## Petter Mostad

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Mathematically optimal decisions in forensic age assessment. International Journal of Legal Medicine, 2022, 136, 765-776.	2.2	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. Preventive Veterinary Medicine, 2019, 162, 95-106.	1.9	1
3	Application of the Bayesian framework for forensic interpretation to casework involving postmortem interval estimates of decomposed human remains. Forensic Science International, 2019, 301, 402-414.	2.2	11
4	Error rates for unvalidated medical age assessment procedures. International Journal of Legal Medicine, 2019, 133, 613-623.	2.2	21
5	Determining the optimal forensic DNA analysis procedure following investigation of sample quality. International Journal of Legal Medicine, 2018, 132, 955-966.	2.2	5
6	Detection probability models for bacteria, and how to obtain them from heterogeneous spiking data. An application to Bacillus anthracis. International Journal of Food Microbiology, 2017, 241, 78-88.	4.7	0
7	Dependent markers. , 2016, , 85-129.		Ο
8	Stationary mutation models. Forensic Science International: Genetics, 2016, 23, 217-225.	3.1	11
9	Making decisions. , 2016, , 203-228.		О
10	A general model for likelihood computations of genetic marker data accounting for linkage, linkage disequilibrium, and mutations. International Journal of Legal Medicine, 2015, 129, 943-954.	2.2	26
11	Enhanced low-template DNA analysis conditions and investigation of allele dropout patterns. Forensic Science International: Genetics, 2015, 14, 61-75.	3.1	22
12	Choosing supplementary markers in forensic casework. Forensic Science International: Genetics, 2014, 13, 128-133.	3.1	19
13	A phylogenetic comparative method for studying multivariate adaptation. Journal of Theoretical Biology, 2012, 314, 204-215.	1.7	139
14	Using Object Oriented Bayesian Networks to Model Linkage, Linkage Disequilibrium and Mutations between STR Markers. PLoS ONE, 2012, 7, e43873.	2.5	5
15	Using X-chromosomal markers in relationship testing: Calculation of likelihood ratios taking both linkage and linkage disequilibrium into account. Forensic Science International: Genetics, 2011, 5, 506-511.	3.1	41
16	Response to: DNA identification by pedigree likelihood ratio accommodating population substructure and mutations. Investigative Genetics, 2011, 2, 7.	3.3	2
17	Empirical Bayes models for multiple probe type microarrays at the probe level. BMC Bioinformatics, 2008, 9, 156.	2.6	9
18	Transcriptome analysis of a respiratory Saccharomyces cerevisiae strain suggests the expression of its phenotype is glucose insensitive and predominantly controlled by Hap4, Cat8 and Mig1. BMC Genomics. 2008, 9, 365.	2.8	27

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19	Analysis of linkage and linkage disequilibrium for eight X-STR markers. Forensic Science International: Genetics, 2008, 3, 37-41.	3.1	52
20	Glomerulus-specific mRNA transcripts and proteins identified through kidney expressed sequence tag database analysis. Kidney International, 2007, 71, 889-900.	5.2	32
21	Improved Covariance Matrix Estimators for Weighted Analysis of Microarray Data. Journal of Computational Biology, 2007, 14, 1353-1367.	1.6	4
22	DNA-testing for immigration cases: The risk of erroneous conclusions. Forensic Science International, 2007, 172, 144-149.	2.2	35
23	HeliCis: a DNA motif discovery tool for colocalized motif pairs with periodic spacing. BMC Bioinformatics, 2007, 8, 418.	2.6	9
24	Large-scale identification of genes implicated in kidney glomerulus development and function. EMBO Journal, 2006, 25, 1160-1174.	7.8	196
25	Design of improved membrane protein production experiments: Quantitation of the host response. Protein Science, 2005, 14, 1729-1740.	7.6	62
26	Predictive screening for regulators of conserved functional gene modules (gene batteries) in mammals. BMC Genomics, 2005, 6, 68.	2.8	35
27	Stochastic Structural Modeling. Mathematical Geosciences, 2003, 35, 899-914.	0.9	61
28	Estimating the number of contributors to a DNA profile. International Journal of Legal Medicine, 2003, 117, 271-275.	2.2	42
29	Quantitative Real-Time PCR Method for Detection of B-Lymphocyte Monoclonality by Comparison of κ and λ Immunoglobulin Light Chain Expression. Clinical Chemistry, 2003, 49, 51-59.	3.2	128
30	Prediction of Cell Type-Specific Gene Modules: Identification and Initial Characterization of a Core Set of Smooth Muscle-Specific Genes. Genome Research, 2003, 13, 1838-54.	5.5	32
31	A clustering algorithm using DNA marker information for sub-pedigree reconstruction. Journal of Forensic Sciences, 2003, 48, 1239-48.	1.6	2
32	Havana — a fault modeling tool. Norwegian Petroleum Society Special Publications, 2002, , 157-171.	0.1	30
33	DNA MICROARRAY ANALYSIS OF TRANSFORMING GROWTH FACTOR-Î <sup>2</sup> AND RELATED TRANSCRIPTS IN NASAL BIOPSIES FROM PATIENTS WITH ALLERGIC RHINITIS. Cytokine, 2002, 18, 20-25.	3.2	30
34	Statistical Genetics and Genetical Statistics: a Forensic Perspective*. Scandinavian Journal of Statistics, 2002, 29, 297-307.	1.4	19
35	Estimation of Gross Rock Volume of Filled Geological Structures With Uncertainty Measures. SPE Reservoir Evaluation and Engineering, 2000, 3, 304-309.	1.8	4