

# Bioinformatics

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## DISCOVERY NOTE

### *Genome analysis*

**Enriched transcription factor binding sites in hypermethylated gene promoters in drug resistant cancer cells**

M.Li, H.-i.H.Paik, C.Balch, Y.Kim, L.Li, T.H.-M.Huang, K.P.Nephew and S.Kim

## ORIGINAL PAPERS

### *Genome analysis*

**A probe-density-based analysis method for array CGH data: simulation, normalization and centralization**

H.-I.H.Chen, F.-H.Hsu, Y.Jiang, M.-H.Tsai, P.-C.Yang, P.S.Meltzer, E.Y.Chuang and Y.Chen

**Database indexing for production MegaBLAST searches**

A.Morgulis, G.Coulouris, Y.Raytselis, T.L.Madden, R.Agarwala and A.A.Schäffer

### *Sequence analysis*

**Efficient functional clustering of protein sequences using the Dirichlet process**

D.P.Brown

**Memory-efficient dynamic programming backtrack and pairwise local sequence alignment**

L.A.Newberg

**Predicting sub-Golgi localization of type II membrane proteins**

A.D.J.van Dijk, D.Bosch, C.J.Fter Braak, A.R.van der Krol and R.C.H.J.van Ham

**Predicting functional regulatory polymorphisms**

A.Torkamani and N.J.Schork

**Sequence analysis of GerM and SpoVS, uncharacterized bacterial 'sporulation' proteins with widespread phylogenetic distribution**

D.J.Rigden and M.Y.Galperin

### *Structural bioinformatics*

**Intrinsic disorder prediction from the analysis of multiple protein fold recognition models**

L.J.McGuffin

### *Genetics and population analysis*

**Systematic biological prioritization after a genome-wide association study: an application to nicotine dependence**

S.F.Saccone, N.L.Saccone, G.E.Swan, P.A.F.Madden, A.M.Goate, J.P.Rice and L.J.Bierut

### *Data and text mining*

**Biomarker selection and sample prediction for multi-category disease on MALDI-TOF data**

J.H.Oh, Y.B.Kim, P.Gurnani, K.P.Rosenblatt and J.X.Gao

## APPLICATIONS NOTE

### *Structural bioinformatics*

**MINS2: Revisiting the molecular code for transmembrane-helix recognition by the Sec61 translocon**

Y.Park and V.Helms

### *Genetics and population analysis*

**ForSim: a tool for exploring the genetic architecture of complex traits with controlled truth**

B.W.Lambert, J.D.Terwilliger and K.M.Weiss

### *Databases and ontologies*

**BioMAJ: a flexible framework for databanks synchronization and processing**

O.Filangi, Y.Beausse, A.Assi, L.Legrand, J.-M.Larré, V.Martin, O.Collin, C.Caron, H.Leroy and D.Allouche

