

**UNIVERZITA KOMENSKÉHO
FAKULTA MATEMATIKY, FYZIKY A INFORMATIKY
Zoznam publikačnej činnosti**

Mgr. Bronislava Brejová, PhD.

ABC Kapitoly vo vedeckých monografiách vydané v zahraničných vydavateľstvách

- ABC01 Brejová, Bronislava 45% - Vinař, Tomáš 45% - Li, Ming : Pattern discovery : Methods and software
In: Introduction to Bioinformatics : A Theoretical and Practical Approach. - Totowa : Humana Press, 2003. - S. 491-521. - ISBN 1-58829-064-6
Ohlasy (4):
[o1] 2003 Lisitsa, A. - Archakov, A. - Lewi, P. - Janssen, P.: Bioinformatic insight into the unity and diversity of cytochromes P450. In: Methods and Findings in Experimental and Clinical Pharmacology, Vol. 25, No. 9, 2003, s. 733-745 - SCI ; SCOPUS
[o1] 2005 Ng, Y. K. - Ono, H. - Shinohara, T.: Measuring over-generalization in the minimal multiple generalizations of biosequences. In: Discovery Science : Lecture Notes in Computer Science, Vol. 3735. Berlin : Springer, 2005, S. 176-188 -SCI ; SCOPUS
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[o1] 2009 Singh, R. - Graham, P.: Grouping MPI processes for partial checkpoint and co-migration. In: EURO-PAR 2009: Parallel Processing : Lecture Notes in Computer Science ; Vol. 5704. Berlin : Springer-Verlag, 2009, S. 69-80 - CPCI-S ; SCOPUS

- ABC02 Brejová, Bronislava 45% - Brown, Daniel G. 10% - Vinař, Tomáš 45%: Advances in Hidden Markov models for sequence annotation
Lit. 82 zázn., 16 obr.
In: Bioinformatics Algorithms : Techniques and Applications. - Hoboken : Wiley-Interscience, 2008. - S. 55-91. - ISBN 978-0-470-09773-1
Ohlasy (2):
[o1] 2009 Lifshits, Y. - Mozes, S. - Weimann, O. - Ziv-Ukelson, M.: Speeding up HMM decoding and training by exploiting sequence repetitions. In: Algorithmica, Vol. 54, No. 3, 2009, s. 379-399 - SCI ; SCOPUS
[o1] 2010 Zhou, D. - Wang, X.: The improvement of HMM algorithm using wavelet de-noising in speech recognition. In: Advanced Computer Theory and Engineering. New York : IEEE, 2010, S. V4438-V4441 - SCOPUS

ADC Vedecké práce v zahraničných karentovaných časopisoch

- ADC01 Brejová, Bronislava 100%: Analyzing variants of Shellsort
Lit. 9 zázn.
In: Information Processing Letters. - Vol. 79, No. 5 (2001), s. 223-227
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[o1] 2007 Lucier, B. - Jiang, T. - Li, M.: Average-case analysis of QuickSort and binary insertion tree height using incompressibility. In: Information Processing Letters, Vol. 103, No. 2, 2007, s. 45-51 - SCI ; SCOPUS
[o1] 2009 Bunse, C. - Hoepfner, H. - Mansour, E. - Roychoudhury, S.: Exploring the energy consumption of data sorting algorithms in embedded and mobile environments. In: MDM 2009: 10th International Conference on Mobile Data Management. New York : IEEE, 2009, S. 600-607 - CPCI-S ; SCOPUS
[o1] 2009 Bunse, C. - Hoepfner, H. - Mansour, E. - Roychoudhury, S.: Choosing the "best" sorting algorithm for optimal energy consumption. In: ICSOFT 2009: 4th International Conference on Software and Data Technologies, Proceedings Vol. 2. Setubal : INSTICC Press, 2009, S. 199-206 - CPCI-S ; SCOPUS

