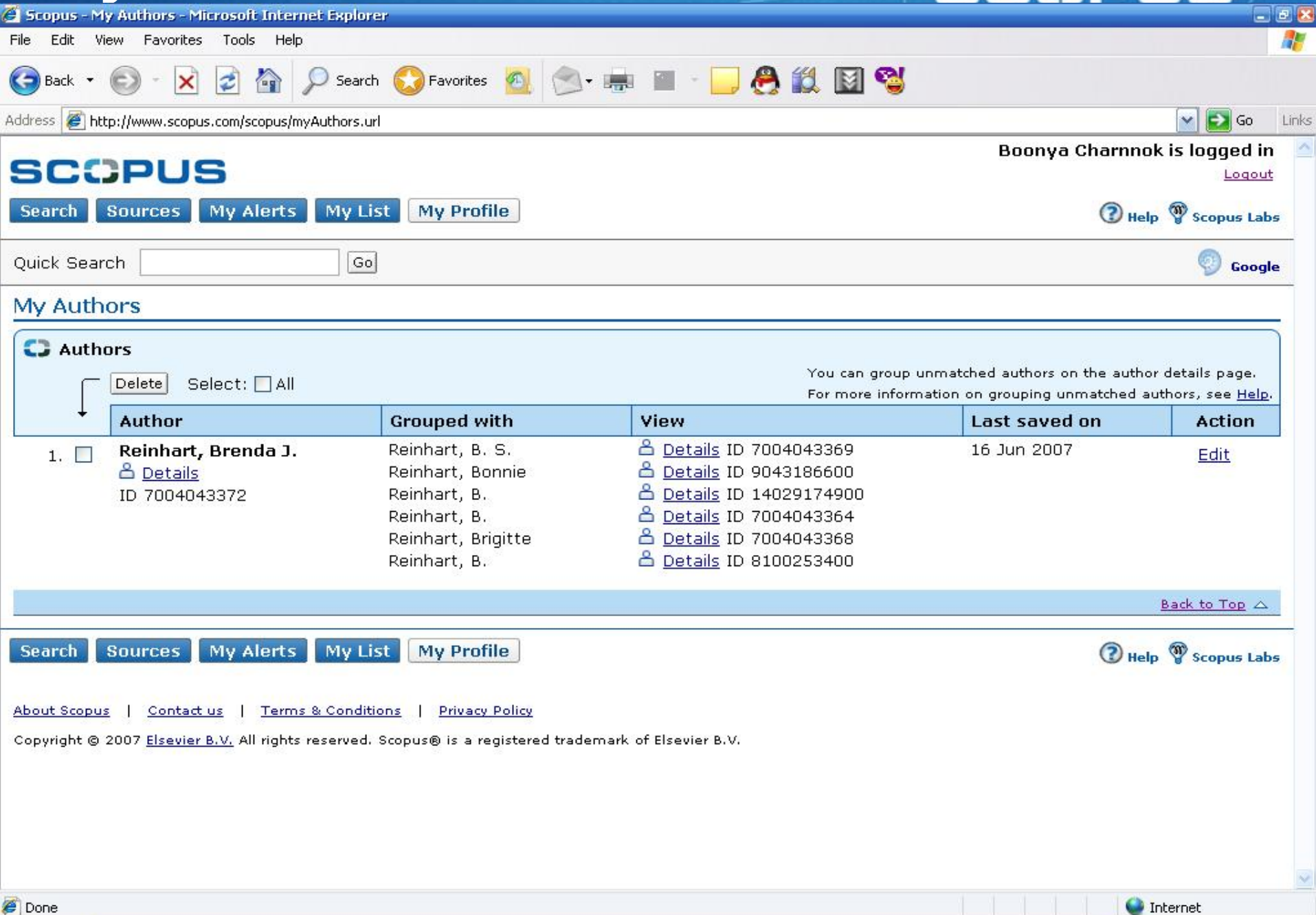
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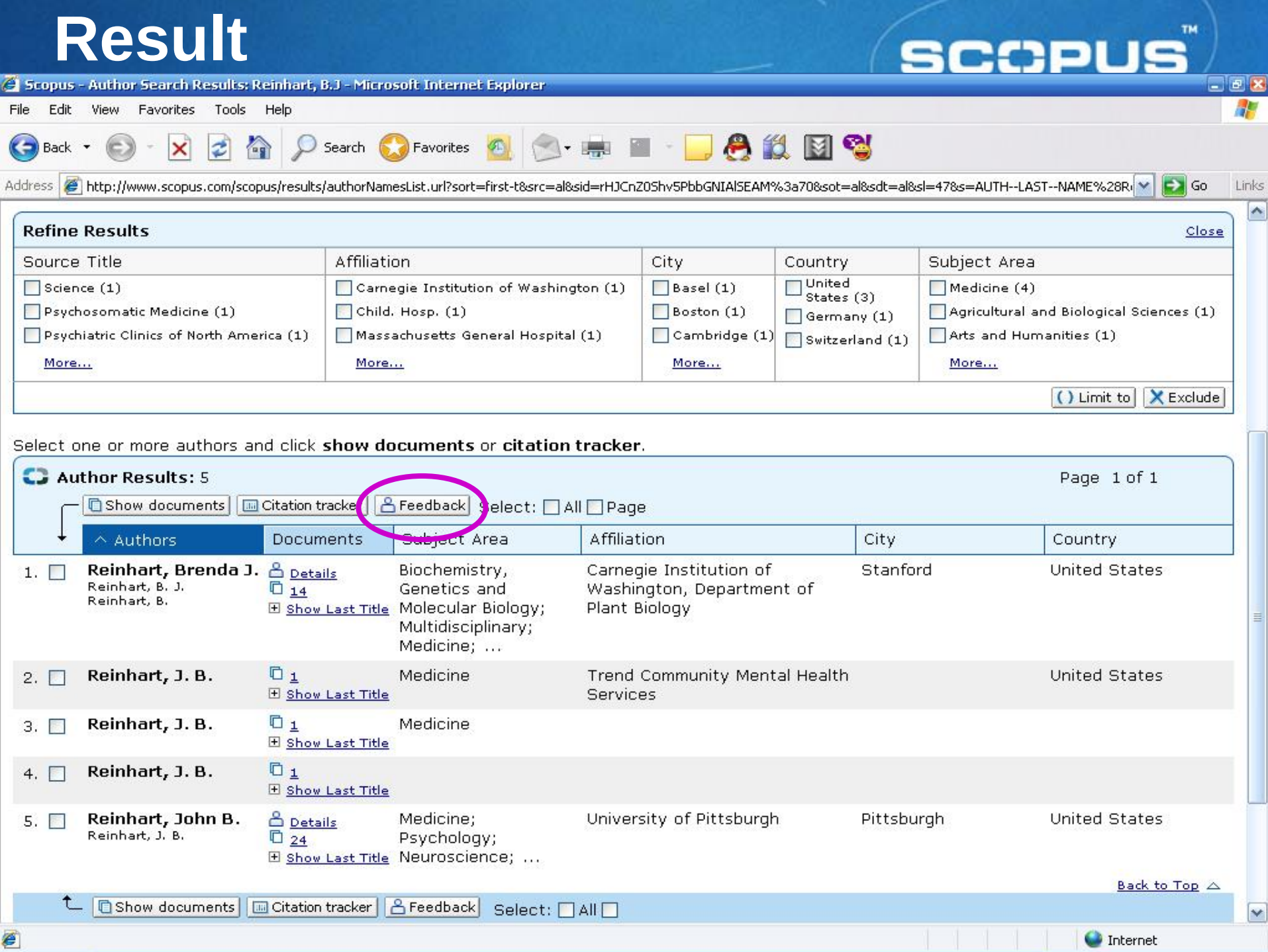
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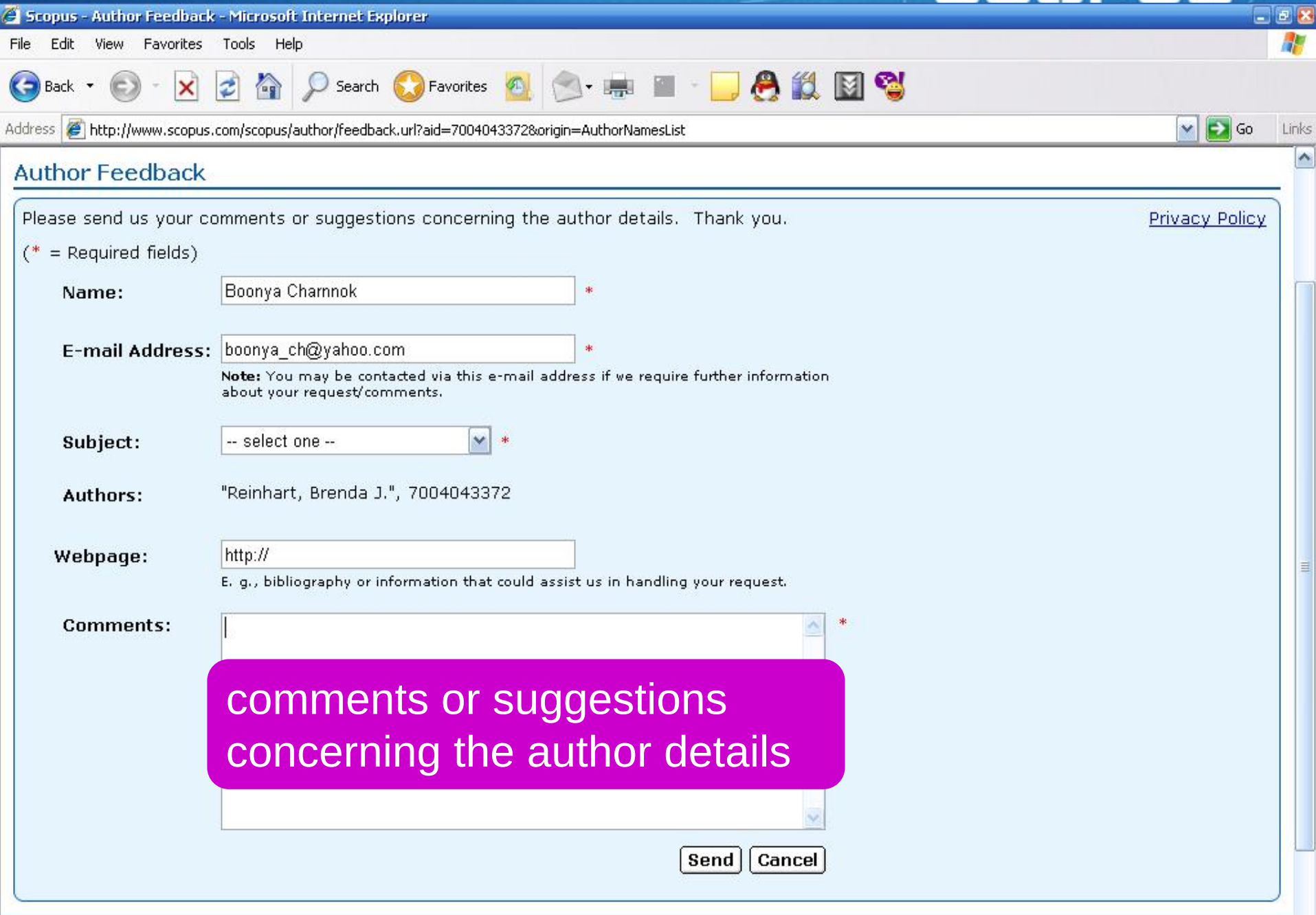

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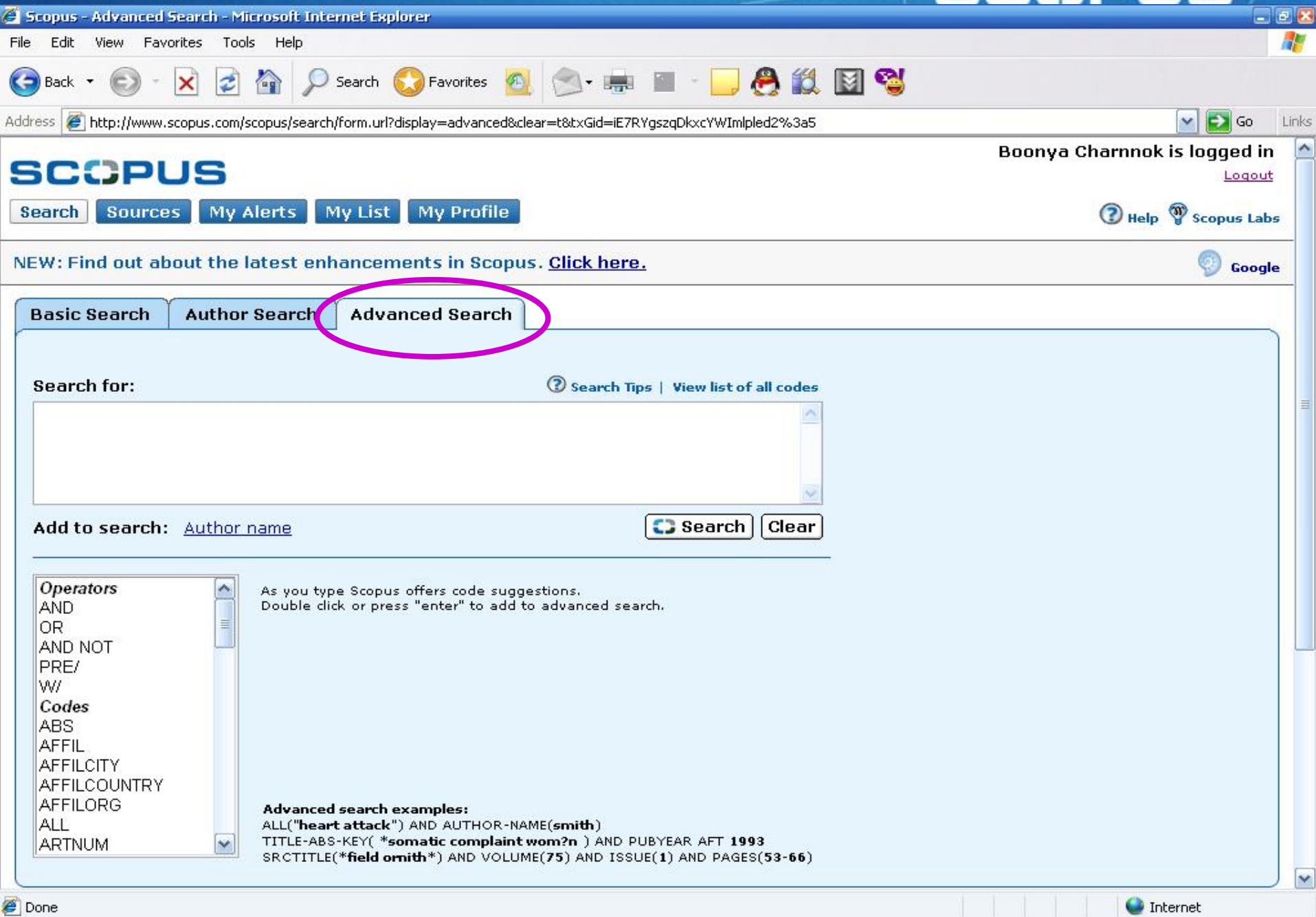

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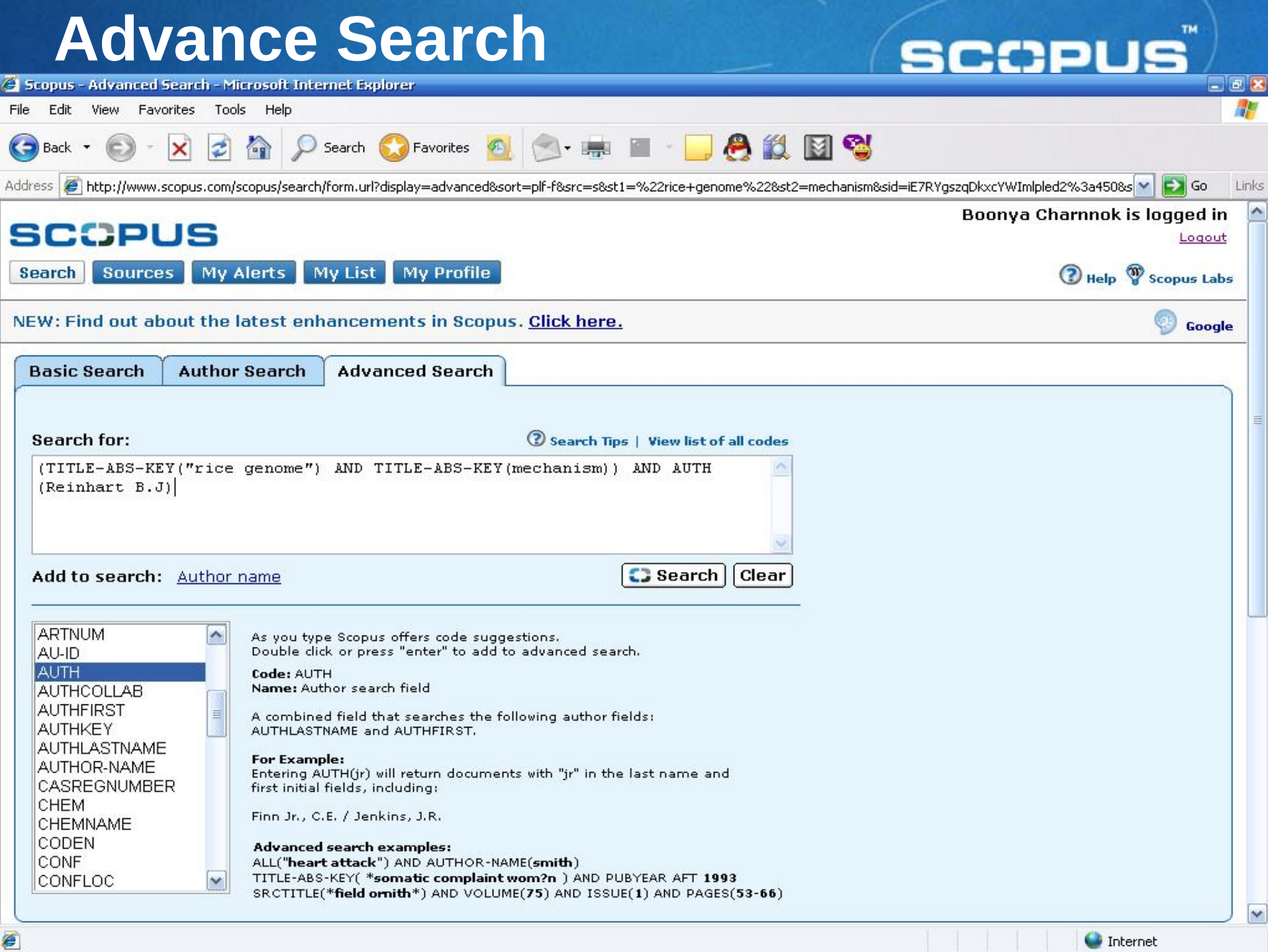

