

目次

| | |
|---|------------------------|
| 构建基于 EBI 数据库的本地 SRS 服务系统 | 毛逸清,李江城,王小磊,赵东升(93) |
| 乙型、丙型流感病毒的长记忆 ARFIMA 模型 | 刘娟,高洁(97) |
| 肾细胞癌 DNA 甲基化标记检测的重复性及其与基因表达改变的相关性 | 姚晨,李红东,郭政(102) |
| 四种常用高通量测序拼接软件的应用比较 | |
| 朱大强,李存,陈斌,姜焕焕,江晓芳,安小平,米志强,陈禹保,童贻刚(106) | |
| 生物网络研究进展述评 | 高蕾,郭进利(113) |
| 基于对数线性模型的酵母基因转录调控模体分析 | 周荣阁,张静(120) |
| 高粱抗坏血酸过氧化物酶基因的电子克隆及序列分析 | 陈国强,孟鹏,刘李黎,陈刚,王萍(125) |
| 树干毕赤酵母(<i>Pichia Stipitic</i>)木糖还原酶(<i>xyl1</i>)基因克隆与序列分析 | 孙博,葛菁萍(131) |
| 细胞色素 P450BM3 催化正十六烷动力学计算 | 姚学峰,宋怡铃(134) |
| R/Bioconductor 在 Affymetrix 表达芯片中的应用 | 甄一松,张伟丽,吴青,肖成路(138) |
| 模拟蛋白质折叠过程的新算法研究 | 张天弛,张菁(142) |
| 基于图形硬件加速的生物序列比对算法研究 | 张林,柴惠,沃立科,袁小凤,黄燕芬(146) |
| 人类和黑猩猩 Y 染色体结构和基因含量的差异性 | 金能智,张晶,沈玉琳,孙一桐(151) |
| 人参皂甙 Rb1 对大鼠脑缺血再灌注神经损伤后的修复作用 | 李明强,曾照芳,尤萍(155) |
| 基于启发式算法预测含假结 RNA 二级结构的研究进展 | 晁江涛,马春森(157) |
| 基于 LNMF 的癌症基因表达谱数据的特征提取 | 王蕊平,王年,苏亮亮,陈乐(164) |
| 一种基于 SVR 的分辨近天然 G 蛋白耦联受体——配体构象的方法 | 杨凌云,吕强(167) |
| 基于最优分割位点的蛋白质亚细胞位点预测方法 | |
| 王伟,郑小琪,窦永超,刘太岗,赵娟,王军(171) | |
| 小鼠 DEAF1 调控基因的生物信息学分析 | 盛德乔(176) |

Contents

| | |
|--|---|
| Construction of local SRS service system based on EBI databases | MAO Yi-qing, LI jiang-yu, WANG Xiao-lei, ZHAO Dong-sheng(93) |
| long-memory ARFIMA models for DNA sequences of influenza B, C virus | LIU Juan, GAO jie(97) |
| Reproducibility of DNA methylation signatures in kidney renal cell carcinoma and their relationship with expression change | YAO Chen, LI Hong-dong, GUO Zheng(102) |
| Comparison of the widely used high-throughput sequencing assembly software | ZHU Da-qiang, LI Cun, CHENG Bin, JIANG Huan-huan, JIANG Xiao-fang, AN Xiao-ping, MI Zhi-qiang, CHEN Yu-bao, TONG Yi-gang(106) |
| Review in Research on Biological networks | GAO Lei, GUO Jin-li(113) |
| Analysis of transcription regulation motifs in yeast genes based on log-linear model | ZHOU Rong-ge, ZHANG Jing(120) |
| In Silico Cloning and Characterization of Sorghum APX Gene | CHEN Guo-qiang, MENG Peng, LIU Li-li, CHEN Gang, WANG Ping(125) |
| Cloning and Sequence Analysis of the Xylose Reductase Gene(xyl1) from Pichia Stipitis | SUN Bo, GE Jing-ping(131) |
| Binding Dynamics calculation for Cytochrome P450 BM - 3 Catalyzing n-hexadecane | YAO Xue-feng, SONG Yi-ling(134) |
| Application of R/BioConductor software in microarray analysis | ZHEN Yi-song, ZHANG wei-li, WU Qing, XIAO Cheng-lu(138) |
| A New Algorithm for Simulation of Protein Folding Process | ZHANG Tian-chi, ZHANG Jing(142) |
| Biological Sequence Alignment Algorithm Research Based on Graphics Hardware Acceleration | ZHANG Lin, CHAI Hui, WO Li-ke, YUAN Xiao-feng, HUANG Yan-fen(146) |
| Divergent in structure and gene content between human and chimpanzee MSY region | JIN Neng-zhi, ZHANG Jing, SHEN Yu-lin, SUN Yi-tong(151) |
| Ginsenoside Rb1 on cerebral ischemia-reperfusion nerve injury repair | LI Ming-qiang, ZENG Zhao-fang, YOU Ping(155) |
| Review of prediction of RNA secondary structure with pseudoknots based on heuristic algorithms | CHAO Jiang-tao, MA Chun-sen(157) |
| Feature Extraction for Cancer Gene Expression Profiles Based on Local Non-negative Matrix Factorization | WANG Rui-ping, WANG Nian, SU Liang-liang, CHEN Le(164) |
| A SVR-Based Method for Identifying Near-Native CPCR-Ligand Conformation Decoys | YANG Ling-yun, Lü Qiang(167) |
| Prediction of protein subcellular location using optimal cleavage site | WANG Wei, ZHENG Xiao-Qi, DOU Yong-Chao, LIU Tai-Gang, ZHAO Juan, WANG Jun(171) |
| Bioinformatic Analysis of Mouse Genes Controlled by DEAF1 | SHENG De-qiao(176) |