[o1] 2010 Goodrich, M. T.: Randomized Shellsort: A simple oblivious sorting algorithm. In: Proceedings of the Annual ACM-SIAM Symposium on Discrete Algorithms (SODA). Philadelphia : SIAM, 2009, S. 1262-1277 - SCOPUS

[o1] 2011 Bunse, C. - Hoepfner, H. - Mansour, E. - Roychoudhury, S.: Energy efficient data sorting using standard sorting algorithms. In: Software and Data Technologies : Communications in Computer and Information Science Volume: 50. Berlin: Springer, 2011, S. 247-260 - CPCI-S

ADC02 Biedl, Therese C. - Brejová, Bronislava 30% - Demaine, Erik D. - Hamel, Angele M. - López-Ortiz, Alejandro - Vinař, Tomáš 30%: Finding hidden independent sets in interval graphs
Rozšířená práce
Lit. 27 zázň., 4 obr.

In: Theoretical Computer Science. - Vol. 310, No. 1-3 (2004), s. 287-307

Ohlasy (3):

[o1] 2006 Cohen, J. - Fomin, F. - Heggernes, P. - Kratsch, D. - Kucherov, G.: Optimal linear arrangement of interval graphs. In: Mathematical Foundations of Computer Science 2006 : Lecture Notes in Computer Science, Vol. 4162. Berlin :Springer, 2006, S. 267-279 - SCI ; SCOPUS

[o1] 2010 Tao, Y. - Sheng, C. - Li, J.: Finding maximum degrees in hidden bipartite graphs. In: Proceedings of the ACM SIGMOD International Conference on Management of Data. New York : ACM, 2010, S. 891-902 - SCOPUS

[o1] 2012 Sheng, C. - Tao, Y. - Li, J.: Exact and approximate algorithms for the Most Connected Vertex problem. In: ACM Transactions on Database Systems, Vol. 37, No. 2, 2012, Art. No. 12 - SCI ; SCOPUS

ADC03 Brejová, Bronislava 45% - Brown, Daniel G. - Li, Ming - Vinař, Tomáš 45%: ExonHunter: a comprehensive approach to gene finding
Lit. 31 zázň., 2 obr., 2 tab.

In: Bioinformatics. - Vol. 21, Suppl. 1 (2005), s. i57-i65

[ISMB 2005 : Intelligent Systems for Molecular Biology : Annual International Conference. 13th, Detroit, 25.-29.6.2005]

Ohlasy (26):

[o1] 2006 Carter, D. - Durbin, R.: Vertebrate gene finding from multiple-species alignments using a two-level strategy. In: Genome Biology, Vol. 7, Suppl. 1, 2006, Art. No. S6 - SCI

[o1] 2006 Guigo, R. - Flicek, P. - Abril, J. F. - Raymond, A. - Lagarde, J. - Denoeud, F. - Antonarakis, S. - Ashburner, M. - Bajic, V. B. - Birney, E. - Castelo, R. - Eyraas, E. - Ucla, C. - Gingeras, T. R. - Harrow, J. - Hubbard, T. - Lewis, S. E. - Reese, M. G.: EGASP: the human ENCODE genome annotation assessment project. In: Genome Biology, Vol. 7, Suppl. 1, 2006, Art. No. S2 - SCI

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ADC04 Brejová, Bronislava 25% - Brown, Daniel G. - Vinař, Tomáš 15%: Vector seeds: An extension to spaced seeds

Lit. 13 záz., 3 obr., 5 tab.

In: Journal of Computer and System Sciences. - Vol. 70, No. 3 (2005), s. 364-380

Ohlasy (18):

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- [o1] 2010 Ng, E. Y. K. - Pang, M. P.: Comparison of nucleotide DNA alignment search programmes. In: *International Journal of Medical Engineering and Informatics*, Vol. 2, No. 2, 2010, s. 163-176 - SCOPUS
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ADC05 Brejová, Bronislava 50% - Brown, Daniel G. - Vinař, Tomáš 40%: The most probable annotation problem in HMMs and its application to bioinformatics

Rozšířená práce

Lit. 21 zázň., 20 obr.