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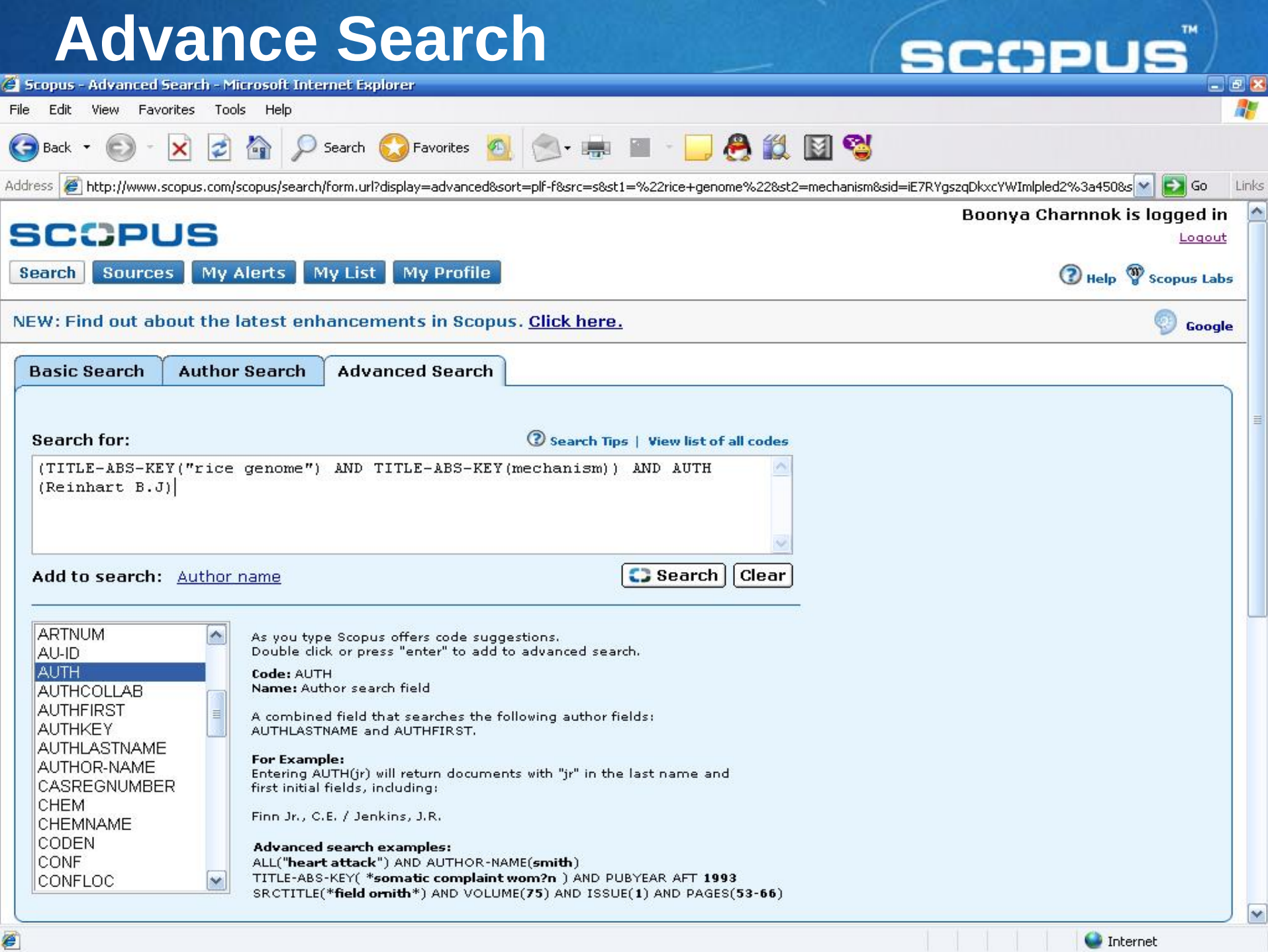

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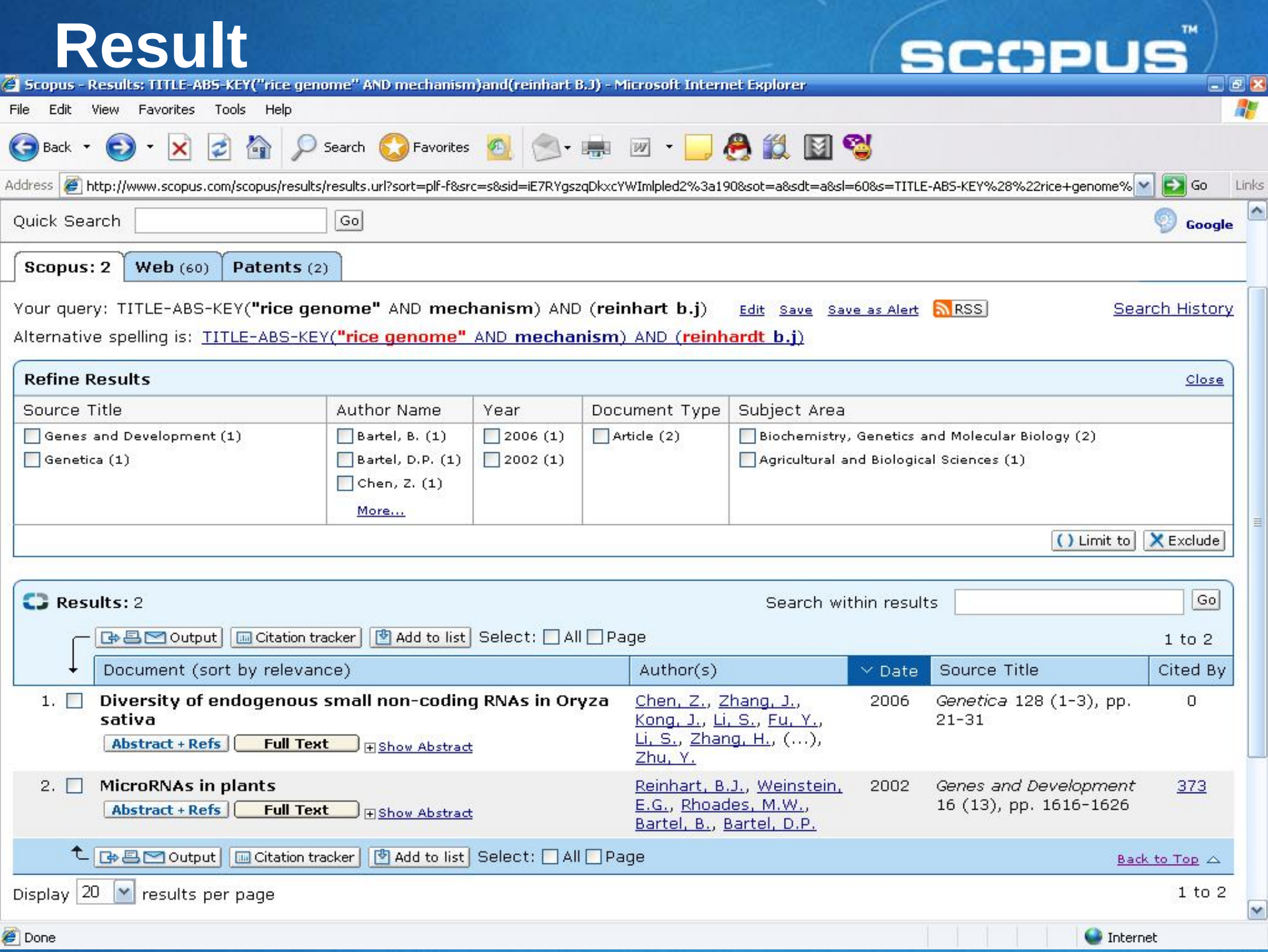
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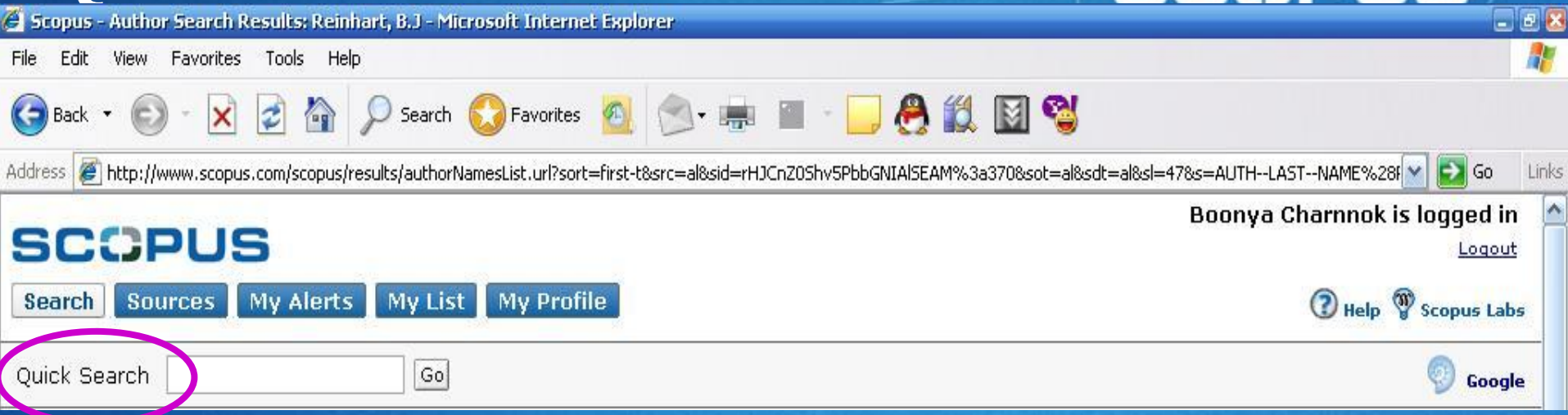

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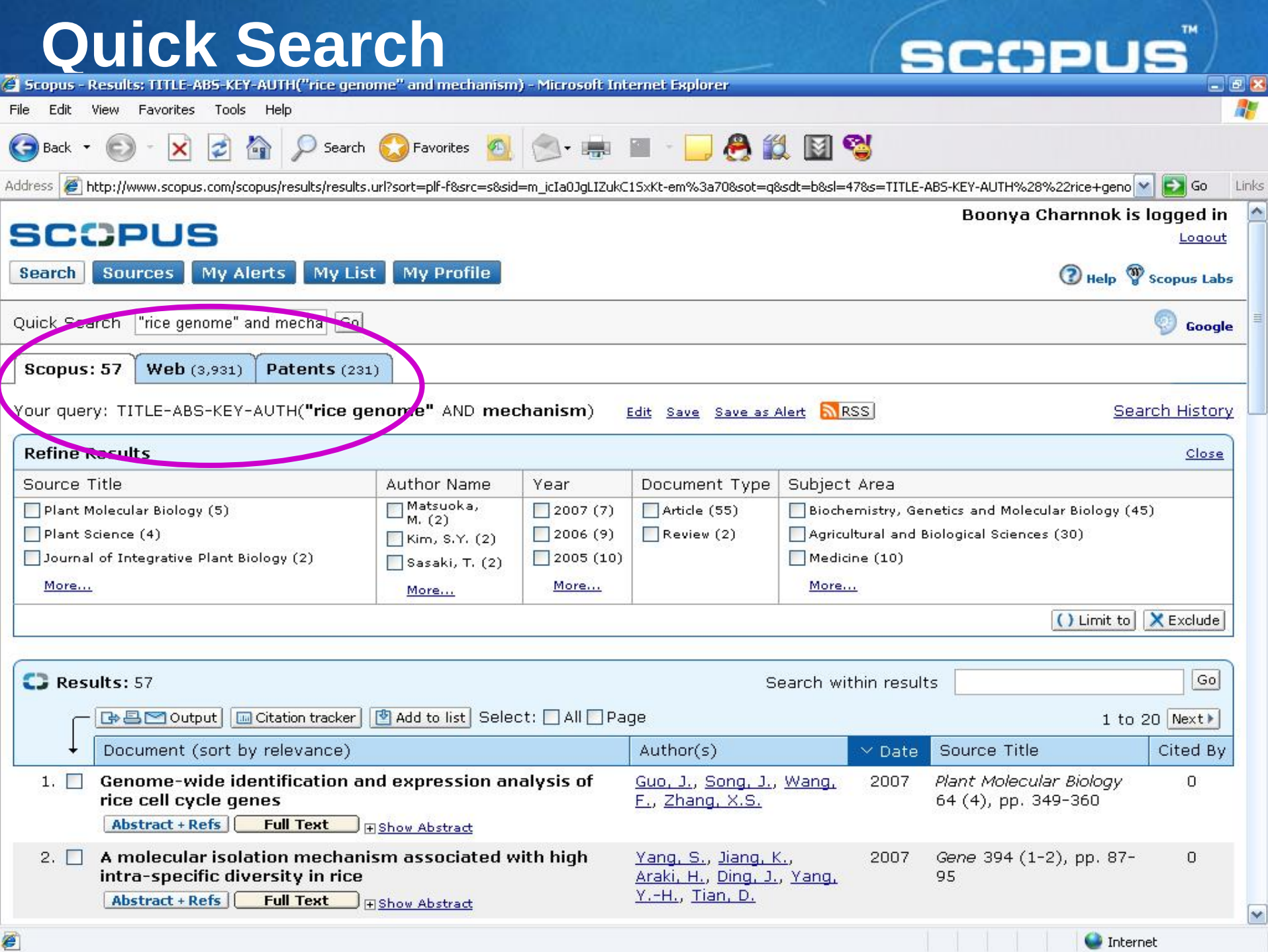

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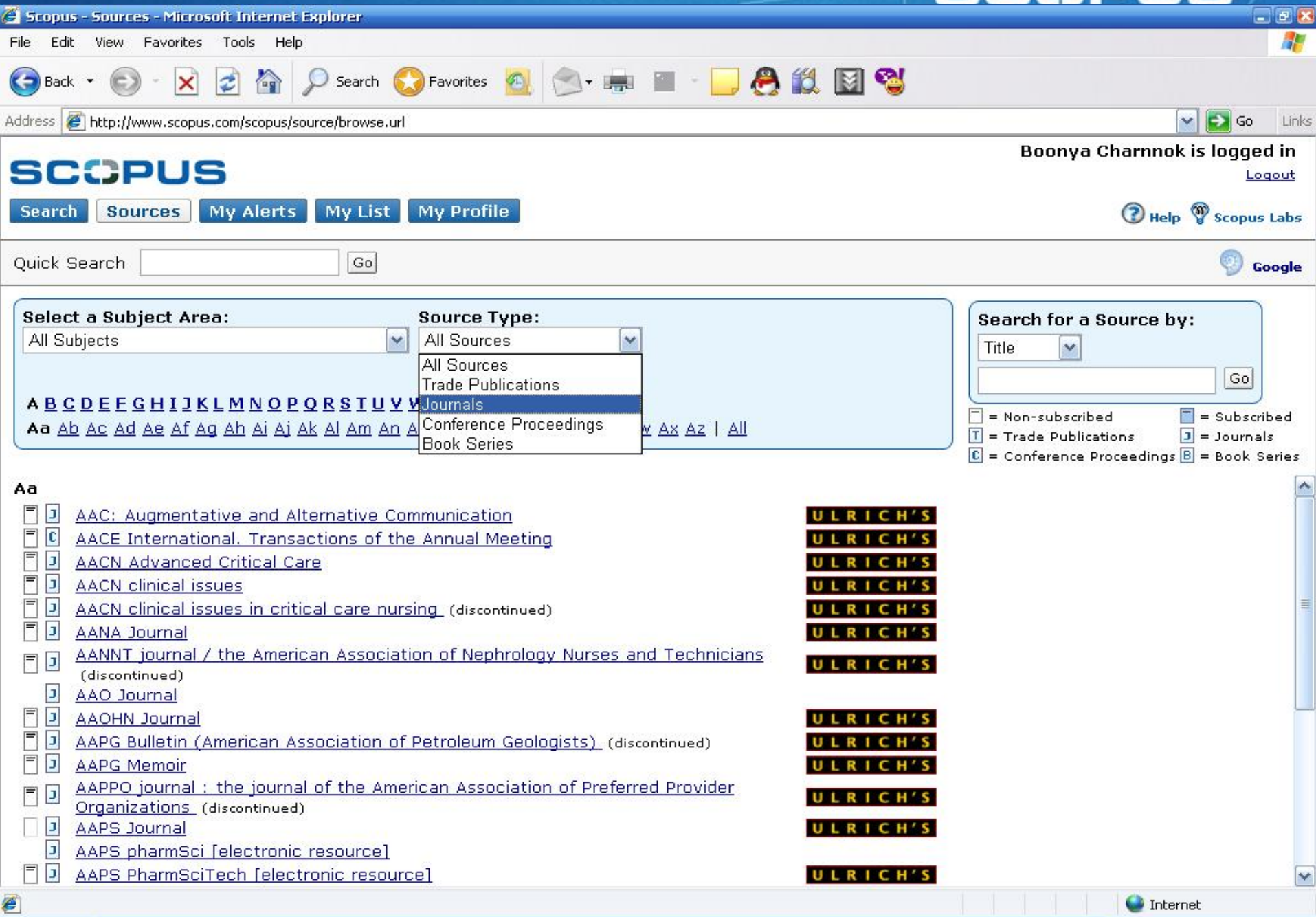

