

International Conference on Bioinformatics, Computational Biology, Genomics and Chemoinformatics 2009

(BCBGC-09)

**Orlando, Florida, USA
13-16 July 2009**

ISBN: 978-1-61567-653-8

Printed from e-media with permission by:

Curran Associates, Inc.
57 Morehouse Lane
Red Hook, NY 12571



Some format issues inherent in the e-media version may also appear in this print version.

Copyright© (2009) by the International Society for Research in Science and Technology
All rights reserved.

Printed by Curran Associates, Inc. (2009)

For permission requests, please contact the International Society for Research in Science and Technology
at the address below.

ISRST (public relations)
PO Box 2464
Tallahassee, FL 32316 - 2464
USA

isrst@isrst.org

Additional copies of this publication are available from:

Curran Associates, Inc.
57 Morehouse Lane
Red Hook, NY 12571 USA
Phone: 845-758-0400
Fax: 845-758-2634
Email: curran@proceedings.com
Web: www.proceedings.com

Contents

Structure Activity Relationship (SAR) Patterns Observed Within a Series of Unrelated Common Consumer Drugs	1
Malcolm J. D'Souza, Fumie Koyoshi, Lynn M. Everett An	
Efficient Context-based Gene Normalization System	7
Yifei Chen, Feng Liu, Bernard Manderick	
A Framework for Secure Access to Medical Images	15
Tariq Javid Ali, Arshad Aziz, Pervez Akhtar, Muhammad Iqbal Bhatti	
Codon Usage Pattern Detection in Human, Mouse, and Chicken Genes Using Artificial Neural Networks	20
Edward Lockhart, Mandy Lucas, Jae Yoo, William Seffens	
Application Coupling and Data Feeding in an Integrative Life Sciences Data Management System	28
Can Turker, Dieter Joho, Christian Panse, Simon Barkow-Oesterreicher, Fuat Akal, Ralph Schlapbach	
OE Matching Algorithm for Searching Biological Sequences	36
Ahmad Fadel Klaib, Hugh Osborne	
Cross-genome knowledge-based expression data fusion	43
Matej Holec, Jiri Klema, Filip Zelezny, Jiri Belohradsky, Jakub Tolar	
Combinatorial Patterns of Promoter Elements in Homo Sapiens	51
Yunkai Liu, Sujuan Ye, Asai Asaithambi	
Improving the Performance of Protein-Protein Interaction Article Selection Using Domain Specific Features	57
Şenay Kafkas, Ekrem Varoglu, Bahar Taneri	
A graph-theoretic model based on primary and predicted secondary structure reveals functional specificity in a set of plant secondary product UDP-glucosyltransferases	65
Debra Knisley, Edith Seier, Daniel Lamb, Daniel Owens, Cecelia McIntosh	
An Efficient Approach in Comparing Protein Structures using Matrix Alignment Techniques	73
Zoran Dimov, Georgina Mirceva, Danco Davcev	
Classification and Cluster Analysis of Complex Time-of-Flight Secondary Ion Mass Spectrometry for Biological Samples	78
Xue Tian, Stephen E. Reichenbacha, Qingping Tao, Alex Henderson	

Characterizing Position-Specific Properties of siRNAs86
Wei Hu, John Hu

Optimal Clone Identifier based on Dynamic Rules and Process Algebra92
Mauricio E. Cantão, Luciano V. Araújo, Eliana G. M. Lemos, João E. Ferreira

In-silico Approach to Study the Gene Expression for Acute Myeloid Leukemia(AML)100
Rajendra Singh, Priyanka Narad, Gulshan Wadhwa

AUTHOR INDEX