In: *Journal of Computer and System Sciences*. - Vol. 73, No. 7 (2007), s. 1060-1077

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ADC06 Cui, Xuefeng - Vinař, Tomáš 30% - Brejová, Bronislava 10% - Shasha, Dennis - Li, Ming : Homology search for genes

Lit. 22 zázň., 5 obr., 8 tab.

In: *Bioinformatics*. - Vol. 23, No. 13 (2007), s. i97-i103

[ISMB 2007 : Intelligent Systems for Molecular Biology : Annual International Conference. 15th, Vienna, 21.-25.7.2007]

[ECCB 2007 : European Conference on Computational Biology. 6th, Vienna, 21.-25.7.2007]

Ohlasy (8):

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[o1] 2009 She, R. - Chu, J. S. C. - Wang, K. - Pei, J. - Chen, N. S.: genBlastA: Enabling BLAST to identify homologous gene sequences. In: *Genome Research*, Vol. 19, No. 1, 2009, s. 143-149 - SCI ; SCOPUS

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[o1] 2010 Siva, R. - Doss, F. P. - Kundu, K. - Satyanarayana, V. S. V. - Kumar, V.: Molecular characterization of bixin-An important industrial product. In: *Industrial Crops and Products*, Vol. 32, No. 1, 2010, s. 48-53 - SCI ; SCOPUS

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ADC07 Siepel, Adam - Diekhans, Mark - Brejová, Bronislava 10% - Langton, Laura - Stevens, Michael - Comstock, Charles L. G. - Davis, Colleen - Ewing, Brent - Oommen, Shelly - Lau, Christopher - Yu, Hung-Chun - Li, Jianfeng - Roe, Bruce A. - Green, Phil - Gerhard, Daniela S. - Temple, Gary - Haussler, David - Brent, Michael R. : Targeted discovery of novel human exons by comparative genomics

Lit. 60 zázň., 6 obr.

In: *Genome Research*. - Vol. 17, No. 12 (2007), s. 1763-1773

Ohlasy (16):

[o1] 2008 Rexroad III, C. E. - Palti, Y. - Gahr, S. A. - Vallejo, R. L.: A second generation genetic map for rainbow trout (*Oncorhynchus mykiss*). In: *BMC Genetics*, Vol. 9, 2007, Art. No. 74 - SCI ; SCOPUS

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[o1] 2010 Chen, X. - Tompa, M.: Comparative assessment of methods for aligning multiple genome sequences. In: *Nature Biotechnology*, Vol. 28, No. 6, 2010, s. 567-572 - SCI ; SCOPUS

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[o1] 2010 Wagner, J. R. - Ge, B. - Pokholok, D. - Gunderson, K. L. - Pastinen, T. - Blanchette, M.: Computational analysis of whole-genome differential allelic expression data in human. In: *PLoS Computational Biology*, Vol. 6, No. 7, 2010, Art.No. e1000849 - SCI ; SCOPUS

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ADC08 The Schistosoma japonicum Genome Sequencing and Functional Analysis Consortium - Zhou, Yan - Vinař, Tomáš 2% - Brejová, Bronislava 2%: The Schistosoma japonicum genome reveals features of host-parasite interplay

Lit. 69 zázn.

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Lit. 35 zázň., 5 obr., 3 tab.

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Popis urobený 25.3.2009

Lit. 26 zázň., 5 obr., 3 tab.

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URL: doi:10.1093/nar/gkp052

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ADC11 Vesteg, Matej 40% - Vacula, Rostislav 10% - Steiner, Jürgen M. 5% - Mateášiková, Bianka 5% - Löffelhardt, Wolfgang 10% - Brejová, Bronislava 5% - Krajčovič, Juraj 25%: A possible role for short introns in the acquisition of stroma-targeting peptides in the flagellate *Euglena gracilis*

Lit.: 66 zázň., 1 obr., 4 tab.