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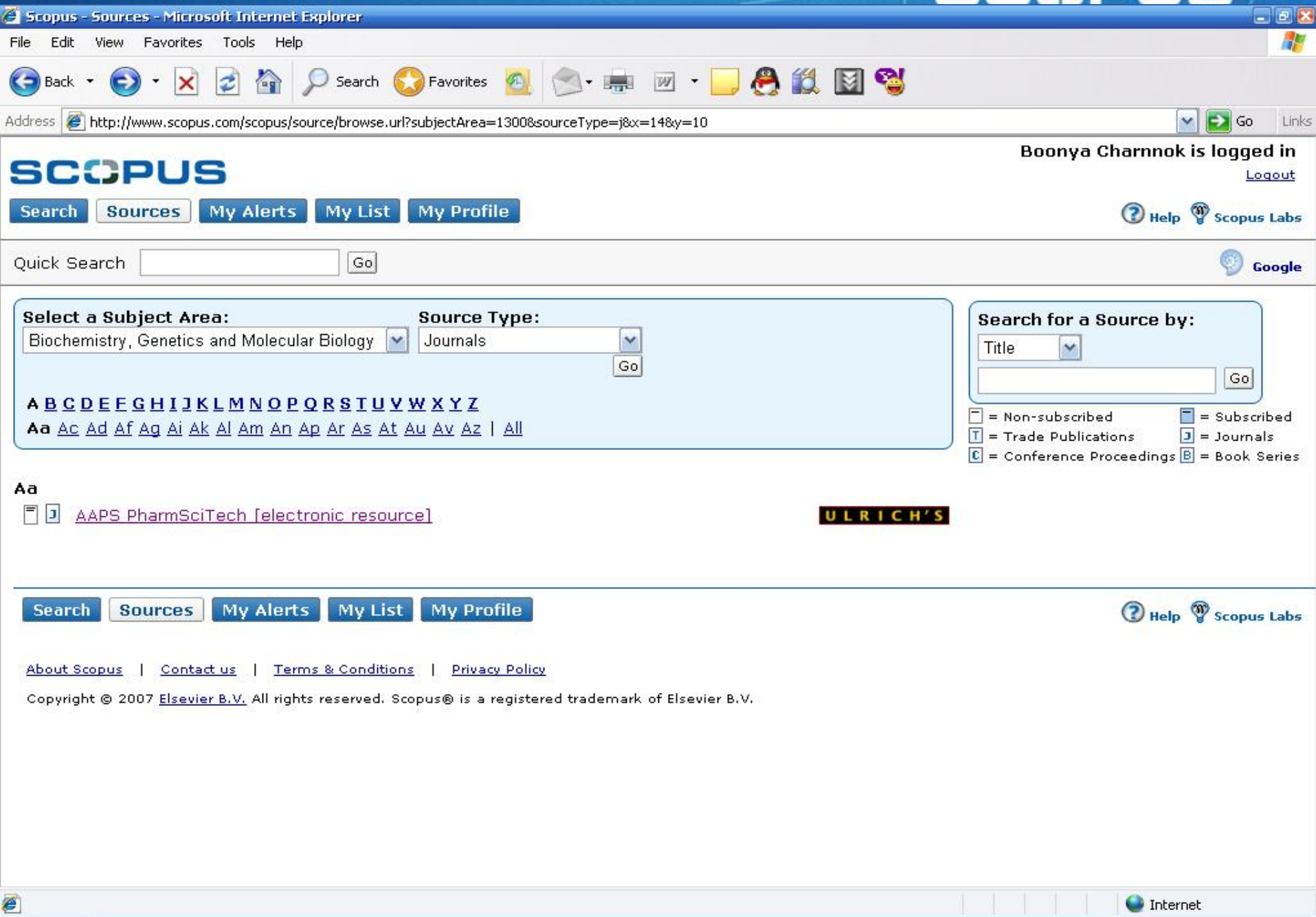

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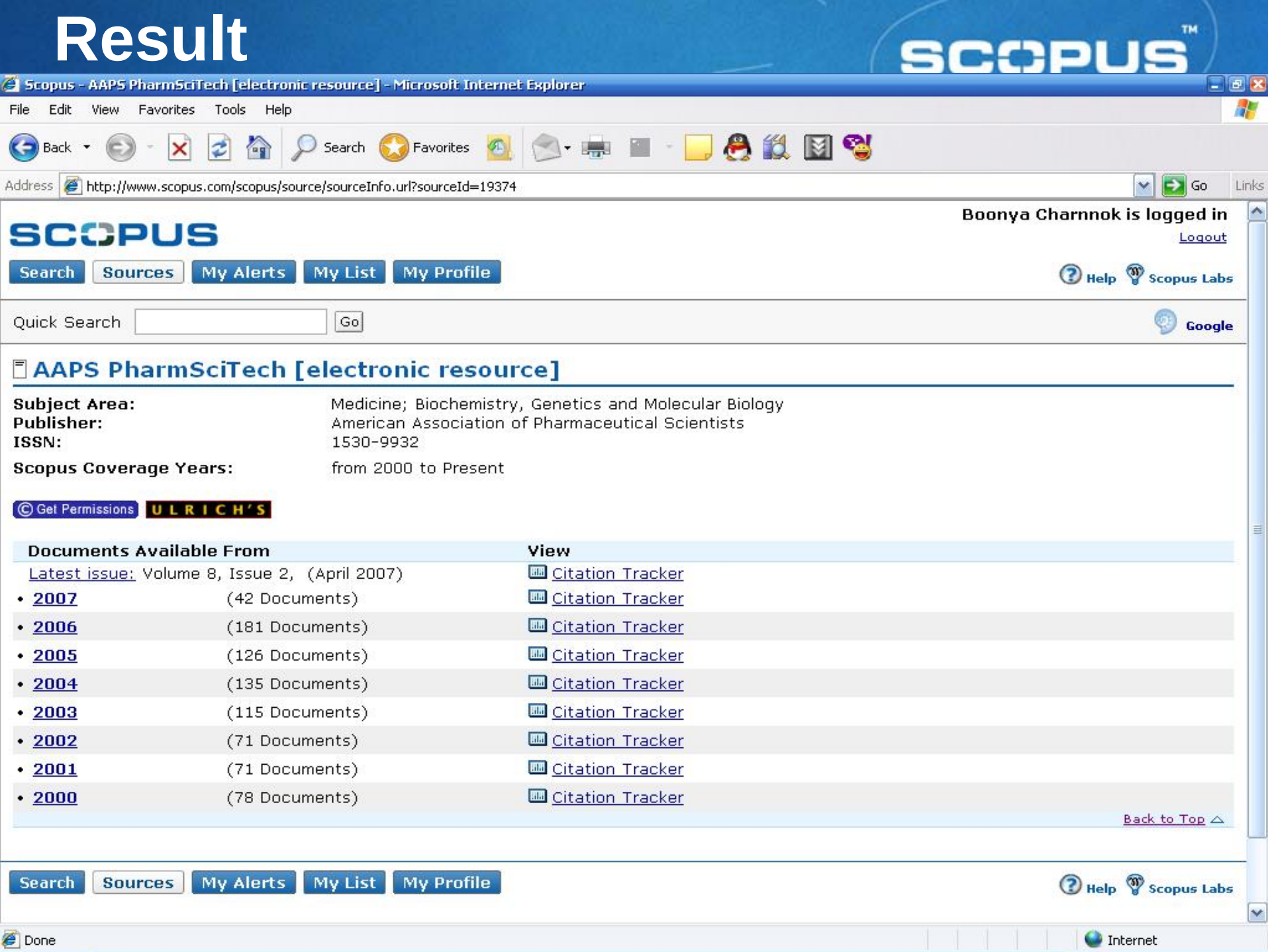
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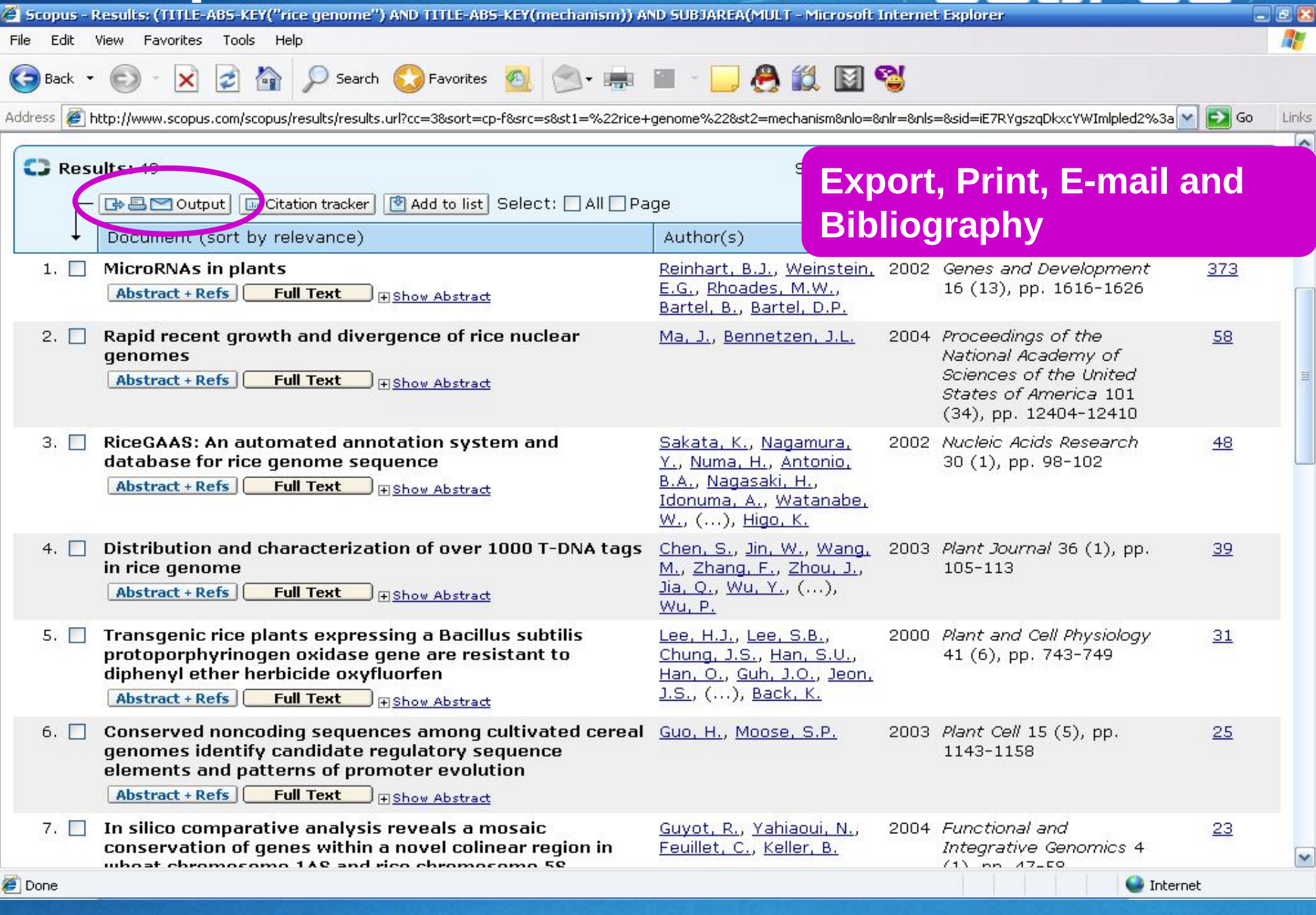
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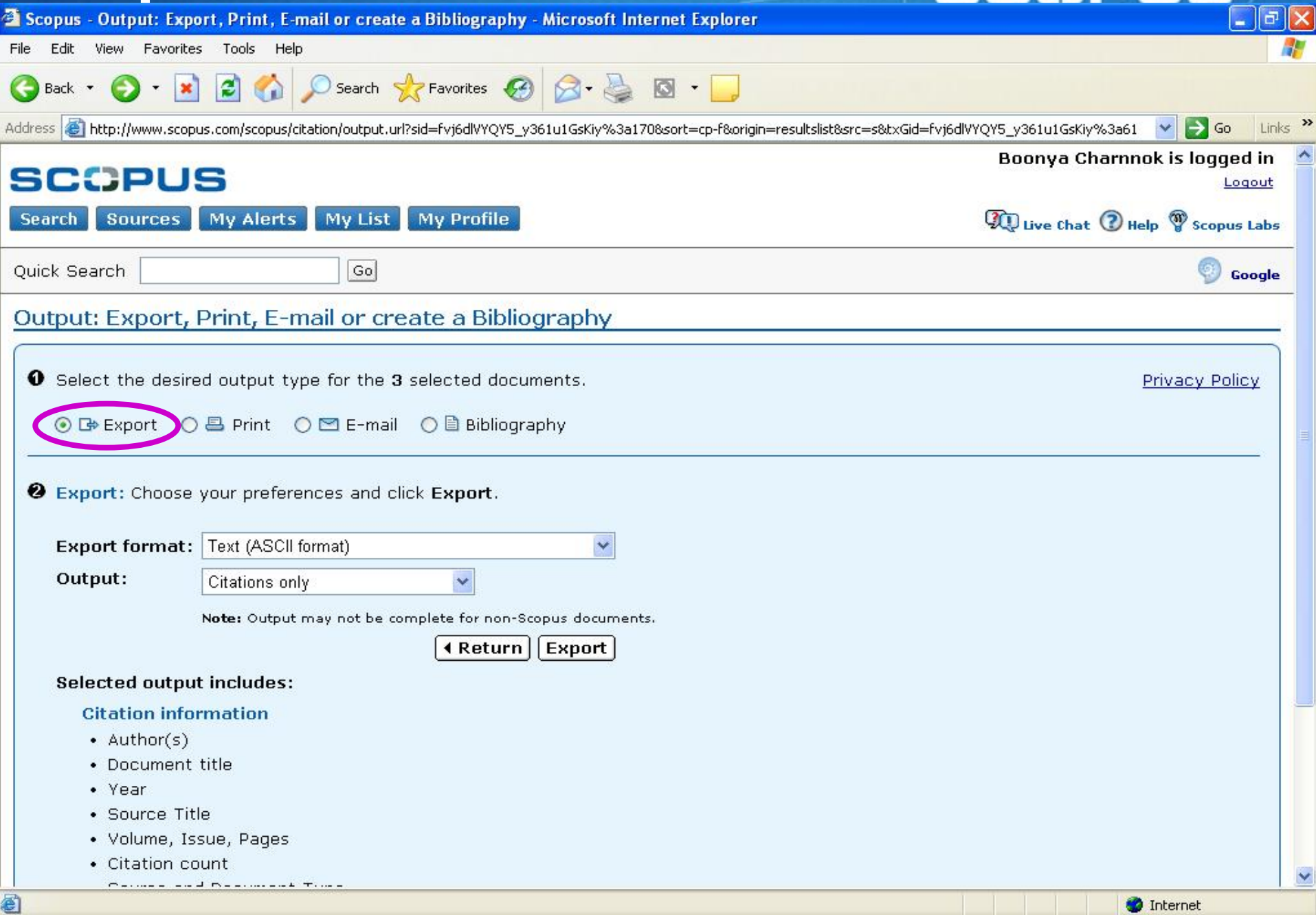
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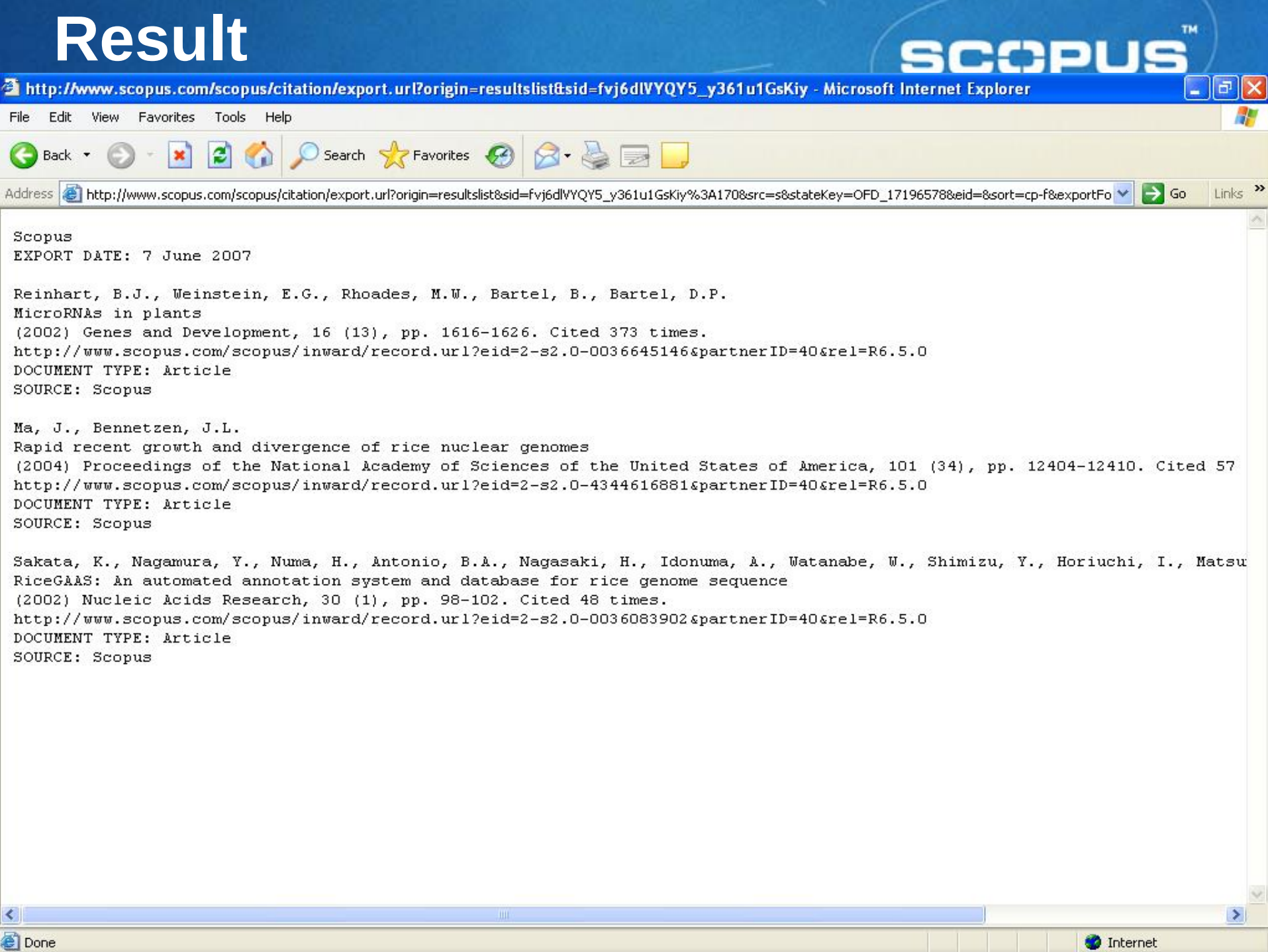
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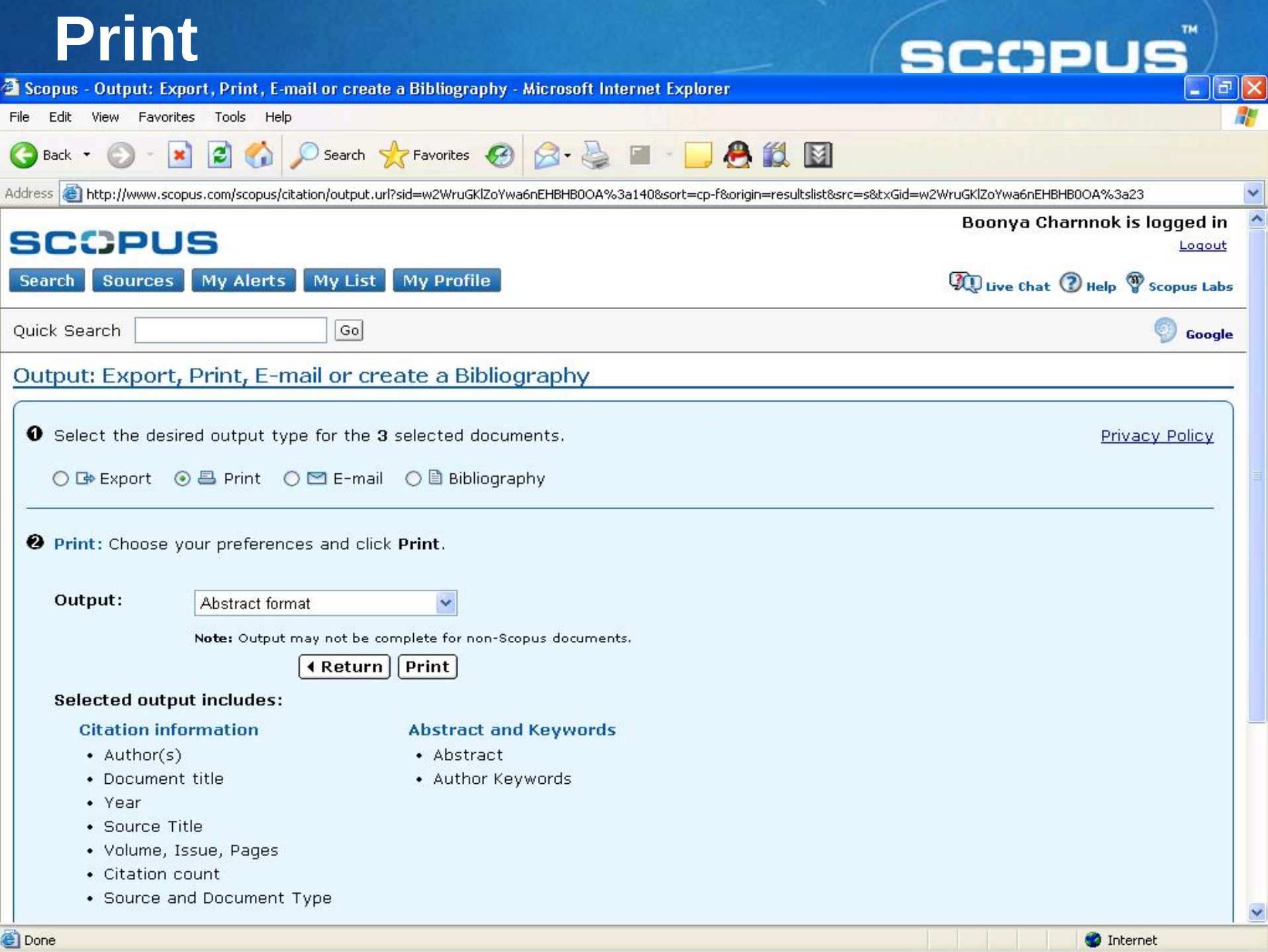
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Whitehead Inst. for Biomed. Research, Department of Biology, Massachusetts Inst. of Technology, Cambridge, MA 02142, United States

