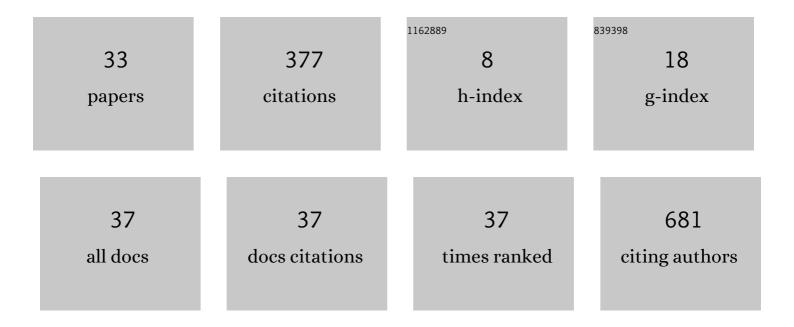
Erinija Pranckeviciene

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7834439/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Advances in sports genomics. Advances in Clinical Chemistry, 2022, 107, 215-263.	1.8	33
2	Perspectives in Sports Genomics. Biomedicines, 2022, 10, 298.	1.4	24
3	Donor Splice Site Variant in SLC9A6 Causes Christianson Syndrome in a Lithuanian Family: A Case Report. Medicina (Lithuania), 2022, 58, 351.	0.8	0
4	Galaxy Dnpatterntools for Computational Analysis of Nucleosome Positioning Sequence Patterns. International Journal of Molecular Sciences, 2022, 23, 4869.	1.8	0
5	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	Ο
6	Variants in the Myostatin Gene and Physical Performance Phenotype of Elite Athletes. Genes, 2021, 12, 757.	1.0	4
7	Total Genotype Score Modelling of Polygenic Endurance-Power Profiles in Lithuanian Elite Athletes. Genes, 2021, 12, 1067.	1.0	7
8	Novel In-Frame Deletion in HTRA1 Gene, Responsible for Stroke at a Young Age and Dementia—A Case Study. Genes, 2021, 12, 1955.	1.0	4
9	Inferring Effective Population Size and Divergence Time in the Lithuanian Population According to High-Density Genotyping Data. Genes, 2020, 11, 293.	1.0	3
10	Nucleosome positioning sequence patterns as packing or regulatory. PLoS Computational Biology, 2020, 16, e1007365.	1.5	4
11	Gene Prioritization Using Semantic Similarity. , 2019, , 898-906.		0
12	Adopting High-Resolution Allele Frequencies Substantially Expedites Variant Interpretation in Genetic Diagnostic Laboratories. Journal of Molecular Diagnostics, 2019, 21, 602-611.	1.2	0
13	Validation of bcbio-nextgen Pipeline Based on NextSeq500 Exome Sequencing. , 2019, , .		1
14	Features of <i>KAT6B</i> -related disorders in a patient with 10q22.1q22.3 deletion. Ophthalmic Genetics, 2017, 38, 383-386.	0.5	2
15	Challenges in exome analysis by LifeScope and its alternative computational pipelines. BMC Research Notes, 2015, 8, 421.	0.6	5
16	Trichostatin A Enhances Vascular Repair by Injected Human Endothelial Progenitors through Increasing the Expression of TAL1-Dependent Genes. Cell Stem Cell, 2014, 14, 644-657.	5.2	48
17	Comparative expression profiling identifies differential roles for Myogenin and p38α MAPK signaling in myogenesis. Journal of Molecular Cell Biology, 2012, 4, 386-397.	1.5	64
18	Gene variants related to the power performance of the Lithuanian athletes. Open Life Sciences, 2011, 6, 48-57.	0.6	7

Erinija Pranckeviciene

#	Article	IF	CITATIONS
19	HIV-1 Modulates the tRNA Pool to Improve Translation Efficiency. Molecular Biology and Evolution, 2011, 28, 1827-1834.	3.5	94
20	Relating fitness phenotypes to genotypes in Lithuanian elite athletes. Acta Medica Lituanica, 2010, 17, 1-10.	0.2	17
21	Integrating Liknon Feature Selection and Committee Training. Studies in Computational Intelligence, 2009, , 233-250.	0.7	0
22	Feature/Model Selection by the Linear Programming SVM Combined with State-of-Art Classifiers: What Can We Learn About the Data. Neural Networks (IJCNN), International Joint Conference on, 2007, , .	0.0	6
23	Class Separability in Spaces Reduced By Feature Selection. , 2006, , .		9
24	On Classification Models of Gene Expression Microarrays: The Simpler the Better. , 2006, , .		3
25	Identification of signatures in biomedical spectra using domain knowledge. Artificial Intelligence in Medicine, 2005, 35, 215-226.	3.8	10
26	Using Domain Knowledge in the Random Subspace Method: Application to the Classification of Biomedical Spectra. Lecture Notes in Computer Science, 2005, , 336-345.	1.0	10
27	Consensus-based identification of spectral signatures for classification of high-dimensional biomedical spectra. , 2004, , .		1
28	A Data-Driven, Flexible Machine Learning Strategy for the Classification of Biomedical Data. , 2004, , 67-85.		11
29	Control of Sparseness for Feature Selection. Lecture Notes in Computer Science, 2004, , 707-715.	1.0	1
30	Automatic Ischemic Stroke Segmentation Using Various Techniques. , 2003, , 498-503.		4
31	Application of the Biologically Inspired Network for Electroencephalogram Analysis. Lecture Notes in Computer Science, 2001, , 18-27.	1.0	0
32	On Classification Models of Gene Expression Microarrays: The Simpler the Better. , 0, , .		0
33	Procedure and datasets to compute links between genes and phenotypes defined by MeSH keywords. F1000Research, 0, 4, 47.	0.8	1