In: *DNA Research*. - Vol. 17, No. 4 (2010), s. 223-231

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Lit. 34 záz. n.

In: Journal of Computational Biology. - Vol. 17, No. 9 (2010), s. 1267-1279

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Lit. 30 záz. n.

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ADC14 Valach, Matúš 10% - Farkaš, Zoltán 10% - Fričová, Dominika 10% - Kováč, Jakub 10% - Brejová, Bronislava 10% - Vinař, Tomáš 10% - Pfeiffer, Ilona 10% - Kucsera, Judit 5% - Tomáška, Ľubomír 10% - Lang, Franz B. 5% - Nosek, Jozef 10%: Evolution of linear chromosomes and multipartite genomes in yeast mitochondria

Lit. 89 záz. n., 9 obr., 3 tab.

In: Nucleic Acids Research. - Vol. 39, No. 10 (2011), s. 4202-4219

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ADE Vedecké práce v zahraničných nekarentovaných časopisoch

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Lit. 11 zázň., 3 obr., 6 tab.
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AFC10 Kováč, Jakub 50% - Vinař, Tomáš 20% - Brejová, Bronislava 30%: Predicting gene structures from multiple RT-PCR tests

Recenzované

Lit. 17 zázň., 4 obr.

In: Algorithms in Bioinformatics. - Berlin : Springer-Verlag, 2009. - S. 181-193. - ISBN 978-642-042040-9. - (Lecture Notes in Computer Science: Lecture Notes in Bioinformatics ; Vol. 5724)

[WABI 2009 : Algorithms in Bioinformatics : International Workshop. 9th, Philadelphia, 12.-13.9.2009]

AFC11 Vinař, Tomáš 45 % - Brejová, Bronislava 45 % - Song, Giltae - Siepel, Adam : Reconstructing histories of complex gene clusters on a phylogeny

Recenzované

Lit. 30 zázň.

In: Comparative Genomics. - Berlin : Springer-Verlag, 2009. - S. 150-163. - ISBN 978-3-642-04743-5. - (Lecture Notes in Bioinformatics ; Vol. 5817)

[RECOMB-CG 2009 : Comparative Genomics : International Workshop. 7th, Budapest, 27.-29.9.2009]

Ohlasy (1):

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AFC12 Nánási, Michal 50 % - Vinař, Tomáš 20 % - Brejová, Bronislava 30 %: The highest expected reward decoding for HMMs with application to recombination detection

Recenzované. - Prezentované na 2 konferenciách

Lit. 12 zázň.

In: Combinatorial Pattern Matching. - Berlin : Springer-Verlag, 2010. - S. 164-176. - ISBN 3-642-13508-0. - (Lecture Notes on Computer Science ; Vol. 6129)

[CPM 2010 : Combinatorial Pattern Matching : Annual Symposium. 21st, New York, 21.-23.6.2010]

[ECCB 2010 : European Conference on Computational Biology. 9th, Ghent, 26.-29.9.2010]

POZNÁMKA: Vyšlo aj ako poster - ECCB 10 [elektronický zdroj]. - Leuven : Katholieke Universiteit, 2010. - S. 9 [CD-ROM]. -

Ohlasy (2):

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AFC13 Brejová, Bronislava 34% - Landau, Gad M. 33% - Vinař, Tomáš 33%: Fast computation of a string duplication history under no-breakpoint-reuse

Recenzované

Lit. 18 zázň.

In: String Processing and Information Retrieval. - Berlin ; Heidelberg : Springer-Verlag, 2011. - S. 144-155. - ISBN 978-3-642-24582-4. - (Lecture Notes in Computer Science ; Vol. 7024)

[SPIRE 2011 : String Processing and Information Retrieval : International Symposium. 18th, Pisa, 17.-21.10.2011]

AFC14 Brejová, Bronislava 25% - Dobrev, Štefan 25% - Kráľovič, Rastislav 25% - Vinař, Tomáš 25%: Routing in carrier-based mobile networks

Recenzované

Lit. 25 zázň., 1 obr.