Abstract
MicroRNAs (miRNAs) are an extensive class of ~22-nucleotide noncoding RNAs thought to regulate gene expression in metazoans. We find that miRNAs are also present in plants, indicating that this class of noncoding RNA arose early in eukaryotic evolution. In this paper 16 Arabidopsis miRNAs are described, many of which have differential expression patterns in development. Eight are absolutely conserved in the rice genome. The plant miRNA loci potentially encode stem-loop precursors similar to those processed by Dicer (a ribonuclease III) in animals. Mutation of an Arabidopsis Dicer homolog, CARPEL FACTORY, prevents the accumulation of miRNAs, showing that similar mechanisms direct miRNA processing in plants and animals. The previously described roles of CARPEL FACTORY in the development of Arabidopsis embryos, leaves, and floral meristems suggest that the miRNAs could play regulatory roles in the development of plants as well as animals.

Author Keywords
CARPEL FACTORY; Dicer; miRNA; ncRNA; siRNA

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Department of Genetics, University of Georgia, Athens, GA 30602, United States

Abstract
By employing the nuclear DNA of the African rice Oryza glaberrima as a reference genome, the timing, natures, mechanisms, and specificities of recent sequence evolution in the indica and japonica subspecies of Oryza sativa were identified. The data indicate that the genome sizes of both indica and japonica have increased substantially, >2% and >6%, respectively, since their divergence from a common ancestor, mainly because of the amplification of LTR-retrotransposons. However, losses of all classes of DNA sequence through unequal homologous recombination and illegitimate recombination have attenuated the growth of the rice genome. Small deletions have been particularly frequent throughout the

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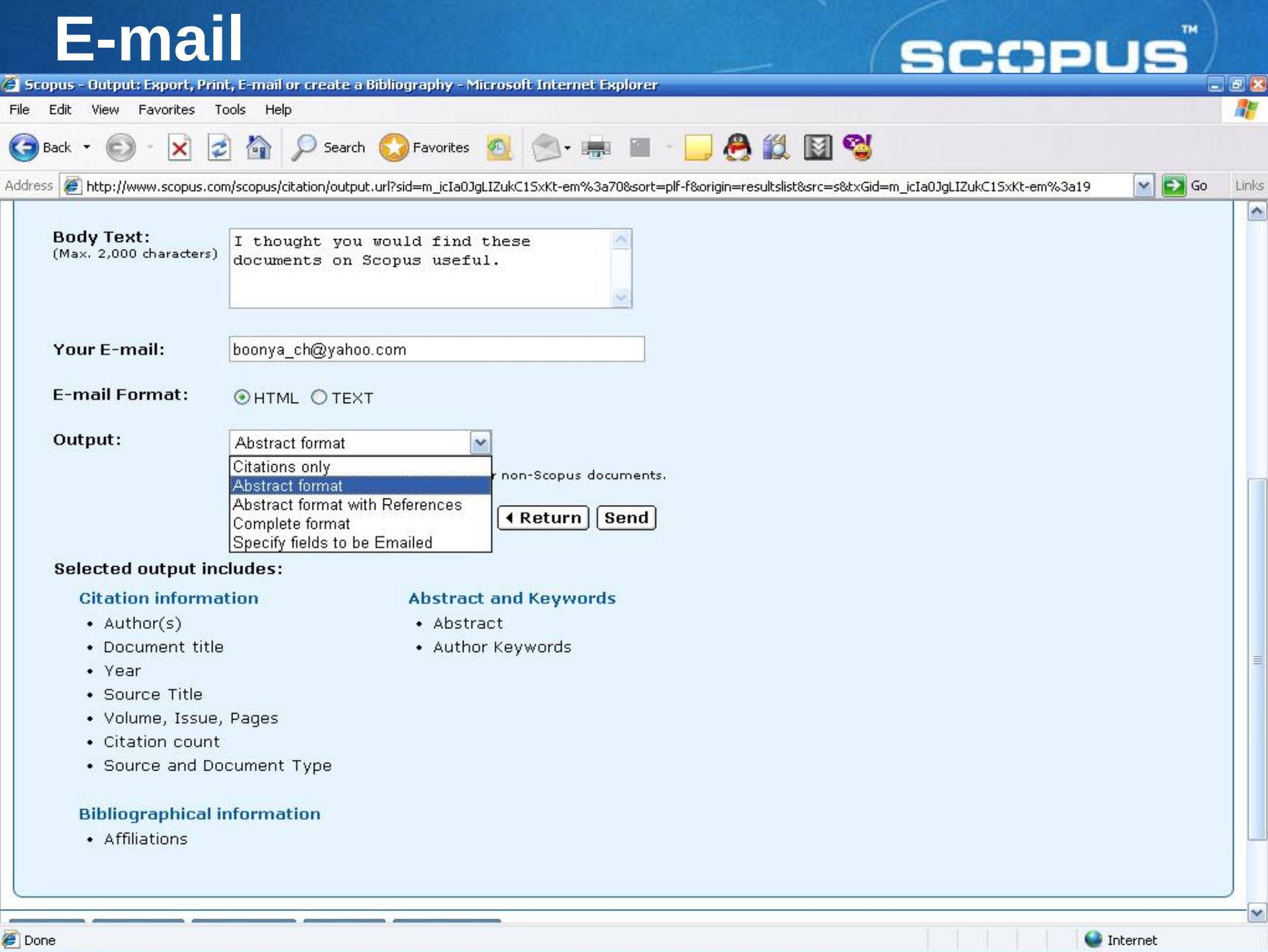
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Abstract
Cyclins, cyclin-dependent kinases, and a number of other proteins control the progression of plant cell cycle. Although extensive studies have revealed the roles of some cell cycle regulators and the underlying mechanisms in Arabidopsis, relatively a small number of cell cycle regulators were functionally analyzed in rice. In this study, we describe 41 regulators in the rice genome. Our results indicate that the rice genome contains a less number of the core cell cycle regulators than the Arabidopsis one does, although the rice genome is much larger than the Arabidopsis one. Eight groups of CDKs similar to those in Arabidopsis were identified in the rice genome through phylogenetic analysis, and the corresponding members in the different groups include E2F, CKI, Rb, CKS and Wee. The structures of the core cell regulators were relatively conserved between the rice and Arabidopsis genomes. Furthermore, the expression of the majority of the core cell cycle genes was spatially regulated, and the most closely related ones showed very similar patterns of expression, suggesting functional redundancy and conservation between the highly similar core cell cycle genes in rice and Arabidopsis. Following auxin or cytokinin treatment, the expression of the core cell cycle genes was either upregulated or downregulated, suggesting that auxin and/or cytokinin may directly regulate the expression of the core cell cycle genes. Our results provide basic information to understand the mechanism of cell cycle regulation and the functions of the rice cell cycle genes. © 2007 Springer Science+Business Media B.V.

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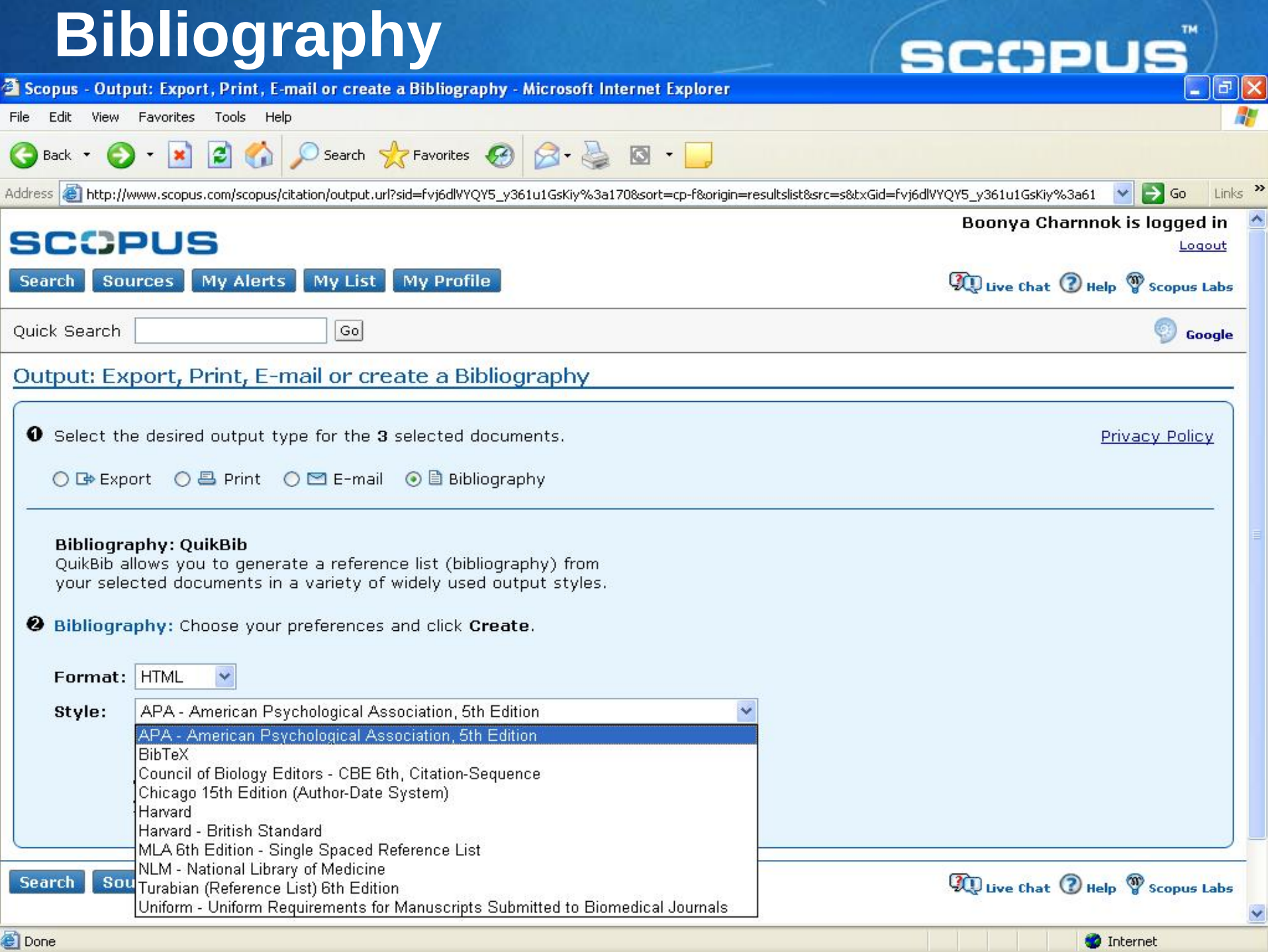

