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☐ **Effects of 25-Hydroxyvitamin D_3 and 1,25-Dihydroxyvitamin D_3 on Cytokine Production by Human Decidual Cells**

Katie N. Evans, Lisa Nguyen, Junny Chan, Barbara A. Innes, Judith N. Bulmer, Mark D. Kilby, and Martin Hewison

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Abstract

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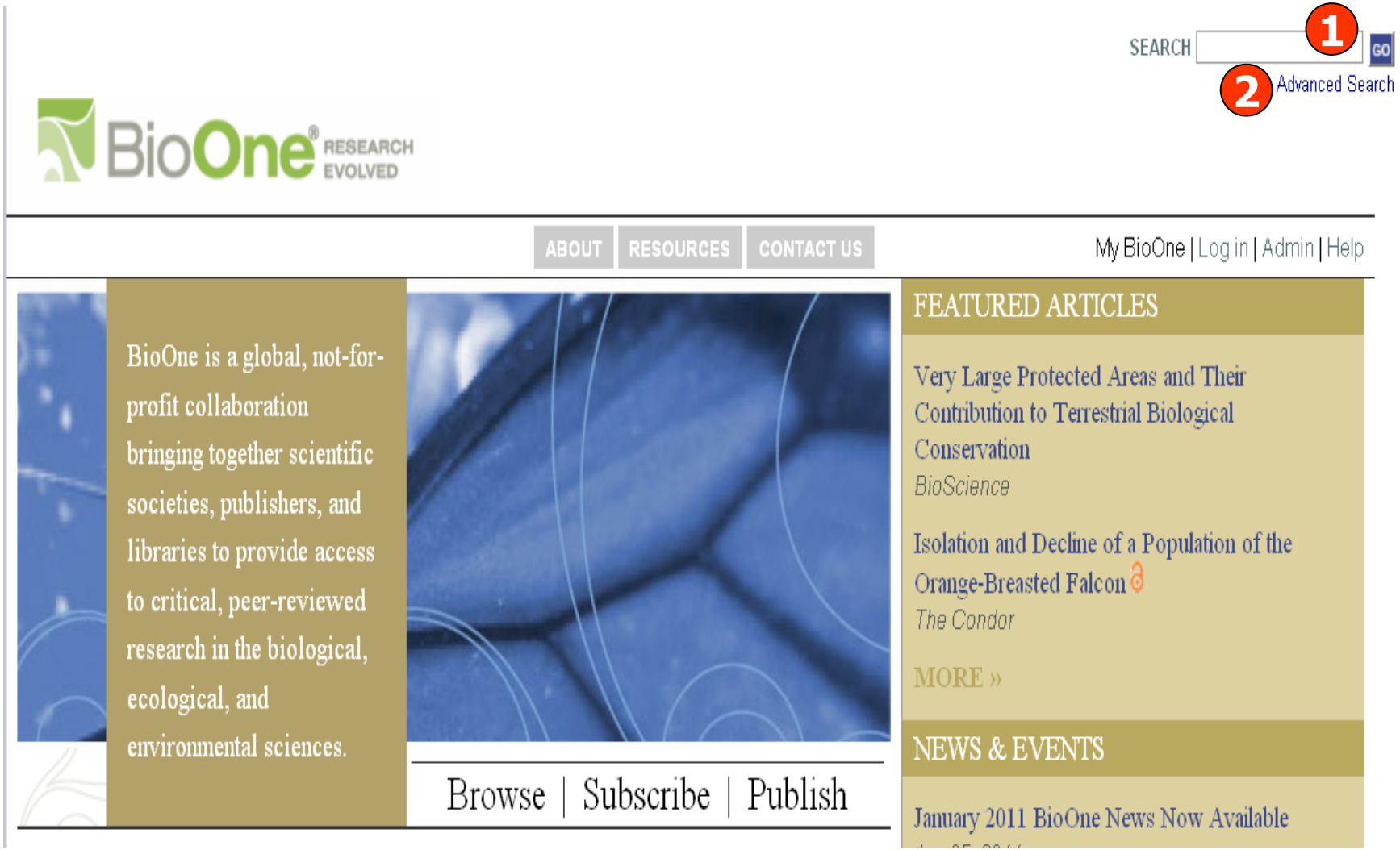