In: Structural Information and Communication Complexity. - Berlin : Springer, 2011. - S. 222-233. - ISBN 978-3-642-22211-5. - (Lecture Notes in Computer Science ; Vol. 6796)

[SIROCCO 2011 : Structural Information and Communication Complexity : International Colloquium. 18th, Gdańsk, 26.-29.6.2011]

AFC15 Brejová, Bronislava 40% - Burger, Michal 20% - Vinař, Tomáš 40%: Automated segmentation of DNA sequences with complex evolutionary histories

Recenzované. - Prezentované na 2 konferenciách

Lit. 28 zázň., 4 obr., 4 tab.

In: Algorithms in Bioinformatics. - Berlin : Springer, 2011. - S. 1-13. - ISBN 978-3-642-23037-0. - (Lecture Notes in Computer Science ; Vol. 6833)

[WABI 2011 : Algorithms in Bioinformatics : International Workshop. 11th, Saarbrücken, 5.-7.9.2011]

[ISMB 2011 : Intelligent Systems for Molecular Biology : Annual International Conference. 19th, Vienna, 17.-19.7.2011]

[ECCB 2011 : European Conference on Computational Biology. 10th, Vienna, 17.-19.7.2011]

POZNÁMKA: Vyšlo aj ako poster - ISMB/ECCB 2011 [elektronický zdroj]. - La Jolla : ISCB, 2011. - Art. No. D12 [USB kľúč]. -

AFC16 Kováč, Jakub 50% - Brejová, Bronislava 25% - Vinař, Tomáš 25%: A practical algorithm for ancestral rearrangement reconstruction

Recenzované. - Prezentované na 2 konferenciách

In: Algorithms in Bioinformatics. - Berlin : Springer, 2011. - S. 163-174. - ISBN 978-3-642-23037-0. - (Lecture Notes in Computer Science ; Vol. 6833)

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POZNÁMKA: Vyšlo aj ako poster - ISMB/ECCB 2011 [elektronický zdroj]. - La Jolla : ISCB, 2011. - Art. No. D07 [USB kľúč]. -

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AFD Publikované príspevky na domácich vedeckých konferenciách

AFD01 Vinař, Tomáš - Brejová, Bronislava : Sút'áže v programovaní ako doplnková forma výučby informatiky
Recenzované

- In: DidInfo '99, zv. 1. - Banská Bystrica : Metodické centrum, 1999. - S. 23-29. - ISBN 80-8041-296-0
[DidInfo 1999 : Kolokvium o vyučovaní informatiky na základných a stredných školách. 5., Banská Bystrica, 18.-23.3.1999]

Ohlasy (1):

- [o1] 2006 Forisek, M. - Winczer, M.: Non-formal activities as scaffolding to informatics achievements. In: Information Technologies at School. Vilnius : Institute of Mathematics and Informatics, 2006, S. 529-534 - CPCI-S

AFD02 Biedl, Therese C. - Brejová, Bronislava 35% - Vinař, Tomáš 35%: Simplifying flow networks

Recenzované

Lit. 9 zázň., 5 obr.

- In: Mathematical Foundations of Computer Science 2000. - Berlin : Springer, 2000. - S. 192-201. - ISBN 3-540-67901-4. - (Lecture Notes in Computer Science ; Vol. 1893)

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URL: <http://www.cs.uwaterloo.ca/research/tr/2000/07/art.pdf>

POZNÁMKA: Vyšlo aj ako preprint - Waterloo : Department of Computer Science University of Waterloo, 2000. - (Technical Report ; CS-2000-07)

Ohlasy (13):