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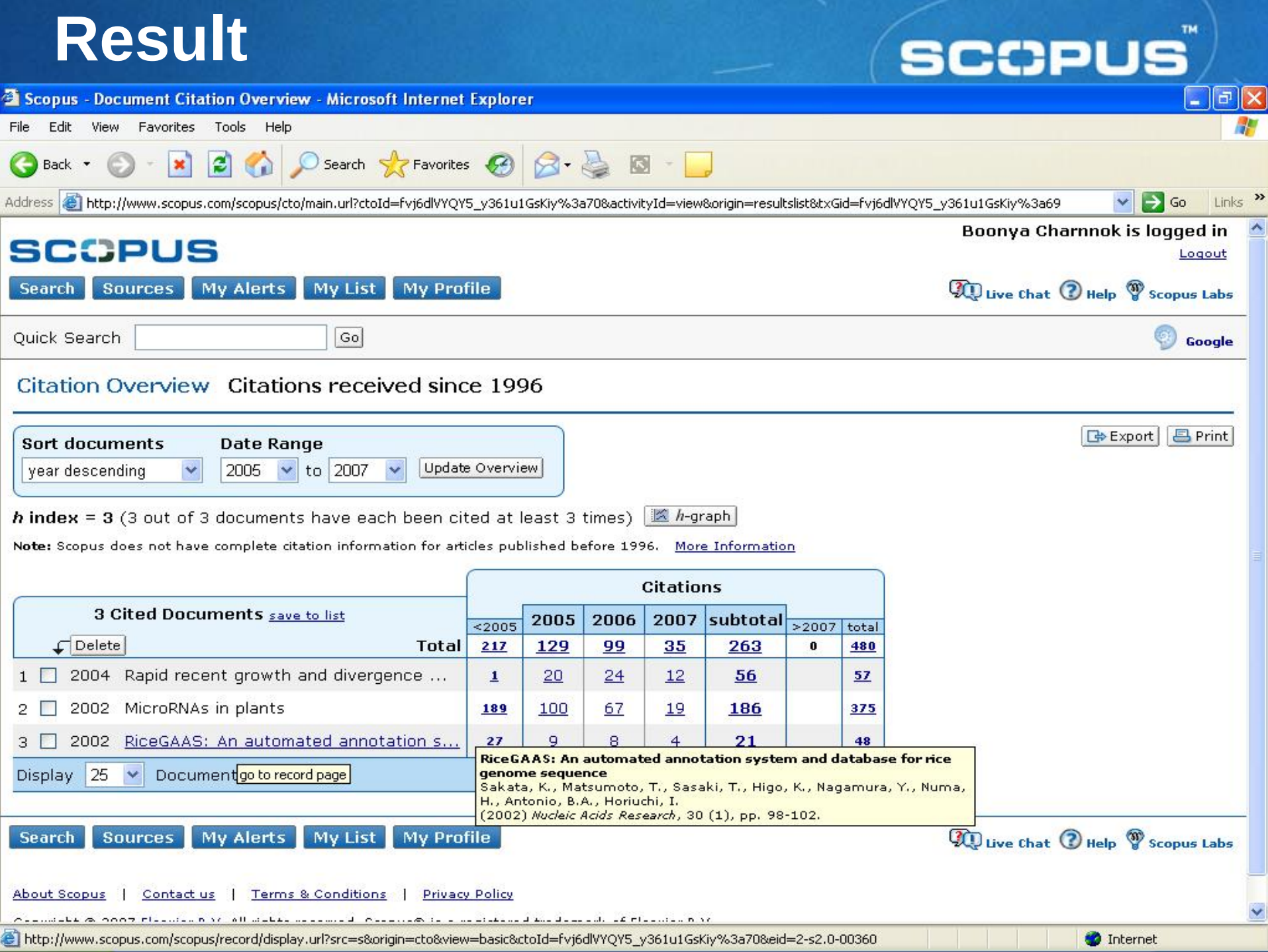
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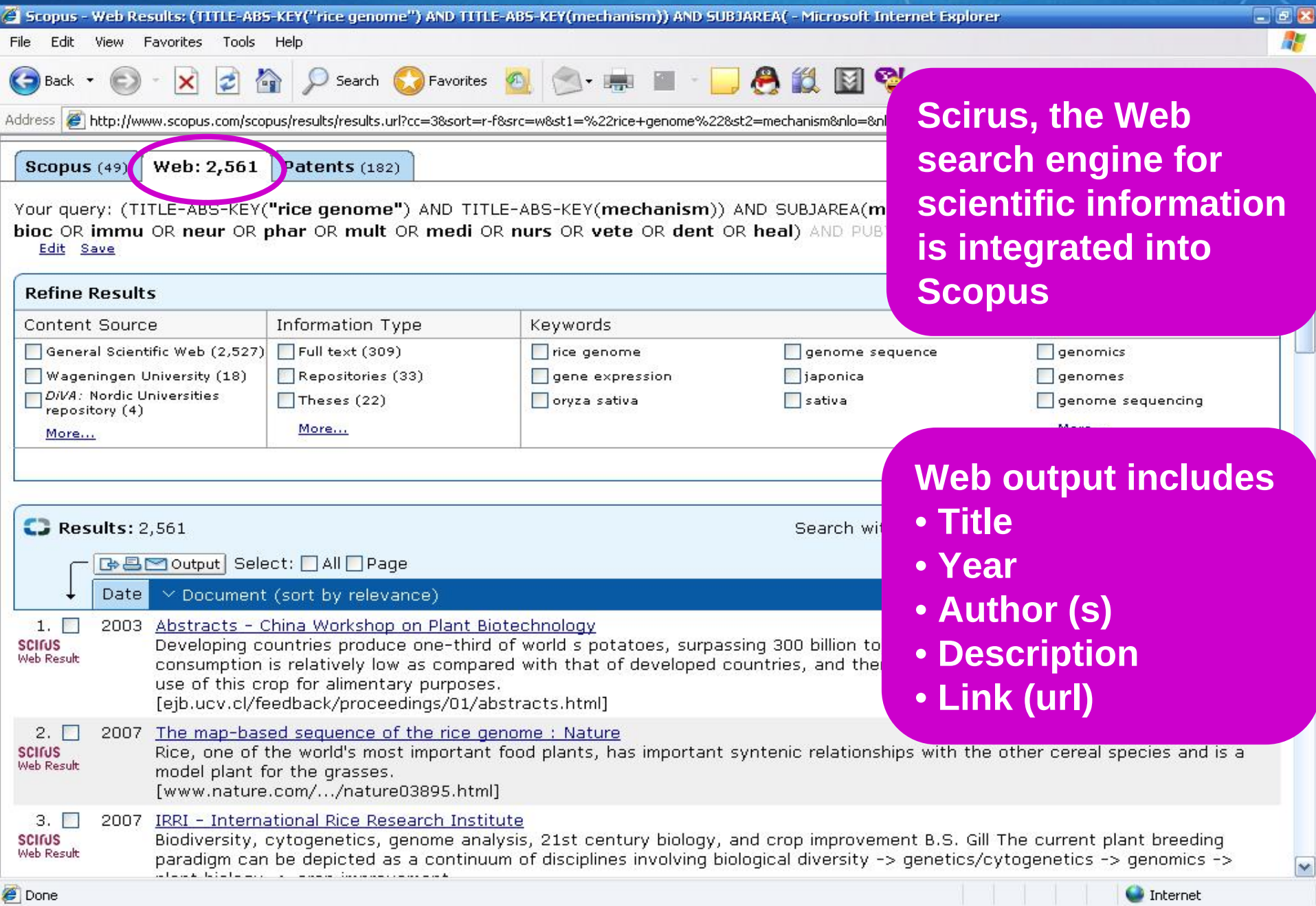

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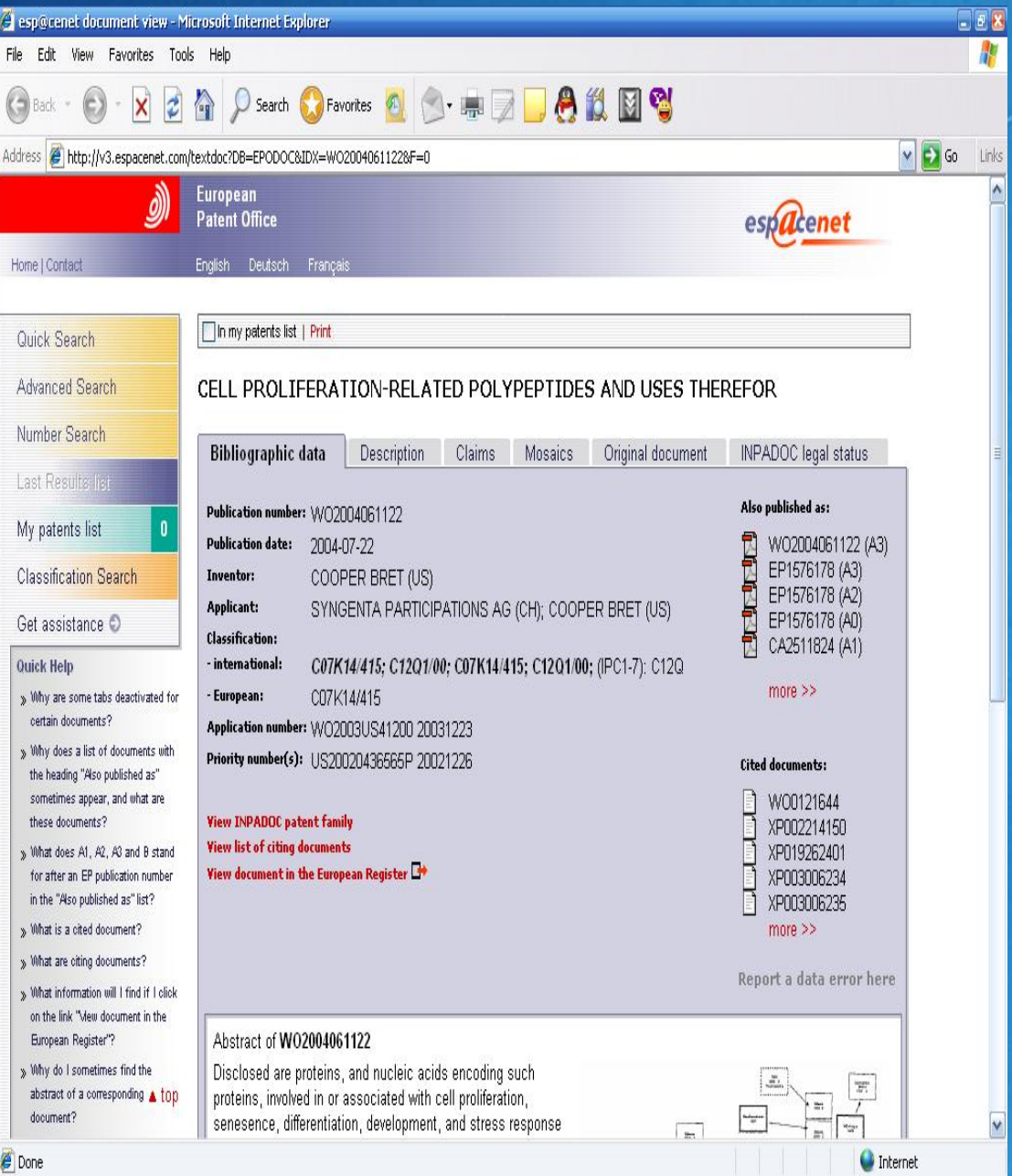