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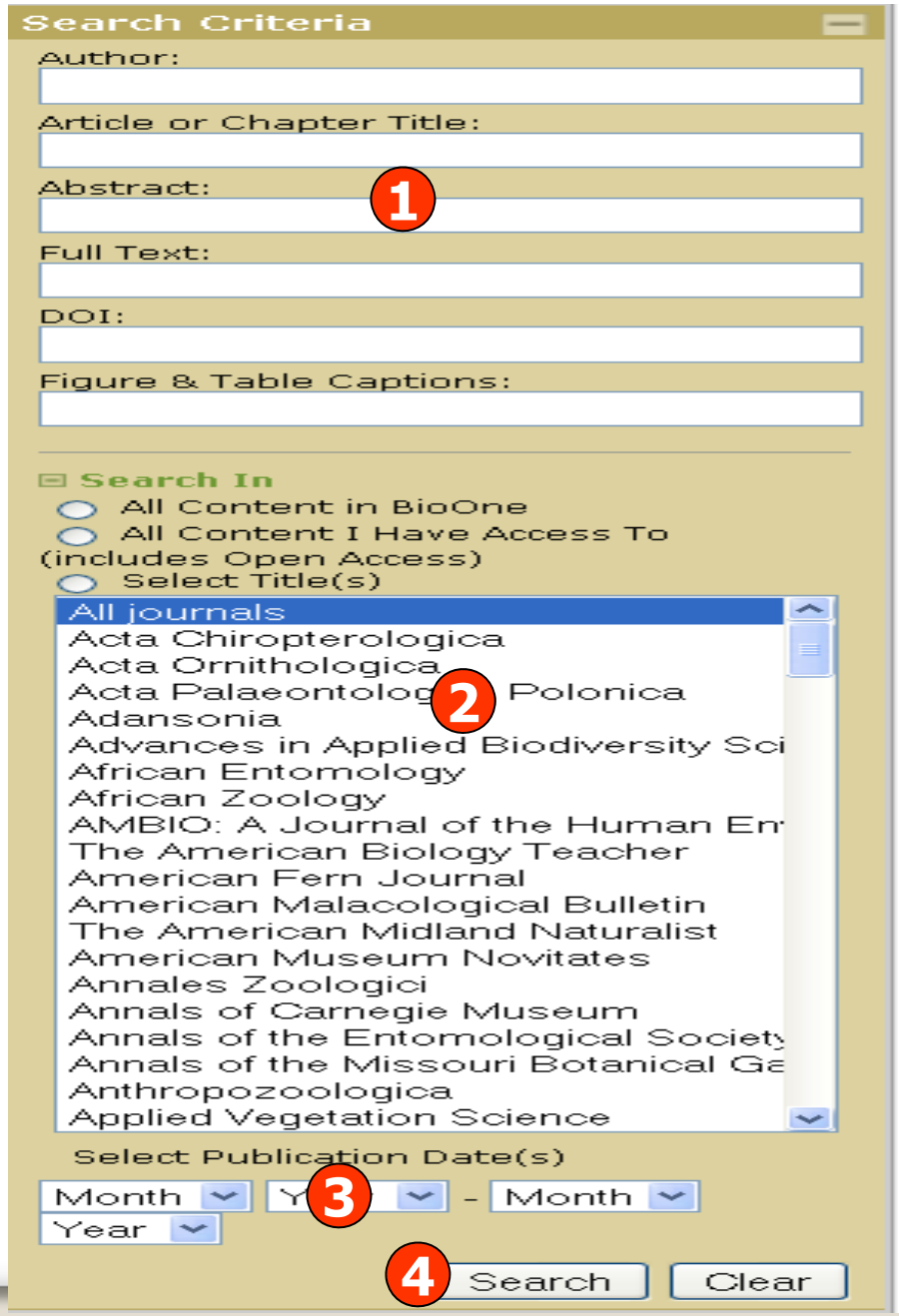

