



ptbi2017.cs.put.poznan.pl

PTBI Symposium 2017

X Symposium of the Polish Bioinformatics Society

27–29 September 2017 | Uniejow, Poland

POSTER SESSION

-
- | | |
|----|---|
| 01 | Jakub Bartoszewicz
Predicting the Pathogenic Potential of Novel DNA Sequences Using Deep Learning |
| 02 | Michał Boniecki
SimRNA: a Coarse-Grained Method for RNA Folding Simulations and 3D Structure Prediction |
| 03 | Juan F. Carrascoza Mayen
On the Origins of Life: Theoretical Studies of Reactions Catalyzed by Montmorillonite on Atmospheric-Like Gases |
| 04 | Kaja Chmielewska
Interleukin 18 Influence on the Cardiovascular System Modeled and Analyzed Using Petri Net-Based Approach |
| 05 | Maciej P. Ciemny
CABS-dock Standalone Application for Protein-Peptide Docking with Large-Scale Flexibility of the Protein Receptor |
| 06 | Aleksandra E. Dawid
SURPASS Low-Resolution Coarse-Grained Protein Modeling |
| 07 | Karolina Dawid
PyMOL Plugin for Visualization and Analysis of Protein-Peptide and Protein-Protein Complex Structures |
| 08 | Witold Dyrka
Where the Probabilistic Grammar Meets the Contact Map |
| 09 | Florian Heinke
Concepts of Protein Energy Profiling: Deciphering Energy Fingerprints in Protein Structures |
| 10 | Paulina Hyży
Ebola Virus Multialignment - Analysis and Visualization |
| 11 | Bogumił Konopka
Sharing the First MinION 3rd Generation Sequencing Experience |
| 12 | Wojciech Lesiński
Predicting Survivor in Neuroblastoma Based on RNA-Seq Data |
| 13 | Wojciech Łabaj
Comparison of Tools for Mutation Detection Using Thyroid Cancer Genome Sequencing Data |
| 14 | Ania Macioszek
Identifying Enrichment in Signal from DNA Sequencing Data Using Hidden Markov Models |
| 15 | Paweł Mackiewicz
Costs of Amino Acid Replacement Can Be Minimized by Mutational Pressure in Bacterial Genomes |
| 16 | Paulina H. Marek
Toward High-Resolution Prediction of Protein-Peptide Complex Structures |
| 17 | Justyna Mika
Reannotation of VDJ Segments in Complementarity Determining Region 3 (CDR3) in Data from TCR Sequencing |

-
- 18 Joanna Miśkiewicz
Bioinformatics Study of Structural Patterns in Plant MicroRNA
-
- 19 Melania Nowicka
An Answer Set Programming Approach to Optimal Design of Synthetic Cell Classifier Circuits
-
- 20 Marcin Pacholczyk
EMQIT: a Machine Learning Approach for Energy Based PWM Matrix Quality Improvement
-
- 21 Marcin Pacholczyk
Searching for Cancer Signatures Using Data Mining Techniques
-
- 22 Agata Perlińska
Role of the Magnesium in a Knotted Methyltransferase
-
- 23 Aneta Polewko-Klim
Identification of Informative Variables in Neuroblastoma Patients
-
- 24 Michał B. Ponczek
Bioinformatics in Blood Coagulation System
-
- 26 Agnieszka Rybarczyk
Tabu Search Algorithm for RNA Partial Degradation Problem
-
- 26 Katarzyna Rżosińska
The Quantitative Model of the Process of Differentiation of Macrophages and Their Effects on Atherosclerosis Plaque Stability Based on Time Petri Nets
-
- 27 Jakub Wiedemann
LCS-TA to Identify Similarity in Molecular Structures
-
- 28 Jakub Wojciechowski
Contact Groups Improve Performance of DCA Contact Prediction
-
- 29 Marta Dudek
Molecular Dynamics Simulations of Heterochiral RNA Complexes
-