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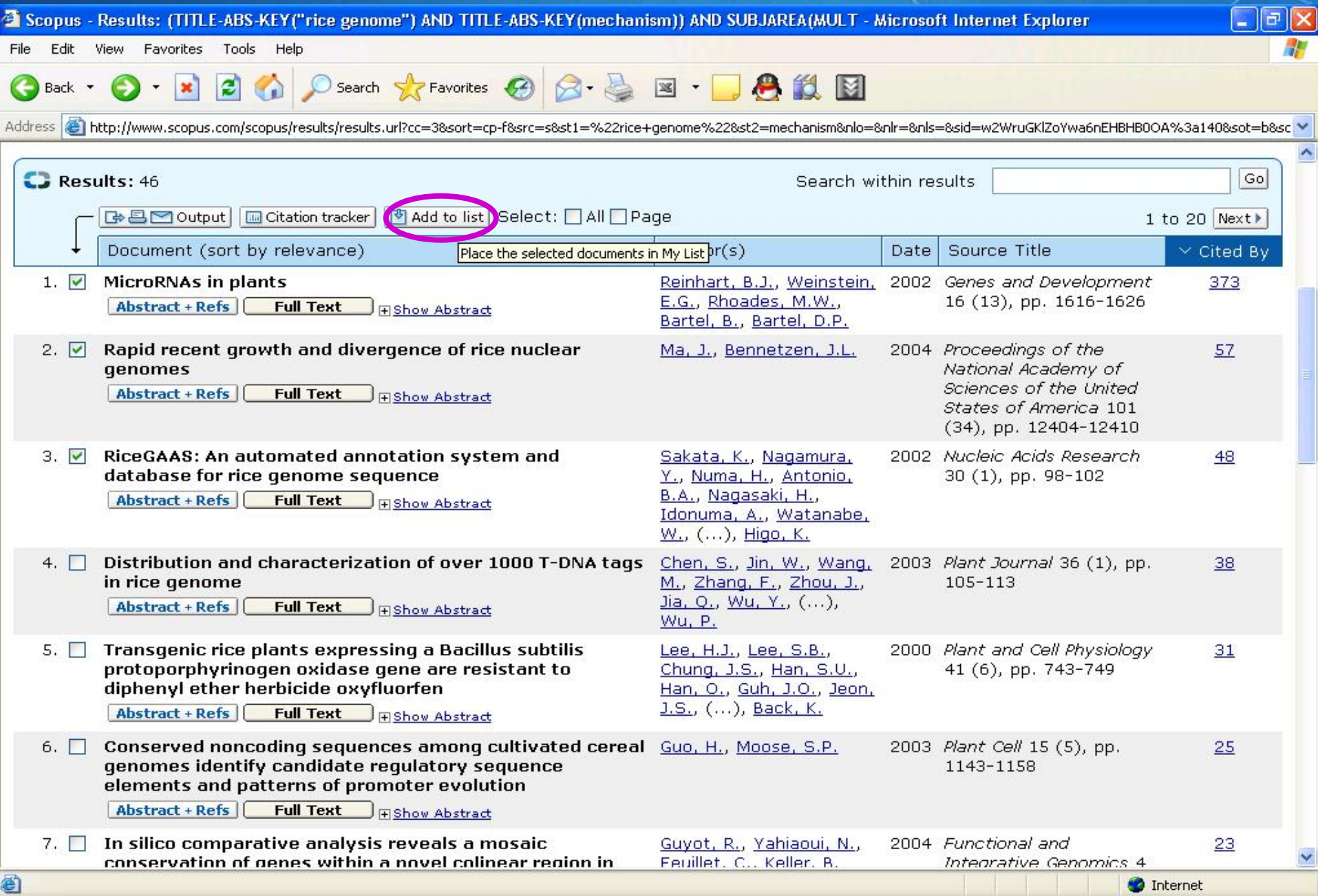
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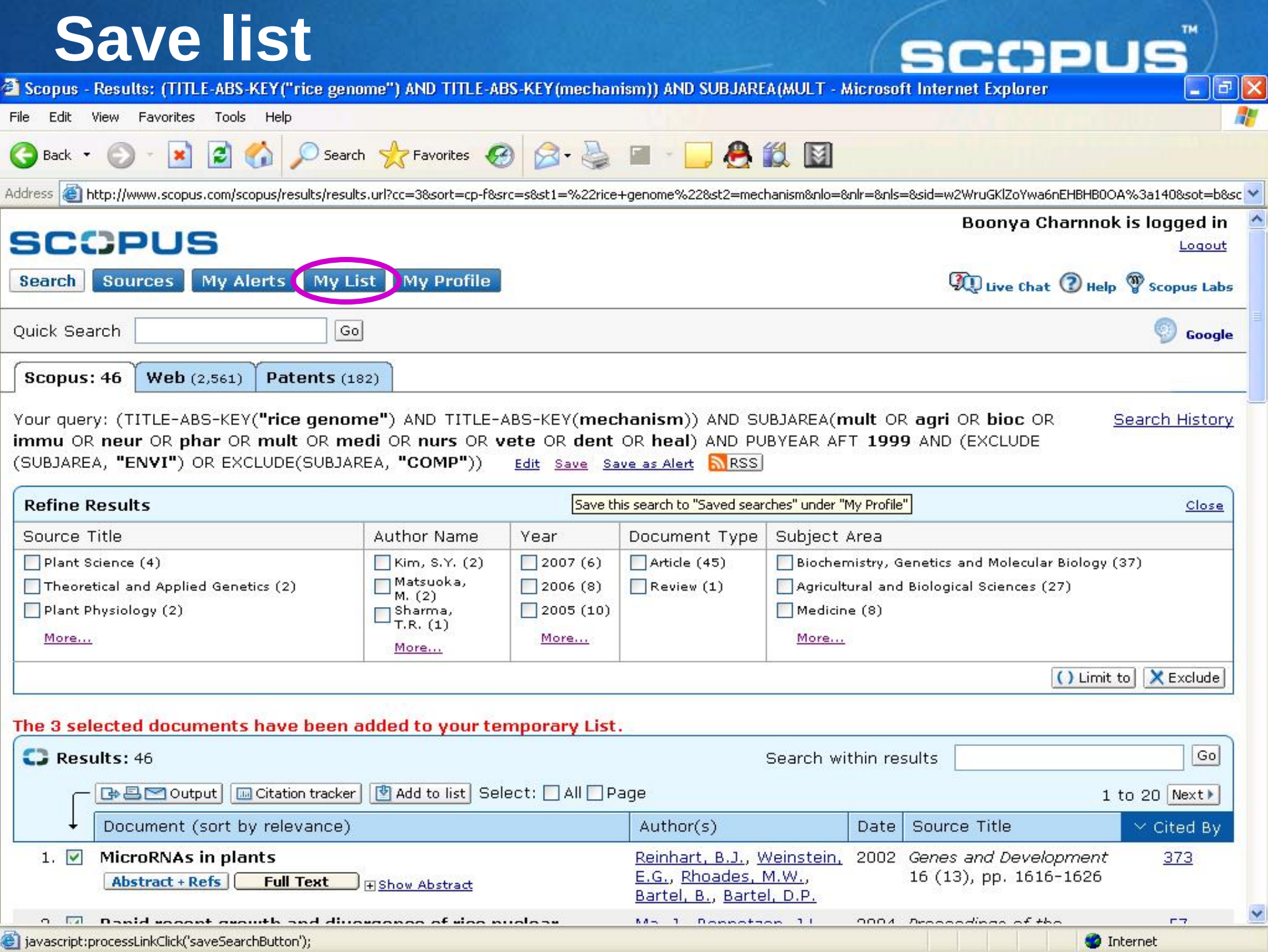
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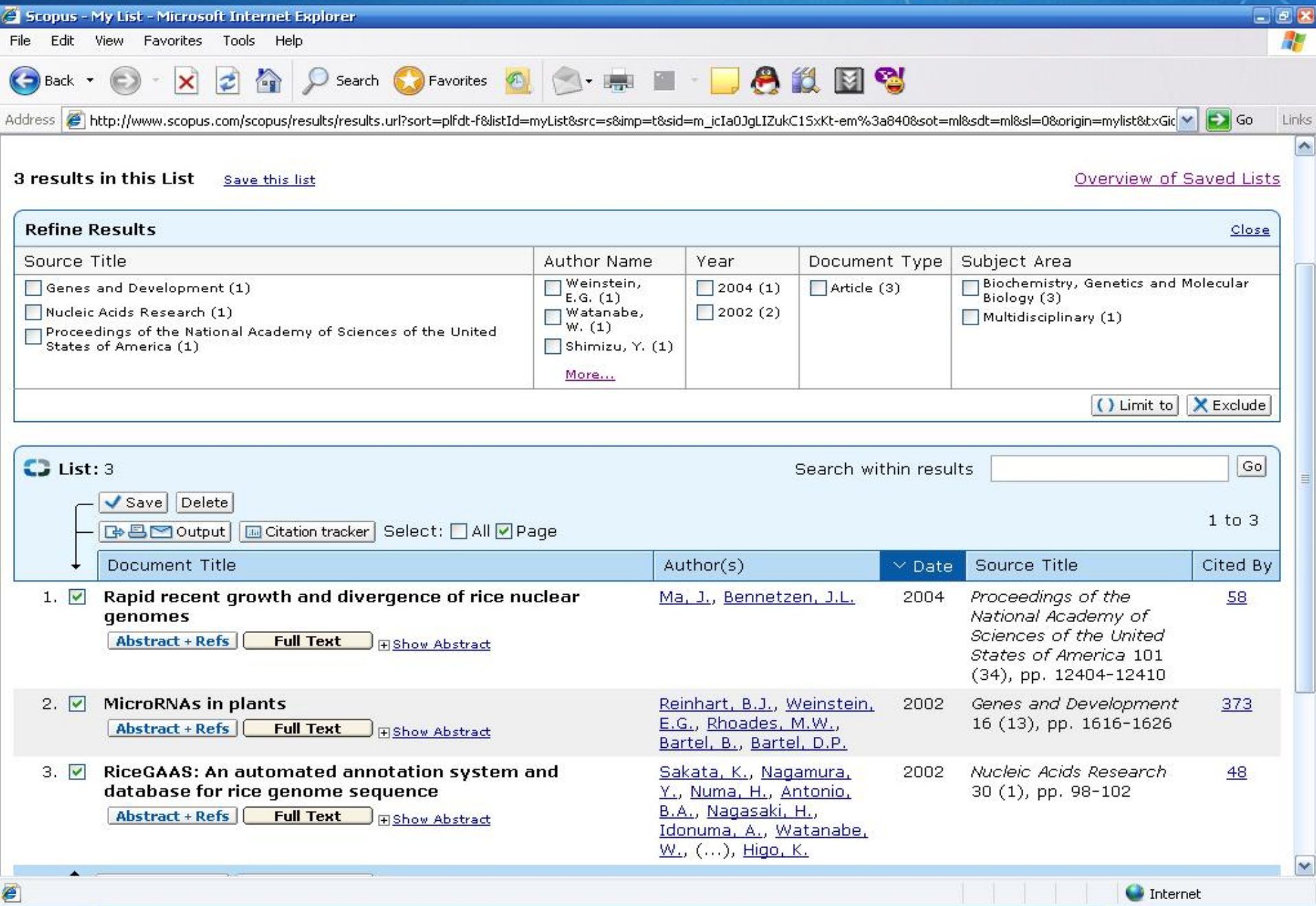
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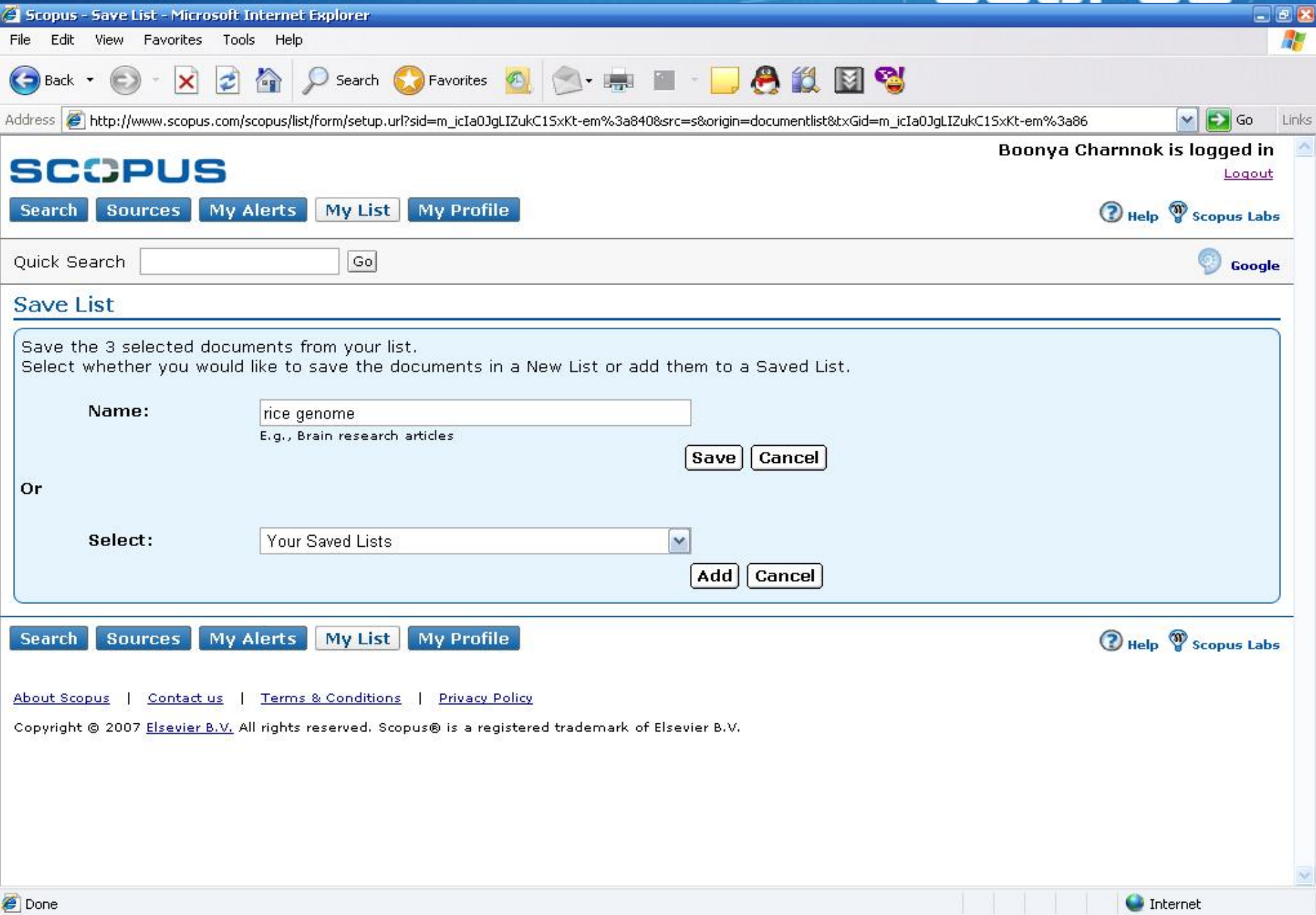
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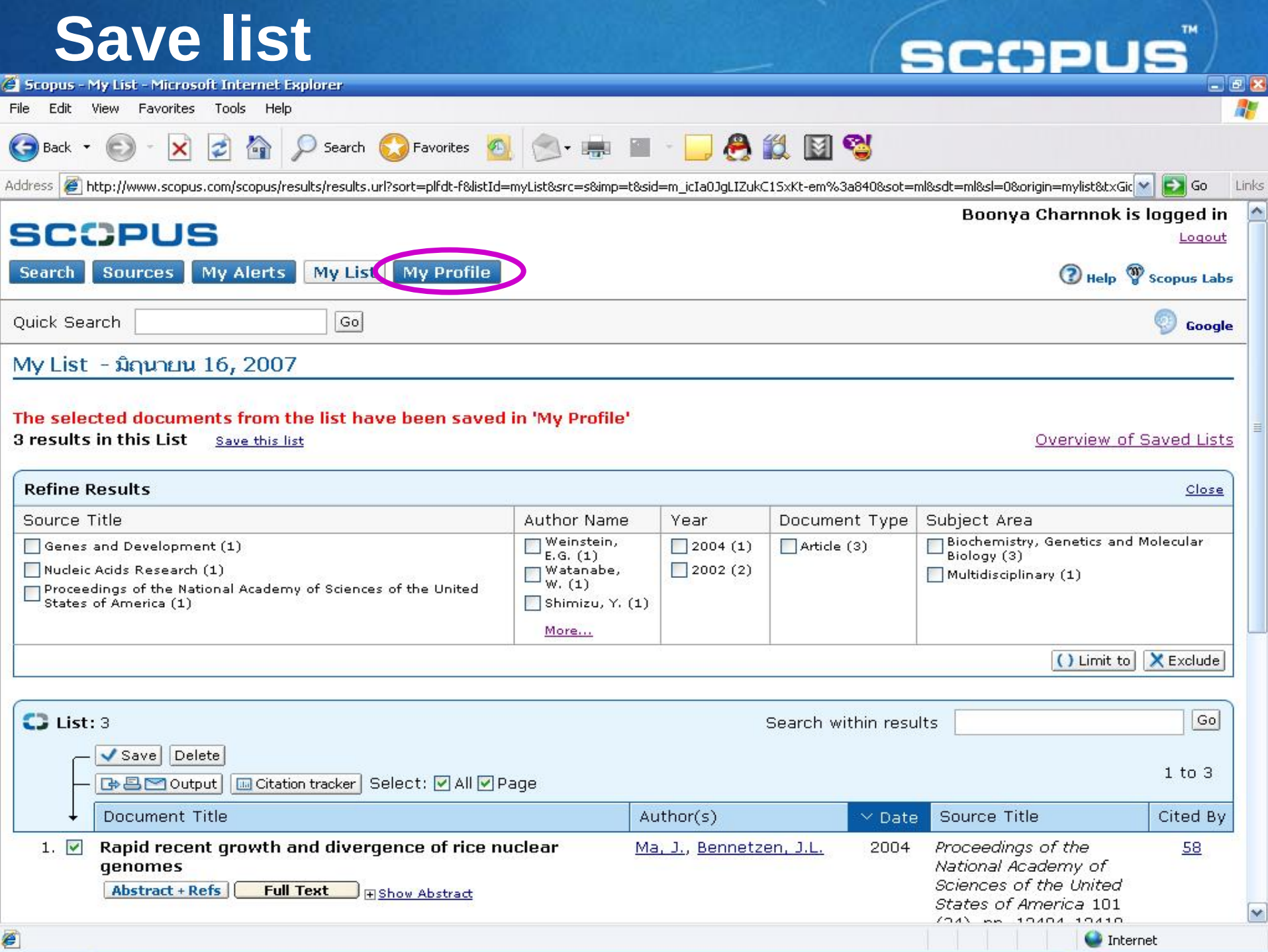
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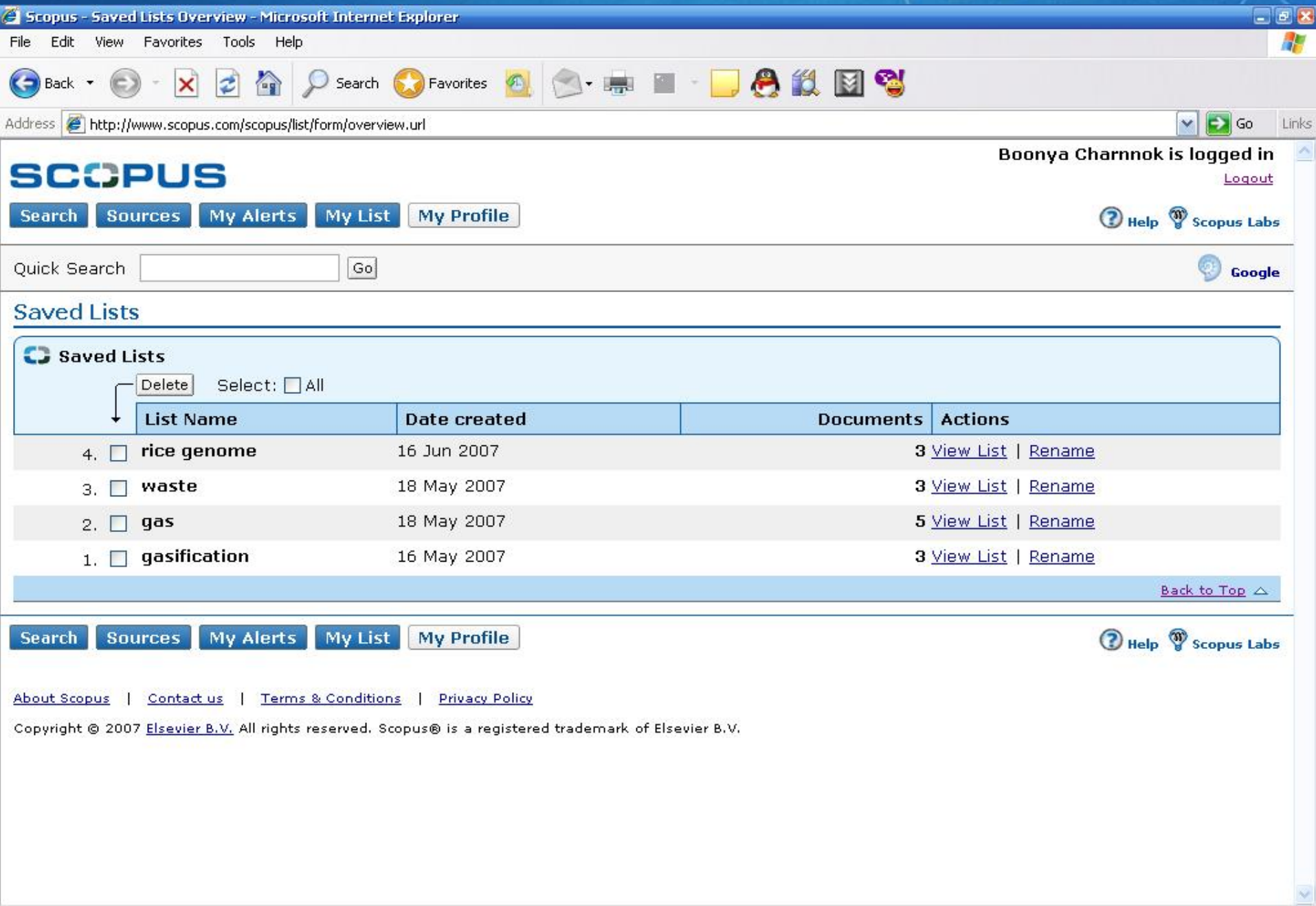
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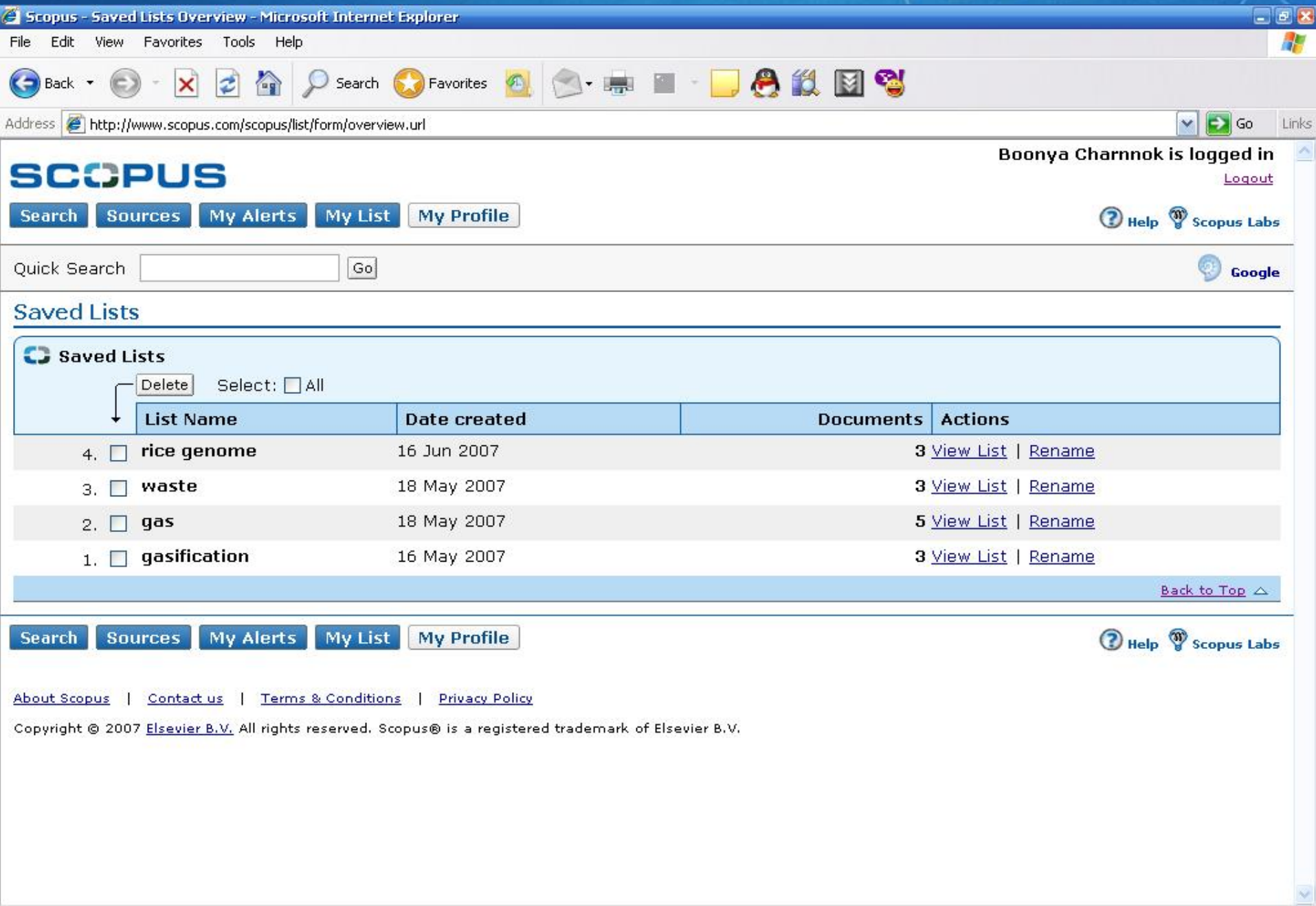
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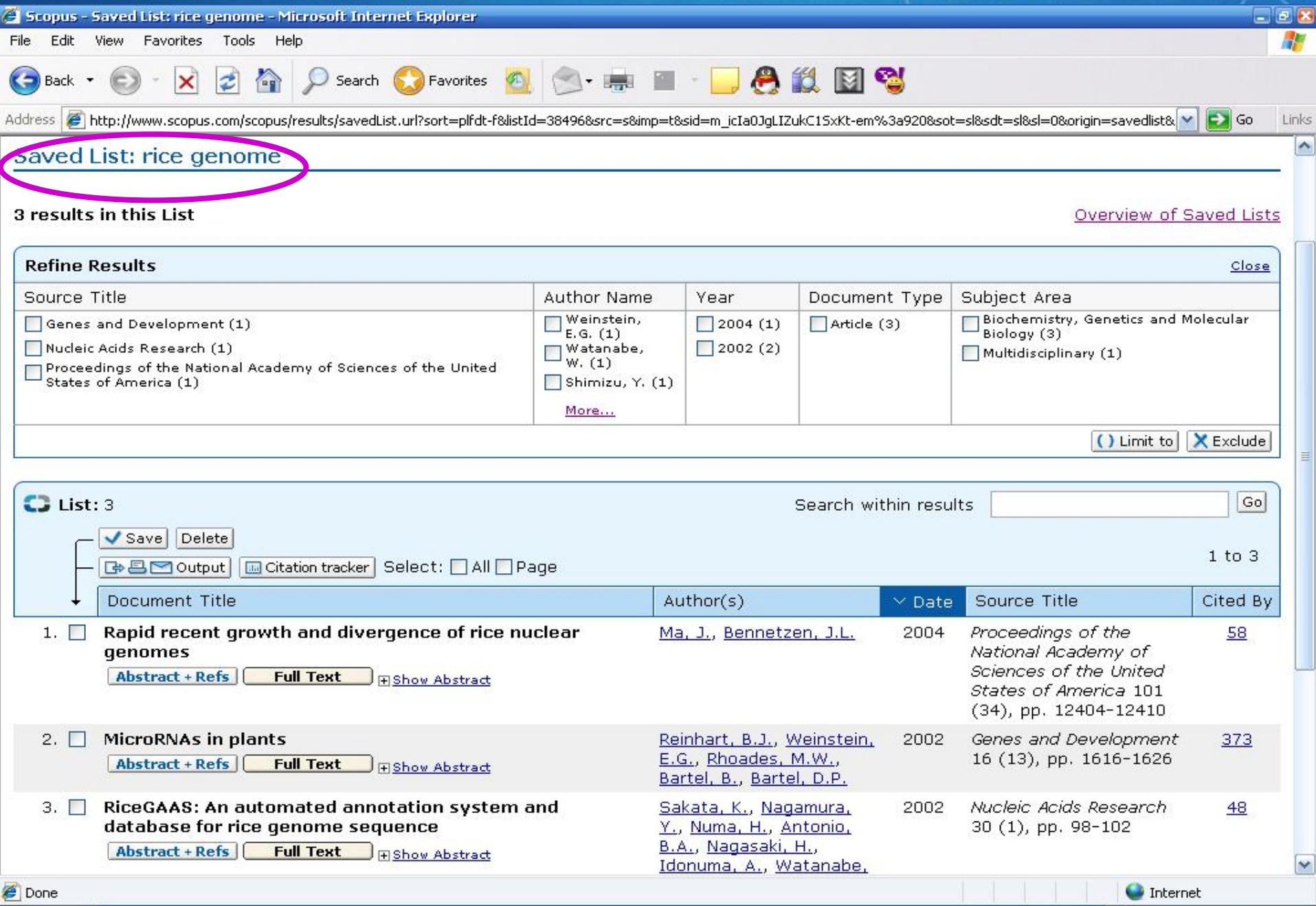
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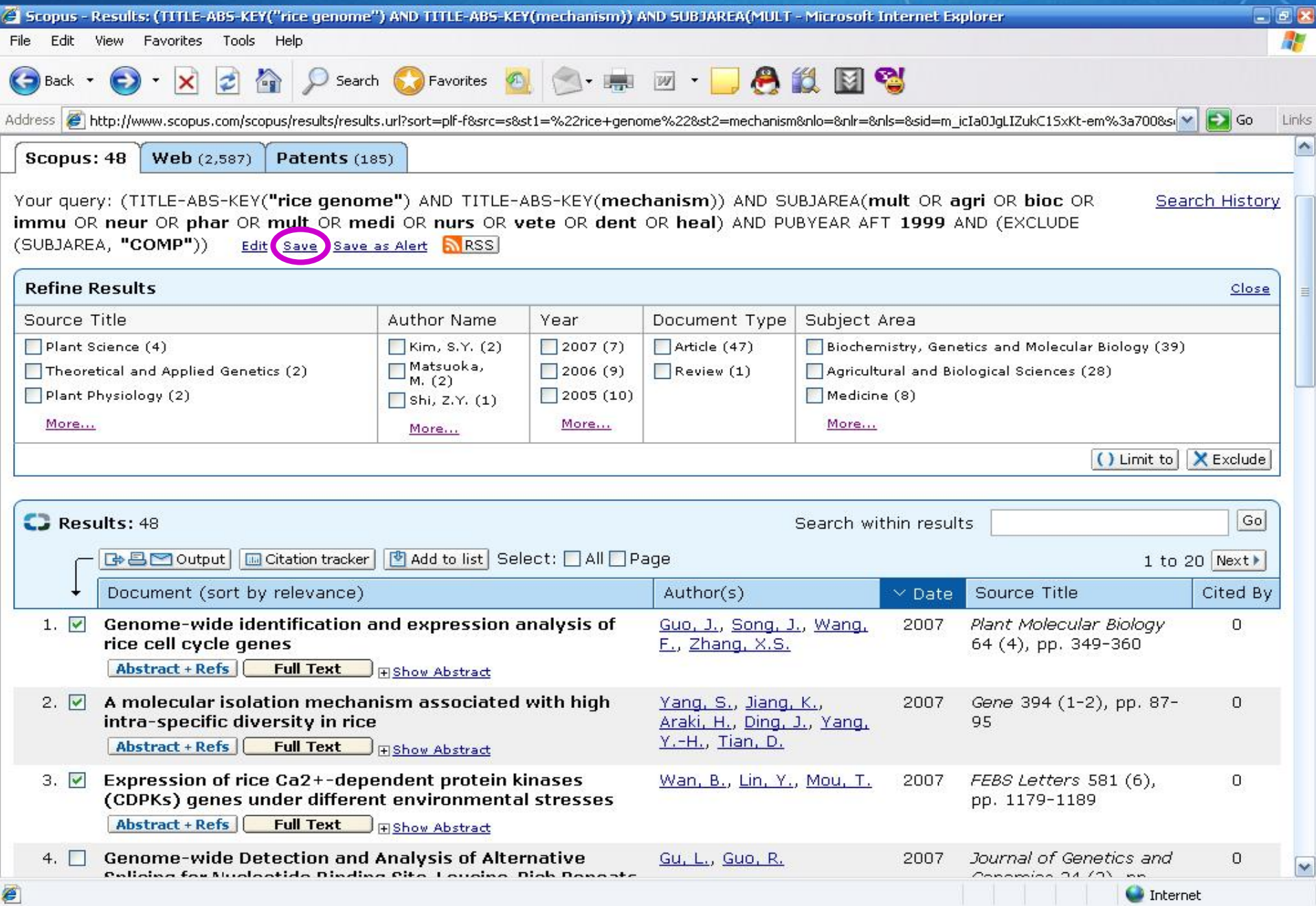
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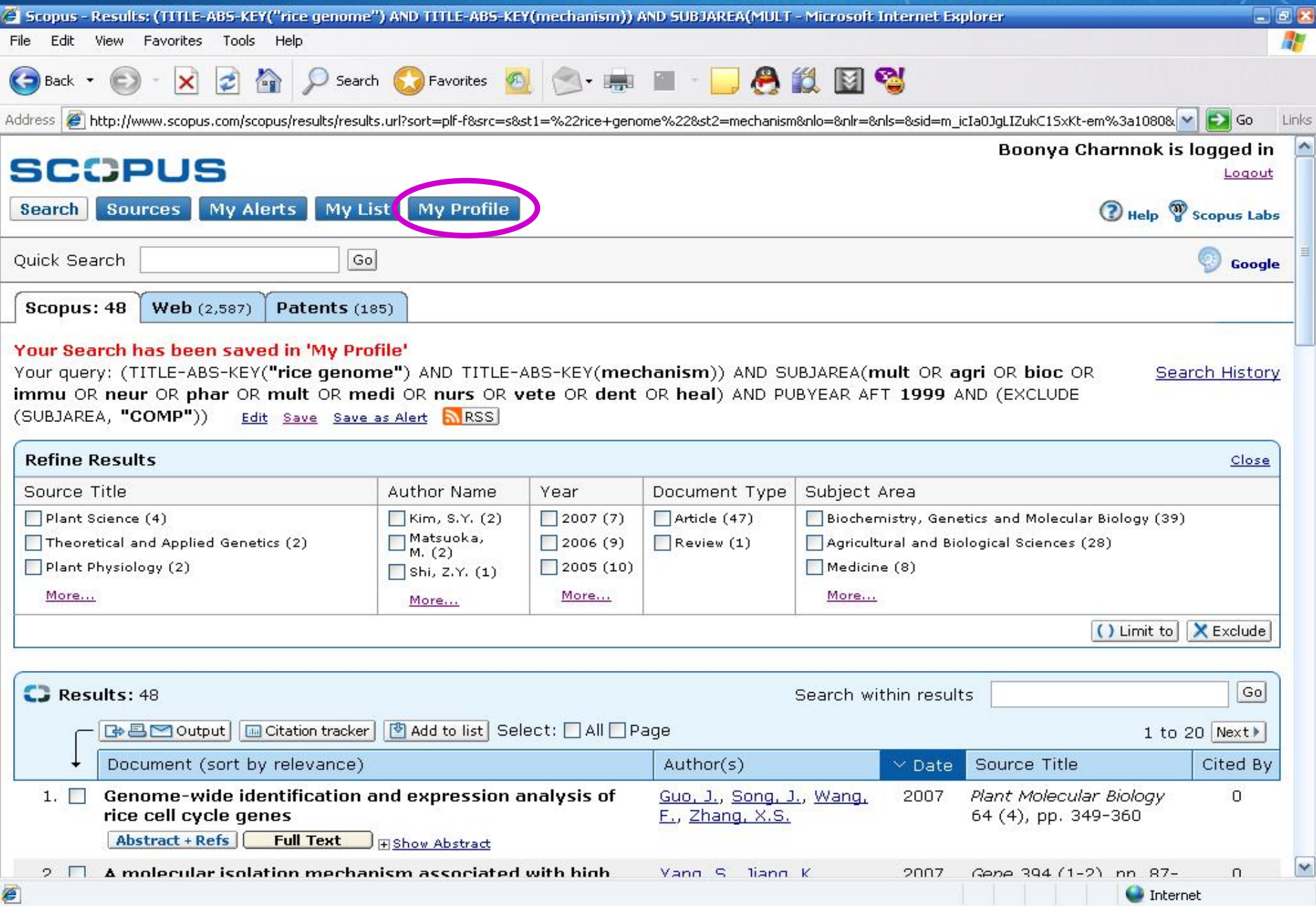
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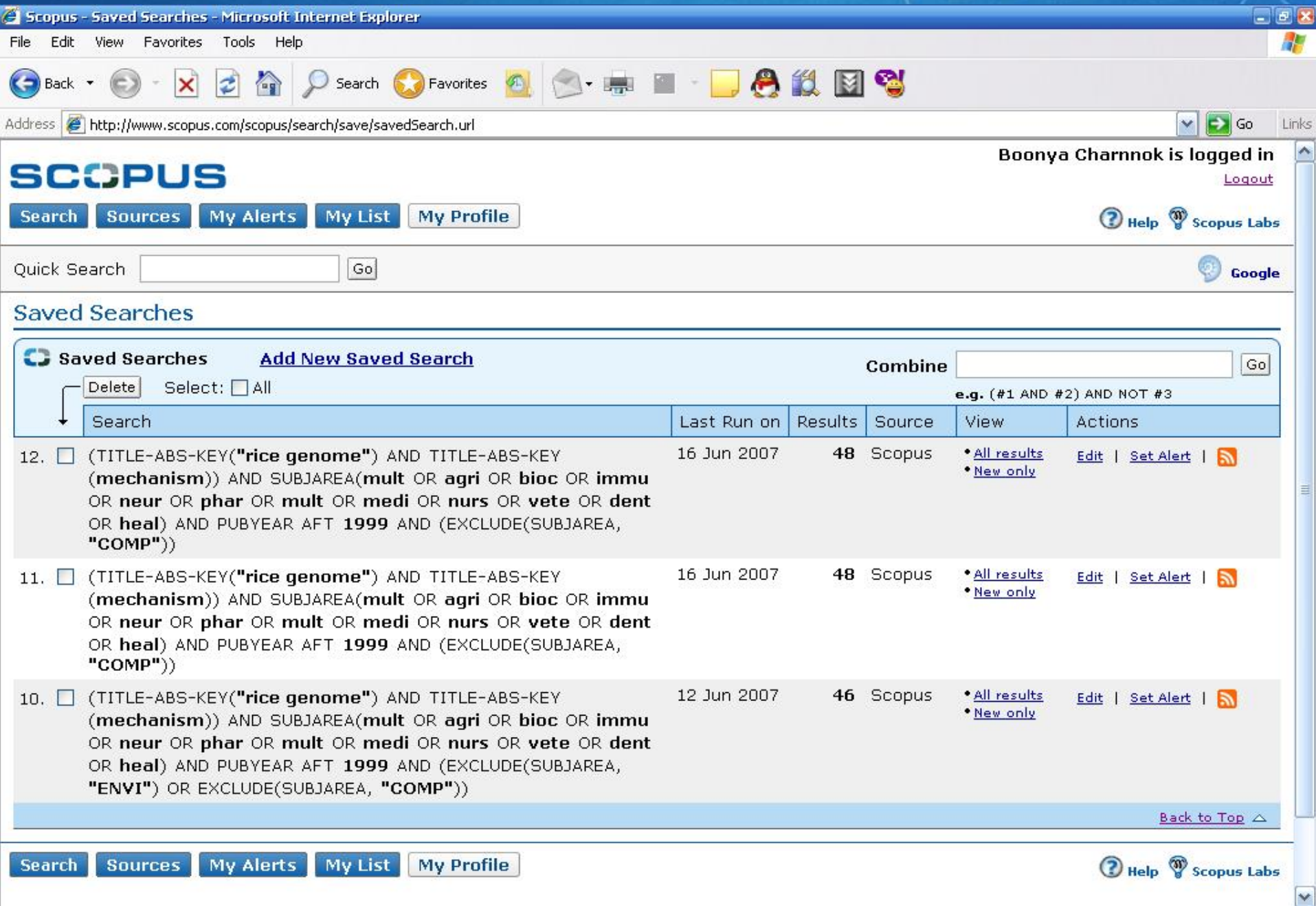
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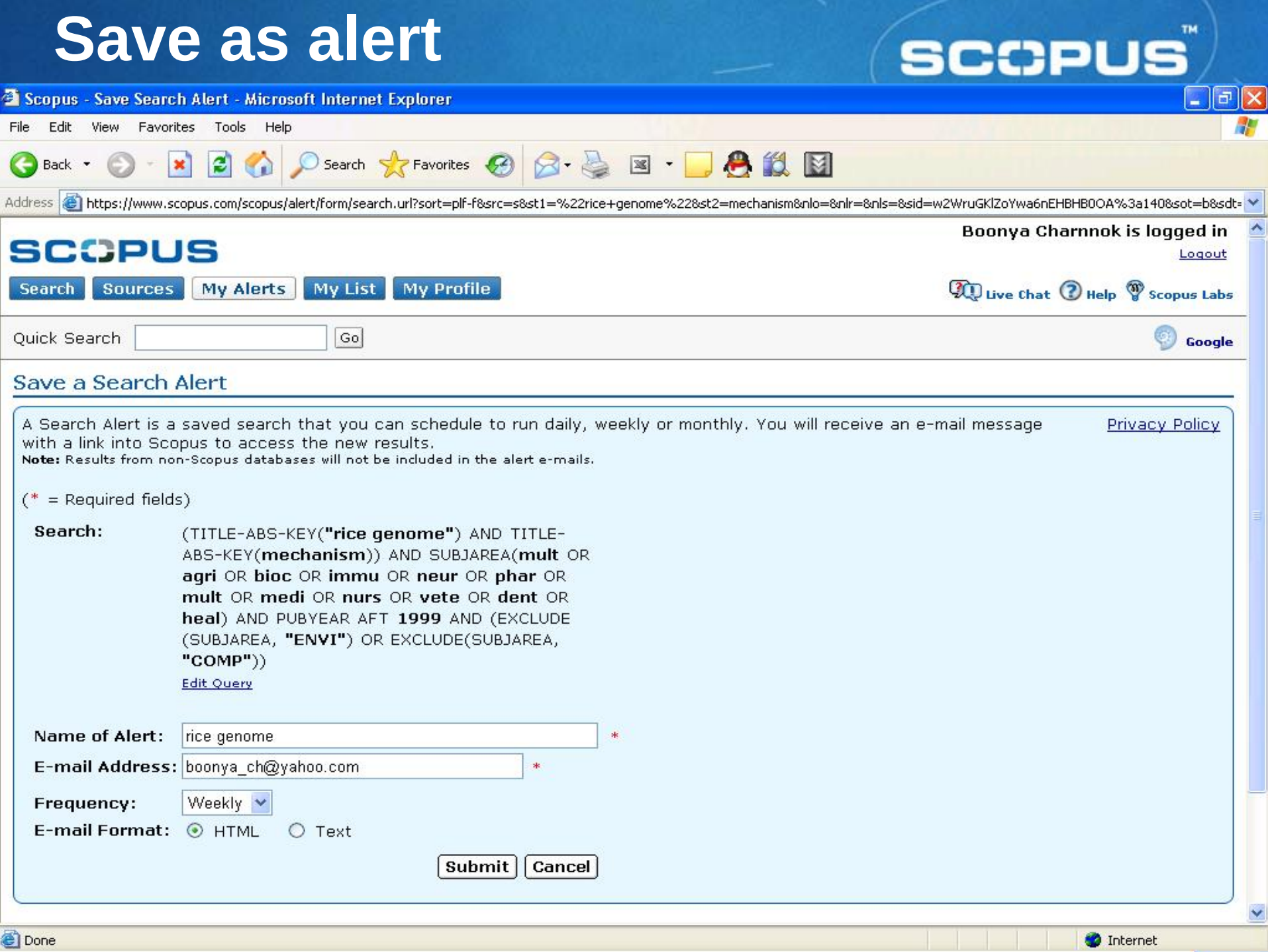

