ポスター賞

最優秀賞

201 SOLUTION STRUCTURE OF CHITINASE-ARGIFIN COMPLEX STUDIED BY MOLECULAR DYNAMICS

Hiroaki Gouda¹, Shuichi Hirono¹

(School of Pharmaceutical Sciences, Kitasato University¹)

優秀賞

111 BioStation Dock: Application of protein-ligand docking to screen

<u>Toshiyuki Sato</u>^{1,2}, Ikuo Okouchi^{1,2}, Kaori Fukuzawa^{1,2}, Kozo Aoki³, Kazuo Koyano¹, Shinji Amari³, Katsuki Amemiya¹, and Tatsuya Nakano⁴

(AdvanceSoft Corporation ¹, Fuji Research Institute Corporation ², University of Tokyo ³, and National Institute of Health Sciences ⁴)

110 Interaction analysis for SARS virus proteinase and its ligands with ab initio FMO method

Shinji Amari¹, Mayuko Takeda-Shitaka², Mitsuo Iwadate², Norio Yamamoto³, Nobutaka Fujii⁴, Naoki Yamamoto³, Hideaki Umeyama², Tatsuya Nakano⁵ (University of Tokyo¹, Kitasato University², Tokyo Medical and Dental University³, Kyoto University⁴, National Institute of Health Sciences⁵)

324 Analysis of transmembrane segment for membrane protein discrimination

Toshiyuki Tsuji 1, Shigeki Mitaku 1

(Division of Applied Physics Graduate School of Engineering Nagoya University 1)

分野優秀賞

MD simulation of asymmetric phospholipid bilayers (POPC/POPE-POPS) with the physiological concentration of ions and cholesterols Kenichi Mori, Masayuki Hata, Saburo Neya, Tyuji Hoshino (Graduate School of Pharmaceutical Sciences, Chiba University)

204 Generation of a novel equation for logP estimation using a neural network

<u>Sumie Tajima</u>¹, Kenji Yamagishi², Makoto Haraguchi¹, Umpei Nagashima³ (Bestsystems Inc.¹, Rikkyo University², Grid Technology Research Center³)

Analysis of Similar Structural Protein with Low Sequence Identity by Coarse-Grained Charge Distribution in Sequence

Kenichiro Imai, Shigeki Mitaku

(Division of Applied Physics Graduate School of Engineering Nagoya University)

419 Automatic generation of cell-wide pathway model from complete genome

<u>Kazuharu Arakawa</u>^{1,2}, Yohei Yamada^{1,3}, Hiromi Komai^{1,3}, Kosaku Shinoda^{1,4}, Yoichi Nakayama^{1,3}, Masaru Tomita^{1,3}

(Institute for Advanced Biosciences, Keio University ¹, Bioinformatics Program, Graduate School of Media and Governance², Department of Environmental Information³, Department of Policy Management⁴)

502 Analysis and Prediction of Drug Excretion into Human Breast Milk (2nd)

- Additional Analysis Including Hydrophilic Compounds -

<u>Takashi Fujiwara</u>, Yuki Hibino, Masaru Kihara, Aiko Yamauchi, Hiroshi Chuman (Graduate School of Pharmaceutical Sciences, The University of Tokushima)

An Electrophysiological Simulation Model of the Myocardial Cell Using E-CELL System

Sayaka Ishinabe ^{1,2}, Yasuhiro Naito ^{1,3}, Motohiro Yoneda ^{1,2}, Katsuya Kawai ^{1,2}, Shoko Miyamoto ^{1,2}, Shinobu Kuratomi ⁴, Nobuaki Sarai ⁴, Satoru Matsuoka ⁴, Akinori Noma ⁴, Masaru (Institute for Advanced Biosciences, Keio University ¹, Graduate School of Media and Governance, Keio University², Department of Environmental Information, Keio University ³, Department of Physiology and Biophysics, Graduate School of Medicine, Kyoto University ⁴)

710 Development of a molecular memory system based on hairpin DNA

<u>Masahiro Takinoue</u>¹, Akira Suyama^{1, 2} (Institute of Physics University of Tokyo¹, JST CREST²)