

Petter Mostad

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

1,116
citations

393982

19
h-index

414034

32
g-index

36
all docs

36
docs citations

36
times ranked

1383
citing authors

#	ARTICLE	IF	CITATIONS
1	Mathematically optimal decisions in forensic age assessment. <i>International Journal of Legal Medicine</i> , 2022, 136, 765-776.	1.2	4
2	Surveillance of animal diseases through implementation of a Bayesian spatio-temporal model: A simulation example with neurological syndromes in horses and West Nile Virus. <i>Preventive Veterinary Medicine</i> , 2019, 162, 95-106.	0.7	1
3	Application of the Bayesian framework for forensic interpretation to casework involving postmortem interval estimates of decomposed human remains. <i>Forensic Science International</i> , 2019, 301, 402-414.	1.3	11
4	Error rates for unvalidated medical age assessment procedures. <i>International Journal of Legal Medicine</i> , 2019, 133, 613-623.	1.2	21
5	Determining the optimal forensic DNA analysis procedure following investigation of sample quality. <i>International Journal of Legal Medicine</i> , 2018, 132, 955-966.	1.2	5
6	Detection probability models for bacteria, and how to obtain them from heterogeneous spiking data. An application to <i>Bacillus anthracis</i> . <i>International Journal of Food Microbiology</i> , 2017, 241, 78-88.	2.1	0
7	Dependent markers. , 2016, , 85-129.		0
8	Stationary mutation models. <i>Forensic Science International: Genetics</i> , 2016, 23, 217-225.	1.6	11
9	Making decisions. , 2016, , 203-228.		0
10	A general model for likelihood computations of genetic marker data accounting for linkage, linkage disequilibrium, and mutations. <i>International Journal of Legal Medicine</i> , 2015, 129, 943-954.	1.2	26
11	Enhanced low-template DNA analysis conditions and investigation of allele dropout patterns. <i>Forensic Science International: Genetics</i> , 2015, 14, 61-75.	1.6	22
12	Choosing supplementary markers in forensic casework. <i>Forensic Science International: Genetics</i> , 2014, 13, 128-133.	1.6	19
13	A phylogenetic comparative method for studying multivariate adaptation. <i>Journal of Theoretical Biology</i> , 2012, 314, 204-215.	0.8	139
14	Using Object Oriented Bayesian Networks to Model Linkage, Linkage Disequilibrium and Mutations between STR Markers. <i>PLoS ONE</i> , 2012, 7, e43873.	1.1	5
15	Using X-chromosomal markers in relationship testing: Calculation of likelihood ratios taking both linkage and linkage disequilibrium into account. <i>Forensic Science International: Genetics</i> , 2011, 5, 506-511.	1.6	41
16	Response to: DNA identification by pedigree likelihood ratio accommodating population substructure and mutations. <i>Investigative Genetics</i> , 2011, 2, 7.	3.3	2
17	Empirical Bayes models for multiple probe type microarrays at the probe level. <i>BMC Bioinformatics</i> , 2008, 9, 156.	1.2	9
18	Transcriptome analysis of a respiratory <i>Saccharomyces cerevisiae</i> strain suggests the expression of its phenotype is glucose insensitive and predominantly controlled by Hap4, Cat8 and Mig1. <i>BMC Genomics</i> , 2008, 9, 365.	1.2	27

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19	Analysis of linkage and linkage disequilibrium for eight X-STR markers. <i>Forensic Science International: Genetics</i> , 2008, 3, 37-41.	1.6	52
20	Glomerulus-specific mRNA transcripts and proteins identified through kidney expressed sequence tag database analysis. <i>Kidney International</i> , 2007, 71, 889-900.	2.6	32
21	Improved Covariance Matrix Estimators for Weighted Analysis of Microarray Data. <i>Journal of Computational Biology</i> , 2007, 14, 1353-1367.	0.8	4
22	DNA-testing for immigration cases: The risk of erroneous conclusions. <i>Forensic Science International</i> , 2007, 172, 144-149.	1.3	35
23	HeliCis: a DNA motif discovery tool for colocalized motif pairs with periodic spacing. <i>BMC Bioinformatics</i> , 2007, 8, 418.	1.2	9
24	Large-scale identification of genes implicated in kidney glomerulus development and function. <i>EMBO Journal</i> , 2006, 25, 1160-1174.	3.5	196
25	Design of improved membrane protein production experiments: Quantitation of the host response. <i>Protein Science</i> , 2005, 14, 1729-1740.	3.1	62
26	Predictive screening for regulators of conserved functional gene modules (gene batteries) in mammals. <i>BMC Genomics</i> , 2005, 6, 68.	1.2	35
27	Stochastic Structural Modeling. <i>Mathematical Geosciences</i> , 2003, 35, 899-914.	0.9	61
28	Estimating the number of contributors to a DNA profile. <i>International Journal of Legal Medicine</i> , 2003, 117, 271-275.	1.2	42
29	Quantitative Real-Time PCR Method for Detection of B-Lymphocyte Monoclonality by Comparison of \hat{I}^{β} and \hat{I}^{α} Immunoglobulin Light Chain Expression. <i>Clinical Chemistry</i> , 2003, 49, 51-59.	1.5	128
30	Prediction of Cell Type-Specific Gene Modules: Identification and Initial Characterization of a Core Set of Smooth Muscle-Specific Genes. <i>Genome Research</i> , 2003, 13, 1838-54.	2.4	32
31	A clustering algorithm using DNA marker information for sub-pedigree reconstruction. <i>Journal of Forensic Sciences</i> , 2003, 48, 1239-48.	0.9	2
32	Havana "a" a fault modeling tool. <i>Norwegian Petroleum Society Special Publications</i> , 2002, , 157-171.	0.1	30
33	DNA MICROARRAY ANALYSIS OF TRANSFORMING GROWTH FACTOR- \hat{I}^{β} AND RELATED TRANSCRIPTS IN NASAL BIOPSIES FROM PATIENTS WITH ALLERGIC RHINITIS. <i>Cytokine</i> , 2002, 18, 20-25.	1.4	30
34	Statistical Genetics and Genetical Statistics: a Forensic Perspective*. <i>Scandinavian Journal of Statistics</i> , 2002, 29, 297-307.	0.9	19
35	Estimation of Gross Rock Volume of Filled Geological Structures With Uncertainty Measures. <i>SPE Reservoir Evaluation and Engineering</i> , 2000, 3, 304-309.	1.1	4