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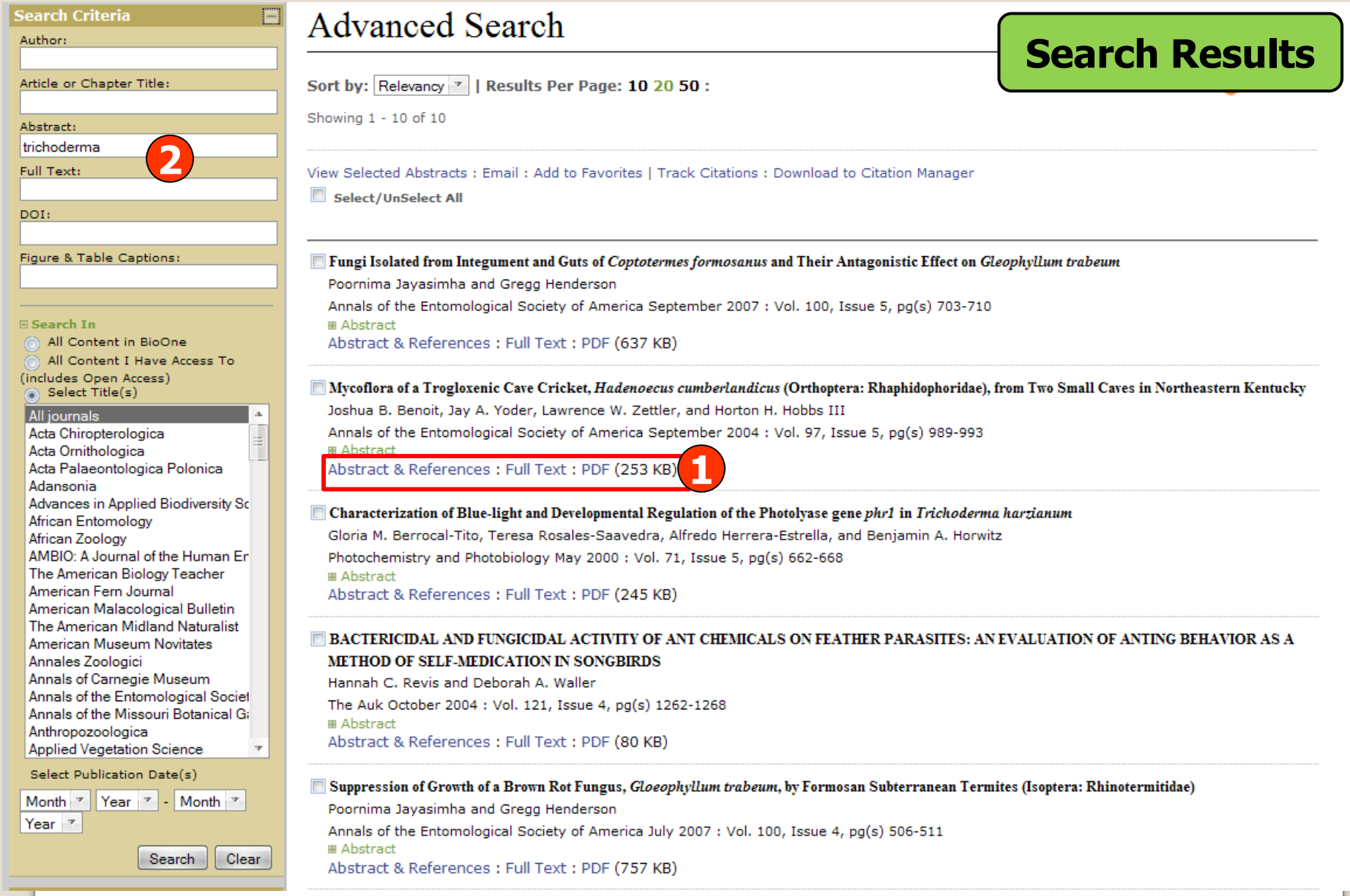

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Biology of Reproduction 75(6):823-835. 2006
doi: 10.1095/biolreprod.106.052290

The Identification of Novel Ovarian Proteases Through the Use of Genomic and Bioinformatic Methodologies[1]

Kei Miyakoshi[3], Melinda J. Murphy[3], Richard R. Yeoman[3], Siddhartha Mitra[4], Christopher J. Dubay[4], and Jon D. Hennebold[2,3,5]

[a]Division of Reproductive Sciences,[3] Oregon National Primate Research Center, Oregon Health & Science University West Campus, Beaverton, Oregon 97006

[b] Departments of Medical Informatics[4] and Obstetrics and Gynecology,[5] Oregon Health & Science University, Portland, Oregon 97239

Abstract

Proteolytic activities are essential for follicular growth, ovulation, as well as for luteal formation and regression. Using suppression subtractive hybridization (SSH), a novel mouse ovary-selective gene

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INTRODUCTION

Proteases comprise a group of structurally and functionally diverse proteins that catalyze the hydrolysis of peptide bonds. The highly selective and limited cleavage of specific protein substrates by the five major groups of proteases (serine-, metallo-, aspartic-, cysteine-, and threonine-proteases) are critical for a number of essential biological processes [1]. For example, proteases remodel extracellular matrix (ECM) proteins, modulate growth factor/cytokine actions by regulating their bioavailability, and control the levels of certain cell surface/receptor proteins. Therefore, proteases are critical determinants of cellular proliferation, differentiation, migration, and adhesion. As such, enzymatic proteolysis is indispensable for maintaining homeostasis, tissue remodeling, and angiogenesis or angiolysis [2, 3]. The recent completion of several large-scale genome sequencing projects and the development of high-throughput differential screening methodologies have led to the identification of hundreds of mouse

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