MCCMB 2015

Proceedings of the International Moscow Conference on Computational Molecular Biology

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Features of miR-574-5p and miR-574-3p binding sites in mRNA of target genes

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Binding sites of miRNAs with transcription factors' genes of Camelus ferus and Homo sapiens

Anna Ivshina, Vladimir Kuznetsov, Zhiqun Tang, Motakis Efthimios, Ghim Siong Ow

Genome wide survival prediction and network analysis stratifies breast cancers into three reproducible subclasses determined by novel genetic grading signatures

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Olga Kalinina, Saskia Metzler, Silvia Caprari

Sequence and structural analysis of related proteins in distant viral species

Anastasia Kalinina, Alexandra Suvorikova, Vladimir Spokoiny, Mikhail Gelfand

The method for homologous recombination detection within bacterial species

PД±nar Kavak, Bekir ErgІjner, Bayram YІjksel, Duran Гьstek, Mahmut Ehamil SaДuДsroДulu, Tunga GІjngІ°r, Can Alkan

Improving genome assemblies using multi-platform sequence data

Sergey Kazakov, Vladimir Ulyantsev, Veronika Dubinkina, Alexander Tyakht, Dmitry Alexeev

MetaFast: fast reference-free graph-based comparison of shotgun metagenomic data

Kamil Khafizov, Rene Staritzbichler, Maxim Ivanov, Marcus Stamm, Lucy Forrest

Anchoring patterns and point mutations in pairwise alignments using AlignMe

Peter Kharchenko

Classifying transcriptional and genetic heterogeneity in single-cell measurements

Matvei Khoroshkin, Semen Leyn, Dmitry Rodionov

Transcriptional Regulation of the Carbohydrate Metabolism in the Bifidobacterium Genus