Alexandros Kanterakis

List of Publications by Year
in descending order

49	1,929	567281 15	414414 32
papers	citations	h-index	g-index

50	50	50	6670
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	21.4	641
2	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
3	Skewed X-inactivation is common in the general female population. European Journal of Human Genetics, 2019, 27, 455-465.	2.8	119
4	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
5	The MOLGENIS toolkit: rapid prototyping of biosoftware at the push of a button. BMC Bioinformatics, 2010, 11, S12.	2.6	102
6	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
7	Improved imputation quality of low-frequency and rare variants in European samples using the â€˜Genome of The Netherlandsâ€™. European Journal of Human Genetics, 2014, 22, 1321-1326.	2.8	92
8	Population-specific genotype imputations using minimac or IMPUTE2. Nature Protocols, 2015, 10, 1285-1296.	12.0	84
9	Transmission of human mtDNA heteroplasmy in the Genome of the Netherlands families: support for a variable-size bottleneck. Genome Research, 2016, 26, 417-426.	5.5	84
10	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
11	Integrated clinical and omics approach to rare diseases: novel genes and oligogenic inheritance in holoprosencephaly. Brain, 2019, 142, 35-49.	7.6	44
12	Exploring public genomics data for population pharmacogenomics. PLoS ONE, 2017, 12, e0182138.	2.5	35
13	Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant. Human Molecular Genetics, 2014, 23, 2481-2489.	2.9	32
14	Association analysis of copy numbers of FC-gamma receptor genes for rheumatoid arthritis and other immune-mediated phenotypes. European Journal of Human Genetics, 2016, 24, 263-270.	2.8	25
15	MinePath: Mining for Phenotype Differential Sub-paths in Molecular Pathways. PLoS Computational Biology, 2016, 12, e1005187.	3.2	23
16	Knowledge Discovery Scientific Workflows in Clinico-Genomics. , 2007, , .		19
17	Exome sequencing in a family segregating for celiac disease. Clinical Genetics, 2011, 80, 138-147.	2.0	16
18	ePGA: A Web-Based Information System for Translational Pharmacogenomics. PLoS ONE, 2016, 11, e0162801.	2.5	14

#	Article	IF	Citations
19	Scanning of Genetic Variants and Genetic Mapping of Phenotypic Traits in Gilthead Sea Bream Through ddRAD Sequencing. Frontiers in Genetics, 2019, 10, 675.	2.3	13
20	Molgenis-impute: imputation pipeline in a box. BMC Research Notes, 2015, 8, 359.	1.4	8
21	WGS-based telomere length analysis in Dutch family trios implicates stronger maternal inheritance and a role for RRM1 gene. Scientific Reports, 2019, 9, 18758.	3.3	8
22	Towards Reproducible Bioinformatics: The OpenBio-C Scientific Workflow Environment. , 2019, , .		7
23	Documentation of clinically relevant genomic biomarker allele frequencies in the nextâ€generation FINDbase worldwide database. Human Mutation, 2020, 41, 1112-1122.	2.5	7
24	A new gene expression signature related to breast cancer estrogen receptor status. , 2008, , .		4
25	Towards a MOLGENIS Based Computational Framework. , 2011, , .		4
26	Two novel HLAâ€A alleles, HLAâ€A*03:399 and â€A*24:17:01:02, detected in inhabitants from the island of Crete. Hla, 2021, 97, 353-356.	0.6	4
27	Two novel <scp>HLAâ€DRB1</scp> alleles detected in inhabitants from the island of Crete. Hla, 2021, 97, 163-166.	0.6	4
28	Significance of regional population HLA immunogenetic datasets in the efficacy of umbilical cord blood banks and marrow donor registries: a study of Cretan HLA genetic diversity. Cytotherapy, 2022, 24, 183-192.	0.7	4
29	Mining Interesting Clinico-Genomic Associations: The HealthObs Approach. , 2007, , 137-145.		4
30	Automated Mortality Prediction in Critically-ill Patients with Thrombosis using Machine Learning. , 2020, , .		4
31	PyPedia: using the wiki paradigm as crowd sourcing environment for bioinformatics protocols. Source Code for Biology and Medicine, 2015, 10, 14.	1.7	3
32	Discovery and Classification of Twitter Bots. SN Computer Science, 2022, 3, .	3.6	3
33	Mining Gene Expression Profiles and Gene Regulatory Networks: Identification of Phenotype-Specific Molecular Mechanisms. Lecture Notes in Computer Science, 2008, , 97-109.	1.3	2
34	On the development of an open and collaborative bioinformatics research environment. Procedia Computer Science, 2018, 126, 1062-1071.	2.0	2
35	Scientific discovery workflows in bioinformatics: a scenario for the coupling of molecular regulatory pathways and gene-expression profiles. Studies in Health Technology and Informatics, 2010, 160, 1304-8.	0.3	2
36	A semantically aware platform for the authoring and secure enactment of bioinformatics workflows. , 2009, 2009, 5625-8.		1

#	Article	IF	Citations
37	Creating Transparent and Reproducible Pipelines: Best Practices for Tools, Data, and Workflow Management Systems. , 2018, , 15-43.		1
38	A Review of Tools to Automatically Infer Chromosomal Positions From dbSNP and HGVS Genetic Variants. , 2018, , 133-156.		1
39	Enabling Ontology-Based Search: A Case Study in the Bioinformatics Domain. , 2019, , .		1
40	Converting Biomedical Text Annotated Resources into FAIR Research Objects with an Open Science Platform. Applied Sciences (Switzerland), 2021, 11, 9648.	2.5	1
41	Biomedical Literature Mining for Text Classification and Construction of Gene Networks. Lecture Notes in Computer Science, 2006, , 469-473.	1.3	1
42	Feature Selection for the Promoter Recognition and Prediction Problem. International Journal of Data Warehousing and Mining, 2007, 3, 60-78.	0.6	0
43	Enabling pharmacogenomic services: Informatics and computational discovery aspects. , 2015, , .		0
44	An Introduction to Tools, Databases, and Practical Guidelines for NGS Data Analysis. , 2018, , 61-89.		0
45	Translating Genomic Information to Rationalize Drug Use. , 2018, , 157-178.		0
46	Zazz: Variant Annotation and Exploration of Next Generation Sequencing Variants. , 2019, , .		0
47	Mining Time Series with Mine Time. Lecture Notes in Computer Science, 2006, , 158-168.	1.3	0
48	Feature Selection for the Promoter Recognition and Prediction Problem. , 2008, , 2248-2262.		0
49	Towards the Discovery of Reliable Biomarkers from Gene-Expression Profiles: An Iterative Constraint Satisfaction Learning Approach. Lecture Notes in Computer Science, 2010, , 233-242.	1.3	0