

Erinija Pranckeviciene

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

377
citations

1162889
8
h-index

839398
18
g-index

37
all docs

37
docs citations

37
times ranked

681
citing authors

#	ARTICLE	IF	CITATIONS
1	HIV-1 Modulates the tRNA Pool to Improve Translation Efficiency. <i>Molecular Biology and Evolution</i> , 2011, 28, 1827-1834.	3.5	94
2	Comparative expression profiling identifies differential roles for Myogenin and p38 β MAPK signaling in myogenesis. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 386-397.	1.5	64
3	Trichostatin A Enhances Vascular Repair by Injected Human Endothelial Progenitors through Increasing the Expression of TAL1-Dependent Genes. <i>Cell Stem Cell</i> , 2014, 14, 644-657.	5.2	48
4	Advances in sports genomics. <i>Advances in Clinical Chemistry</i> , 2022, 107, 215-263.	1.8	33
5	Perspectives in Sports Genomics. <i>Biomedicines</i> , 2022, 10, 298.	1.4	24
6	Relating fitness phenotypes to genotypes in Lithuanian elite athletes. <i>Acta Medica Lituanica</i> , 2010, 17, 1-10.	0.2	17
7	A Data-Driven, Flexible Machine Learning Strategy for the Classification of Biomedical Data. , 2004, , 67-85.		11
8	Identification of signatures in biomedical spectra using domain knowledge. <i>Artificial Intelligence in Medicine</i> , 2005, 35, 215-226.	3.8	10
9	Using Domain Knowledge in the Random Subspace Method: Application to the Classification of Biomedical Spectra. <i>Lecture Notes in Computer Science</i> , 2005, , 336-345.	1.0	10
10	Class Separability in Spaces Reduced By Feature Selection. , 2006, , .		9
11	Gene variants related to the power performance of the Lithuanian athletes. <i>Open Life Sciences</i> , 2011, 6, 48-57.	0.6	7
12	Total Genotype Score Modelling of Polygenic Endurance-Power Profiles in Lithuanian Elite Athletes. <i>Genes</i> , 2021, 12, 1067.	1.0	7
13	Feature/Model Selection by the Linear Programming SVM Combined with State-of-Art Classifiers: What Can We Learn About the Data. <i>Neural Networks (IJCNN)</i> , International Joint Conference on, 2007, , .	0.0	6
14	Challenges in exome analysis by LifeScope and its alternative computational pipelines. <i>BMC Research Notes</i> , 2015, 8, 421.	0.6	5
15	Nucleosome positioning sequence patterns as packing or regulatory. <i>PLoS Computational Biology</i> , 2020, 16, e1007365.	1.5	4
16	Variants in the Myostatin Gene and Physical Performance Phenotype of Elite Athletes. <i>Genes</i> , 2021, 12, 757.	1.0	4
17	Automatic Ischemic Stroke Segmentation Using Various Techniques. , 2003, , 498-503.		4
18	Novel In-Frame Deletion in HTRA1 Gene, Responsible for Stroke at a Young Age and Dementia—A Case Study. <i>Genes</i> , 2021, 12, 1955.	1.0	4

#	ARTICLE	IF	CITATIONS
19	On Classification Models of Gene Expression Microarrays: The Simpler the Better. , 2006, , .		3
20	Inferring Effective Population Size and Divergence Time in the Lithuanian Population According to High-Density Genotyping Data. Genes, 2020, 11, 293.	1.0	3
21	Features of <i>KAT6B</i> -related disorders in a patient with 10q22.1q22.3 deletion. Ophthalmic Genetics, 2017, 38, 383-386.	0.5	2
22	Consensus-based identification of spectral signatures for classification of high-dimensional biomedical spectra. , 2004, , .		1
23	Validation of bcbio-nextgen Pipeline Based on NextSeq500 Exome Sequencing. , 2019, , .		1
24	Control of Sparseness for Feature Selection. Lecture Notes in Computer Science, 2004, , 707-715.	1.0	1
25	Procedure and datasets to compute links between genes and phenotypes defined by MeSH keywords. F1000Research, 0, 4, 47.	0.8	1
26	On Classification Models of Gene Expression Microarrays: The Simpler the Better. , 0, , .		0
27	Gene Prioritization Using Semantic Similarity. , 2019, , 898-906.		0
28	Adopting High-Resolution Allele Frequencies Substantially Expedites Variant Interpretation in Genetic Diagnostic Laboratories. Journal of Molecular Diagnostics, 2019, 21, 602-611.	1.2	0
29	Interplay between probe design and test performance: overlap between genomic regions of interest, capture regions and high quality reference calls influence performance of WES-based assays. Human Genetics, 2021, 140, 289-297.	1.8	0
30	Application of the Biologically Inspired Network for Electroencephalogram Analysis. Lecture Notes in Computer Science, 2001, , 18-27.	1.0	0
31	Integrating Liknon Feature Selection and Committee Training. Studies in Computational Intelligence, 2009, , 233-250.	0.7	0
32	Donor Splice Site Variant in SLC9A6 Causes Christianson Syndrome in a Lithuanian Family: A Case Report. Medicina (Lithuania), 2022, 58, 351.	0.8	0
33	Galaxy Dnpatterntools for Computational Analysis of Nucleosome Positioning Sequence Patterns. International Journal of Molecular Sciences, 2022, 23, 4869.	1.8	0