

## DISCOVERY NOTE

*Sequence analysis*

**Isolated ZP-N domains constitute the N-terminal extensions of Zona Pellucida proteins**

I.Callebaut, J.-P.Mornon and P.Monget

1871

## ORIGINAL PAPERS

*Sequence analysis*

**Predicting functionally important residues from sequence conservation**

J.A.Capra and M.Singh

1875

**RNA Sampler: a new sampling based algorithm for common RNA secondary structure prediction and structural alignment**

X.Xu, Y.Ji and G.D.Stormo

1883

**PALMA: mRNA to genome alignments using large margin algorithms**

U.Schulze, B.Hepp, C.S.Ong and G.Rätsch

1892

*Structural bioinformatics*

**An evaluation of automated homology modelling methods at low target-template sequence similarity**

J.A.R.Dalton and R.M.Jackson

1901

**Secondary structure based analysis and classification of biological interfaces: identification of binding motifs in protein-protein interactions**

M.Guharoy and P.Chakrabarti

1909

**Exploring sequence-structure relationships in the tyrosine kinome space: functional classification of the binding specificity mechanisms for cancer therapeutics**

G.M.Verkhivker

1919

*Gene expression*

**Mining co-regulated gene profiles for the detection of functional associations in gene expression data**

A.Gyenesi, U.Wagner, S.Barkow-Oesterreicher, E.Stolte and R.Schlapbach

1927

**Bayesian modelling of shared gene function**

P.Sykacek, R.Clarkson, C.Print, R.Furlong and G.Micklem

1936

**Logistic regression for disease classification using microarray data: model selection in a large  $p$  and small  $n$  case**

J.G.Liao and K.-V.Chin

1945

*Genetics and population analysis*

**Computational identification of candidate loci for recessively inherited mutation using high-throughput SNP arrays**

M.Laakso, S.Tuupainen, A.Karhu, R.Lehtonen, L.A.Aaltonen and S.Hautaniemi

1952

**The evolutionary forest algorithm**

S.C.Leman, M.K.Uyenoyama, M.Lavine and Y.Chen

1962

*Systems biology*

**Computational methods for diffusion-influenced biochemical reactions**

M.Dobrzyński, J.V.Rodríguez, J.A.Kaandorp and J.G.Blom

1969

**Simple and fast alignment of metabolic pathways by exploiting local diversity**

S.Wernicke and F.Rasche

1978

**Non-parametric quantification of protein lysate arrays**

J.Hu, X.He, K.A.Baggerly, K.R.Coombes, B.T.J.Hennessy and G.B.Mills

1986

*Data and text mining*

**Clustering microarray-derived gene lists through implicit literature relationships**

M.F.Burkart, J.D.Wren, J.I.Herschkowitz, C.M.Perou and H.R.Garner

1995

**Statistical prediction of protein-chemical interactions based on chemical structure and mass spectrometry data**

N.Nagamine and Y.Sakakibara

2004

## APPLICATIONS NOTES

*Genome analysis*

**Tree Gibbs Sampler: identifying conserved motifs without aligning orthologous sequences**

X.Cai, H.Hu and X.S.Li

2013

*Sequence analysis*

**The Cytochrome P450 Engineering Database: a navigation and prediction tool for the cytochrome P450 protein family**

M.Fischer, M.Knoll, D.Sirim, F.Wagner, S.Funke and J.Pleiss

2015

*Structural bioinformatics*

**StrBioLib: a Java library for development of custom computational structural biology applications**

J.-M.Chandonia

2018

*Data and text mining*

**VIPER: an advanced software package to support high-throughput LC-MS peptide identification**

M.E.Monroe, N.Tolić, N.Jaitly, J.L.Shaw, J.N.Adkins and R.D.Smith

2021

**VISDA: an open-source caBIG<sup>TM</sup> analytical tool for data clustering and beyond**

J.Wang, H.Li, Y.Zhu, M.Yousef, M.Nebozhyn, M.Showe, L.Showe, J.Xuan, R.Clarke and Y.Wang

2024

## CORRIGENDUM