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AFD03 Višňovská, Martina 50% - Nánási, Michal 10% - Vinař, Tomáš 10% - Brejová, Bronislava 30%: Estimating effective DNA database size via compression
Recenzované. - Prednesené na 2 konferenciách
Lit. 23 záz., 1 obr., 3 tab.
In: Information Technologies Applications and Theory. - Seňa : PONT, 2010. - S. 63-70. - ISBN 978-80-970179-4-1
[ITAT 2010 : Information Technologies Applications and Theory : Conference. 10th, Smrekovica, 21.-25.9.2010]
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POZNÁMKA: Vyšlo aj ako poster - ECCB 10 (CD ROM). - Leuven : Katholieke universiteit, 2010. - S. 21. -

AFD04 Kucharík, Marcel 50% - Kováč, Jakub 10% - Brejová, Bronislava 40%: Gene finding with complex external information
Recenzované
Lit. 16 záz., 3 obr., 2 tab.
In: Information Technologies Applications and Theory. - Seňa : PONT, 2011. - S. 39-46. - ISBN 978-80-89557-02-8
[ITAT 2011 : Information Technologies Applications and Theory : Conference. 11th, Hotel Boboty, Vrátna dolina, 23.-27.9.2011]

AFD05 Kováč, Peter 60% - Brejová, Bronislava 20% - Vinař, Tomáš 20%: Aligning sequences with repetitive motifs
Recenzované
Lit. 19 záz.
In: ITAT 2012 : Information Technologies Applications and Theory [elektronický dokument]. - Košice : Slovenská spoločnosť pre umelú inteligenciu, 2012. - S. 41-48 [online]. - ISBN 978-80-971144-0-4
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URL: <http://itat.ics.upjs.sk/pmwiki.php?n=Site.Zborniky>

AFG Abstrakty príspevkov zo zahraničných konferencií

AFG01 Brejová, Bronislava 100%: Speeding up RNA motif search by data-driven element ordering
In: Combinatorial Algorithms in Bioinformatics 2012 [elektronický dokument]. - [s.l.]: [s.n.], 2012. - 1 s. [online]
[Combinatorial Algorithms in Bioinformatics 2012 : Workshop. Koper, 13.9.2012]
URL: <http://wiki.techfak.uni-bielefeld.de/gi/CombAlgBioinfWorkshop2012>

AFG02 Jimenez, Randi M. 60% - Rampášek, Ladislav 10% - Brejová, Bronislava 10% - Vinař, Tomáš 10% - Lupták, Andrej 10%: Application of new tools for functional RNA discovery
Lit. 4 záz.
In: ISMB 2012 : Alternative Splicing - Integrative RNA Analysis and Disease (AS-SIG) [elektronický zdroj]. - [La Jolla] : [ISCB], 2012. - S. 12 [online]
[ISMB 2012 : Intelligent Systems for Molecular Biology : Annual International Conference. 20th, Long Beach,

13.-14.7.2012]

URL: http://www.alternative-splicing.org/as-sig-12/download/AS-SIG2012_handout.small_v3.pdf

AFG03 Vinař, Tomáš 50% - Brejová, Bronislava 50%: Three problems illustrating bioinformatics concepts in a standard spreadsheet
In: RECOMB Bioinformatics Education & RECOMB Algorithmic Biology 2012 [elektronický dokument]. - [s.l.] : [s.n.], 2012. - S. 9 [online]
[RECOMB-BE 2012 : Satellite Conference on Bioinformatics Education. 4th, St. Petersburg, 26.8.2012]
[RECOMB-AB 2012 : Satellite Conference on Open Problems in Algorithmic Biology. St. Petersburg, 27.-29.8.2012]
URL: <http://bioinf.spbau.ru/ab2012/sites/default/files/recomb-2012-be-ab-program-v2.pdf>

