

# Contents

<b>Peter Schuster</b>	
Invited Talk: Landscapes in RNA folding and evolution . . . . .	1
<b>Ulrike Mückstein, Hakim Tafer, Jörg Hackermüller, Stephan H. Bernhart, Peter F. Stadler, Ivo L. Hofacker</b>	
Thermodynamics of RNA-RNA Binding . . . . .	3
<b>Ivo L. Hofacker, Peter F. Stadler</b>	
Memory Efficient Folding Algorithms for Circular RNA Secondary Structures . . .	15
<b>Tom Slezak</b>	
Invited Talk: A large-scale application of comparative genomics for biodefense . .	27
<b>Christian Wawra, Mohamed I. Abouelhoda, Enno Ohlebusch</b>	
Efficient mapping of large cDNA/EST databases to genomes: A comparison of two different strategies . . . . .	29
<b>Annette Höglund, Pierre Dönnès, Torsten Blum, Hans-Werner Adolph, Oliver Kohlbacher</b>	
Using N-terminal targeting sequences, amino acid composition, and sequence motifs for predicting protein subcellular localization . . . . .	45
<b>Guo-Ping Zhao</b>	
Invited Talk: SARS molecular epidemiology and SARS-CoV evolution: Combating an emerging infectious disease with the regimen of genomics and bioinformatics . . . . .	61
<b>Alexander Kel, Tatiana Konovalova, Tagir Valeev, Evgeny Cheremushkin, Olga Kel-Margoulis, Edgar Wingender</b>	
Composite Module Analyst: A Fitness-Based Tool for Prediction of Transcription Regulation . . . . .	63
<b>Katrin Fundel, Robert Küffner, Thomas Aigner, Ralf Zimmer</b>	
Data Processing Effects on the Interpretation of Microarray Gene Expression Experiments . . . . .	77
<b>Alexey V. Antonov, Igor V. Tetko, Denis Kosykh, Dmitriy Surmeli, Hans-Werner Mewes</b>	
Exploiting scale-free information from expression data for cancer classification . .	93

<b>Rolf Hilgenfeld</b>	
Invited Talk: Proteins of SARS coronavirus - experimental and theoretical studies . . .	103
<b>Jean-Christophe Nebel</b>	
Generation of 3D templates of active sites of proteins with rigid prosthetic groups . . .	105
<b>Axel Griewel, Matthias Rarey</b>	
From greedy to branch & bound and back: Assessing optimization strategies for incremental construction molecular docking tools . . . . .	119
<b>Li Jin</b>	
Invited Talk: Linkage Disequilibrium Sharing and TagSNP Portability Between Populations . . . . .	131
<b>Hannes Luz, Martin Vingron</b>	
Family specific rates of protein evolution . . . . .	133
<b>David A. Case</b>	
Invited Talk: Macromolecular Simulations Using Continuum Solvent Models . . . . .	145
<b>Alexander Seifert, Michael Krahn, Stephan Tatzel, Rolf D. Schmid, Jürgen Pleiss</b>	
A Model of Specificity and Selectivity of Mammalian Cytochrome P450 Monooxygenases . . . . .	147
<b>Bingding Huang, Michael Schroeder</b>	
Using residue propensities and tightness of fit to improve rigid-body protein-protein docking . . . . .	159
<b>Hugo Kubinyi</b>	
Invited Talk: Chemistry meets Biology: Chemogenomics in Drug Discovery . . . . .	175
<b>Ari Rantanen, Taneli Mielikäinen, Juho Rousu, Esko Ukkonen</b>	
Planning isotopomer measurements for estimation of metabolic fluxes . . . . .	177
<b>Christian Spieth, Felix Streichert, Nora Speer, Andreas Zell</b>	
Inferring Regulatory Systems with Noisy Pathway Information . . . . .	193