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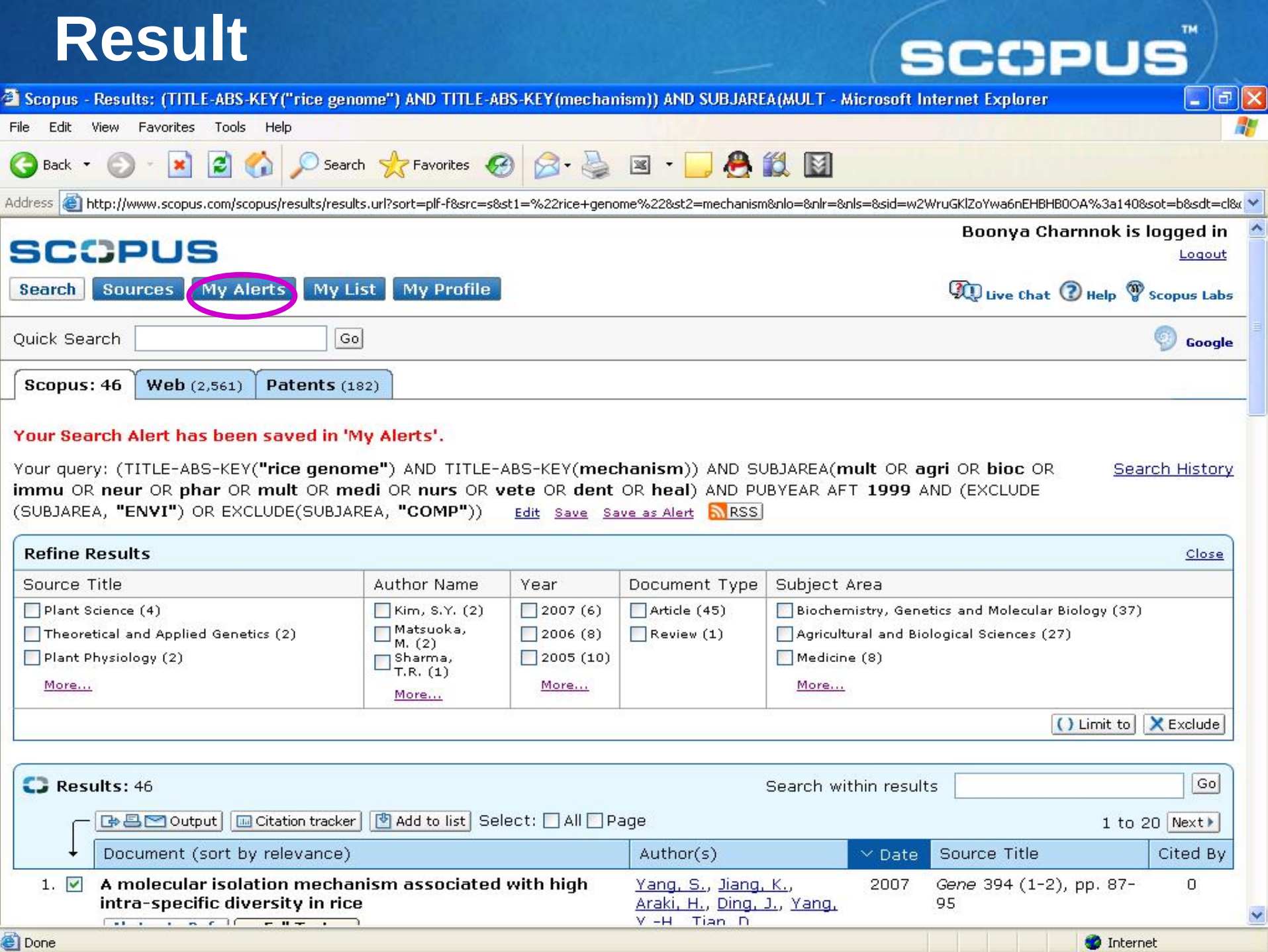
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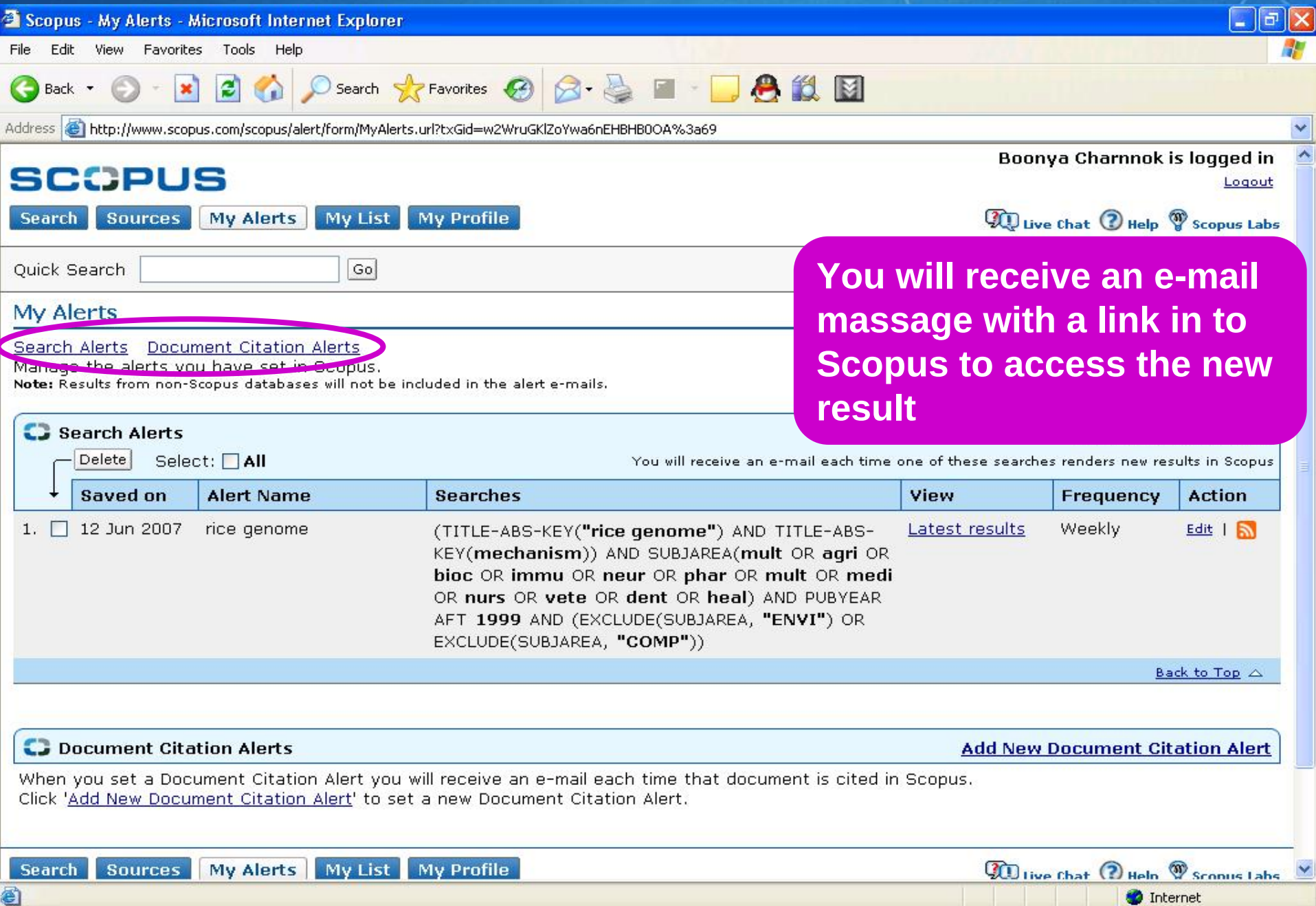