AFH Abstrakty příspěvků z domácích konferencí

AFH01 Kováč, Jakub 20 % - Valach, Matúš 20 % - Nosek, Jozef 20 % - Brejová, Bronislava 20 % - Vinař, Tomáš 20 %: Reconstructing ancestral gene orders in yeast mitochondrial genomes
Lit. 1 záz. n.
In: 38th Annual Conference on Yeasts. - Bratislava : Czechoslovak Society for Microbiology, 2010. - S. 78
[Annual Conference on Yeasts 2010. 38th, Smolenice, 11.-14.5.2010]

AFH02 Mešťánek, Juraj - Brejová, Bronislava 20 %: Software for annotation of protein coding genes in yeast mitochondrial genomes
Lit. 3 záz. n.
In: 38th Annual Conference on Yeasts. - Bratislava : Czechoslovak Society for Microbiology, 2010. - S. 79
[Annual Conference on Yeasts 2010. 38th, Smolenice, 11.-14.5.2010]

AFH03 Vinař, Tomáš 50 % - Brejová, Bronislava 50 %: Bioinformatics research at the Faculty of Mathematics, Physics and Informatics, Comenius University
Lit. 6 záz. n.
In: 38th Annual Conference on Yeasts. - Bratislava : Czechoslovak Society for Microbiology, 2010. - S. 57
[Annual Conference on Yeasts 2010. 38th, Smolenice, 11.-14.5.2010]

AFI Preprinty vědeckých prací vydané v zahraničních vydavatelstvích

AFI01 Brejová, Bronislava 40% - DiMarco, Chrysanne - Vinař, Tomáš 40% - Hildalgo, Sandra Romero - Holguin, Gina - Patten, Cheryl : Finding patterns in biological sequences [elektronický zdroj]. - Waterloo : Department of Computer Science University of Waterloo, 2000. - 49 s. [online]. - (Technical Report ; CS-2000-22), (Project Report ; CS798G)
Popis urobený 6.4.2009
Lit. 66 záz. n., 7 obr.
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AFK Postery zo zahraničných konferencií

AFK01 Valach, Matúš 10% - Farkaš, Zoltán - Kováč, Jakub 3% - Brejová, Bronislava 3% - Vinař, Tomáš 3% - Pfeiffer, Ilona - Fričová, Dominika 10% - Kucsera, Judit - Tomáška, Ľubomír 10% - Nosek, Jozef 21%: Multipartite genomes in yeast mitochondria
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GII01 Brejová, Bronislava 50% - Vinař, Tomáš 50%: Korešpondenčný seminár z programovania vo výuke informatiky na stredných školách

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GII05 Brejová, Bronislava 50 % - Vinař, Tomáš 50 %: Koľko génov má človek?

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Štatistika kategórií (Záznamov spolu: 65):

ABC Kapitoly vo vedeckých monografiách vydané v zahraničných vydavateľstvách (2)

ADC Vedecké práce v zahraničných karentovaných časopisoch (14)

ADE Vedecké práce v zahraničných nekarentovaných časopisoch (3)

AEC Vedecké práce v zahraničných recenzovaných vedeckých zborníkoch, monografiách (1)

AFC Publikované príspevky na zahraničných vedeckých konferenciách (16)

AFD Publikované príspevky na domácich vedeckých konferenciách (5)

AFG Abstrakty príspevkov zo zahraničných konferencií (3)

AFH Abstrakty príspevkov z domácich konferencií (3)

AFI Preprinty vedeckých prác vydané v zahraničných vydavateľstvách (5)

AFK Postery zo zahraničných konferencií (1)

BCI Skriptá a učebné texty (1)

BDF Odborné práce v domácich nekarentovaných časopisoch (1)

DAI Dizertačné a habilitačné práce (1)

GHG Práce zverejnené na internete (1)

GII Rôzne publikácie a dokumenty, ktoré nemožno zaradiť do žiadnej z predchádzajúcich kategórií (8)

Štatistika ohlasov (334):

[o1] Citácie v zahraničných publikáciách registrované v citačných indexoch (334)

9. 1. 2013