# 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 | 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 |
| 2 | Discovery and Classification of Twitter Bots. SN Computer Science, 2022, 3, . | 3.6 | 3 |
| 3 | 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 |
| 4 | Two novel <scp>HLAâ€DRB1</scp> alleles detected in inhabitants from the island of Crete. Hla, 2021, 97, 163-166. | 0.6 | 4 |
| 5 | Converting Biomedical Text Annotated Resources into FAIR Research Objects with an Open Science Platform. Applied Sciences (Switzerland), 2021, 11, 9648. | 2.5 | 1 |
| 6 | Documentation of clinically relevant genomic biomarker allele frequencies in the nextâ€generation FINDbase worldwide database. Human Mutation, 2020, 41, 1112-1122. | 2.5 | 7 |
| 7 | Automated Mortality Prediction in Critically-ill Patients with Thrombosis using Machine Learning. , 2020, , . | | 4 |
| 8 | 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 |
| 9 | Zazz: Variant Annotation and Exploration of Next Generation Sequencing Variants. , 2019, , . | | 0 |
| 10 | Towards Reproducible Bioinformatics: The OpenBio-C Scientific Workflow Environment. , 2019, , . | | 7 |
| 11 | 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 |
| 12 | Enabling Ontology-Based Search: A Case Study in the Bioinformatics Domain. , 2019, , . | | 1 |
| 13 | Skewed X-inactivation is common in the general female population. European Journal of Human Genetics, 2019, 27, 455-465. | 2.8 | 119 |
| 14 | Integrated clinical and omics approach to rare diseases: novel genes and oligogenic inheritance in holoprosencephaly. Brain, 2019, 142, 35-49. | 7.6 | 44 |
| 15 | On the development of an open and collaborative bioinformatics research environment. Procedia Computer Science, 2018, 126, 1062-1071. | 2.0 | 2 |
| 16 | An Introduction to Tools, Databases, and Practical Guidelines for NGS Data Analysis. , 2018, , 61-89. | | 0 |
| 17 | Translating Genomic Information to Rationalize Drug Use. , 2018, , 157-178. | | 0 |
| 18 | Creating Transparent and Reproducible Pipelines: Best Practices for Tools, Data, and Workflow Management Systems. , 2018, , 15-43. | | 1 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | A Review of Tools to Automatically Infer Chromosomal Positions From dbSNP and HGVS Genetic Variants. , 2018, , 133-156. | | 1 |
| 20 | Exploring public genomics data for population pharmacogenomics. PLoS ONE, 2017, 12, e0182138. | 2.5 | 35 |
| 21 | MinePath: Mining for Phenotype Differential Sub-paths in Molecular Pathways. PLoS Computational Biology, 2016, 12, e1005187. | 3.2 | 23 |
| 22 | A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989. | 12.8 | 99 |
| 23 | 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 |
| 24 | 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 |
| 25 | ePGA: A Web-Based Information System for Translational Pharmacogenomics. PLoS ONE, 2016, 11, e0162801. | 2.5 | 14 |
| 26 | PyPedia: using the wiki paradigm as crowd sourcing environment for bioinformatics protocols. Source Code for Biology and Medicine, 2015, 10, 14. | 1.7 | 3 |
| 27 | Enabling pharmacogenomic services: Informatics and computational discovery aspects. , 2015, , . | | 0 |
| 28 | Population-specific genotype imputations using minimac or IMPUTE2. Nature Protocols, 2015, 10, 1285-1296. | 12.0 | 84 |
| 29 | Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801. | 5.5 | 115 |
| 30 | Molgenis-impute: imputation pipeline in a box. BMC Research Notes, 2015, 8, 359. | 1.4 | 8 |
| 31 | Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065. | 12.8 | 45 |
| 32 | 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 |
| 33 | Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant. Human Molecular Genetics, 2014, 23, 2481-2489. | 2.9 | 32 |
| 34 | The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227. | 2.8 | 246 |
| 35 | Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825. | 21.4 | 641 |
| 36 | Exome sequencing in a family segregating for celiac disease. Clinical Genetics, 2011, 80, 138-147. | 2.0 | 16 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Towards a MOLGENIS Based Computational Framework. , 2011, , . | | 4 |
| 38 | The MOLGENIS toolkit: rapid prototyping of biosoftware at the push of a button. BMC Bioinformatics, 2010, 11, S12. | 2.6 | 102 |
| 39 | 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 |
| 40 | 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 |
| 41 | A semantically aware platform for the authoring and secure enactment of bioinformatics workflows. , 2009, 2009, 5625-8. | | 1 |
| 42 | A new gene expression signature related to breast cancer estrogen receptor status. , 2008, , . | | 4 |
| 43 | 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 |
| 44 | Feature Selection for the Promoter Recognition and Prediction Problem. , 2008, , 2248-2262. | | 0 |
| 45 | Knowledge Discovery Scientific Workflows in Clinico-Genomics. , 2007, , . | | 19 |
| 46 | Feature Selection for the Promoter Recognition and Prediction Problem. International Journal of Data Warehousing and Mining, 2007, 3, 60-78. | 0.6 | 0 |
| 47 | Mining Interesting Clinico-Genomic Associations: The HealthObs Approach. , 2007, , 137-145. | | 4 |
| 48 | Mining Time Series with Mine Time. Lecture Notes in Computer Science, 2006, , 158-168. | 1.3 | 0 |
| 49 | Biomedical Literature Mining for Text Classification and Construction of Gene Networks. Lecture Notes in Computer Science, 2006, , 469-473. | 1.3 | 1 |