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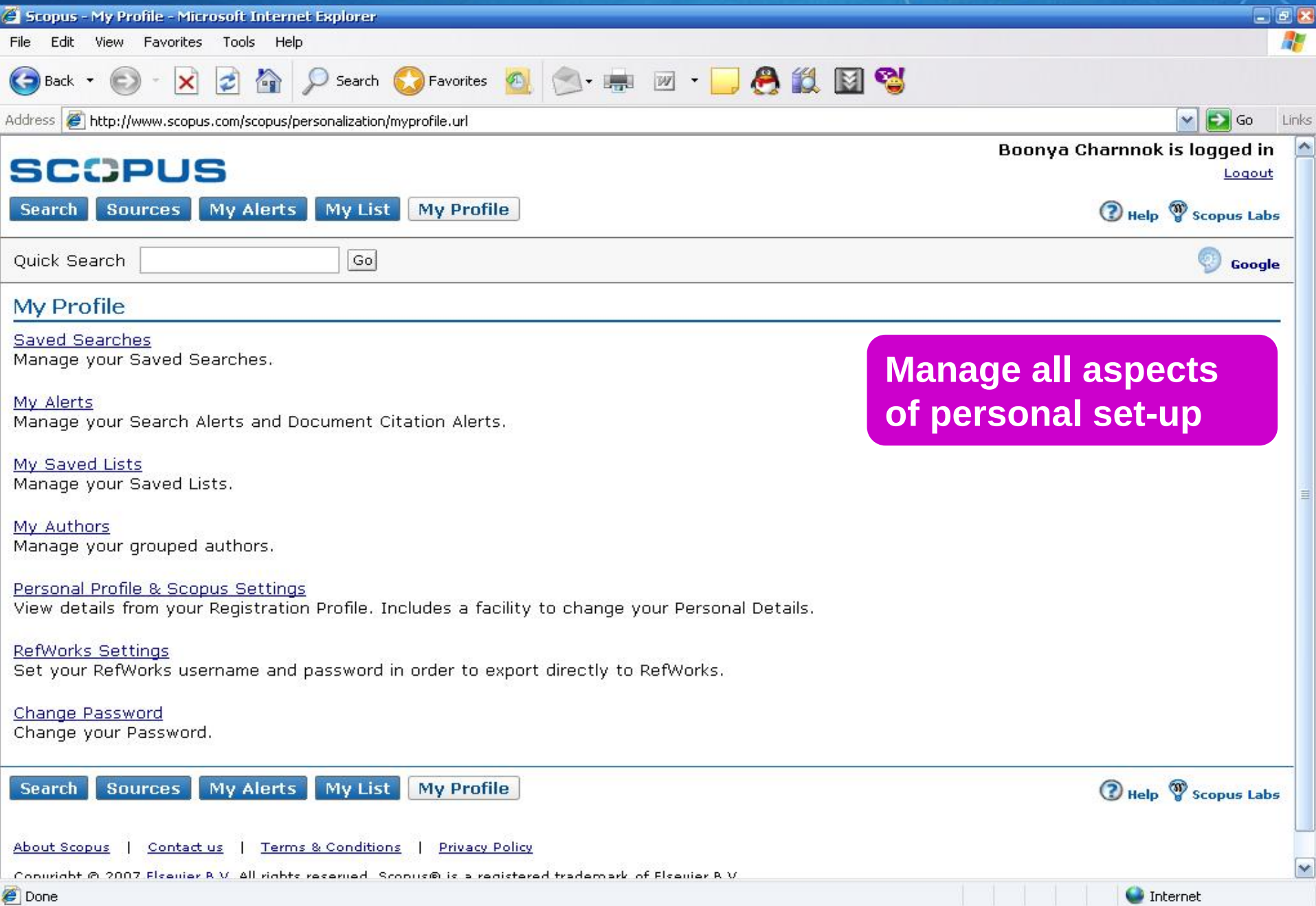

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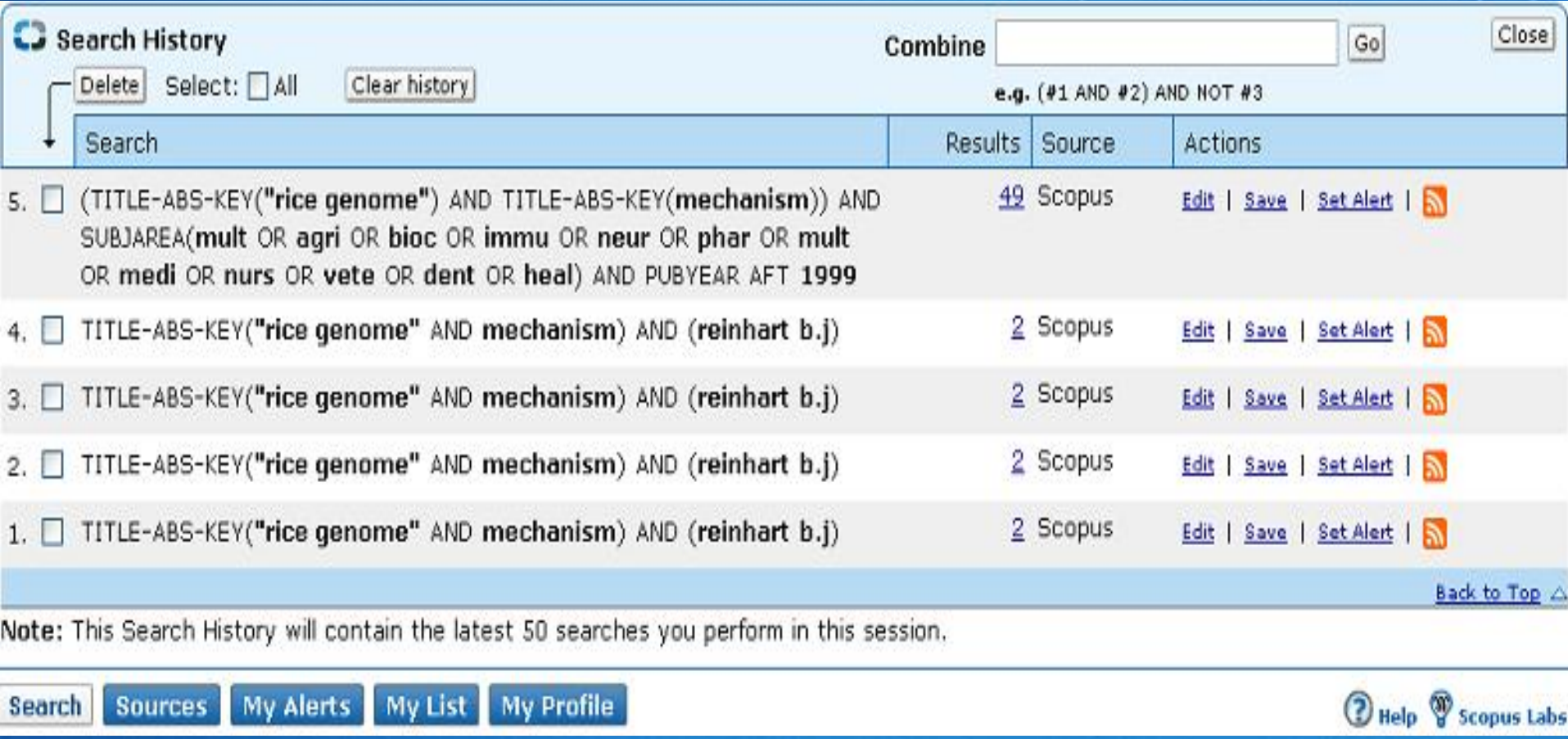

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