

Warren Kibbe

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

18,739
citations

93792

39
h-index

81351

76
g-index

86
all docs

86
docs citations

86
times ranked

38197
citing authors

#	ARTICLE	IF	CITATIONS
1	Demonstrating an approach for evaluating synthetic geospatial and temporal epidemiologic data utility: results from analyzing >1.8 million SARS-CoV-2 tests in the United States National COVID Cohort Collaborative (N3C). Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1350-1365.	2.2	8
2	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	9.0	37
3	Association of Early Aspirin Use With In-Hospital Mortality in Patients With Moderate COVID-19. JAMA Network Open, 2022, 5, e223890.	2.8	31
4	Standardizing, harmonizing, and protecting data collection to broaden the impact of COVID-19 research: the rapid acceleration of diagnostics-underserved populations (RADx-UP) initiative. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1480-1488.	2.2	7
5	Simulating Colorectal Cancer Trials Using Real-World Data. JCO Clinical Cancer Informatics, 2022, , .	1.0	0
6	The National COVID Cohort Collaborative (N3C): Rationale, design, infrastructure, and deployment. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 427-443.	2.2	342
7	Reply: Matters Arising ~Investigating sources of inaccuracy in wearable optical heart rate sensors~™. Npj Digital Medicine, 2021, 4, 39.	5.7	7
8	Cancer Data Science and Computational Medicine. JCO Clinical Cancer Informatics, 2021, 5, 487-489.	1.0	4
9	Cancer Informatics for Cancer Centers: Scientific Drivers for Informatics, Data Science, and Care in Pediatric, Adolescent, and Young Adult Cancer. JCO Clinical Cancer Informatics, 2021, 5, 881-896.	1.0	3
10	Leveraging Clinical Informatics Tools to Extract Cumulative Anthracycline Exposure, Measure Cardiovascular Outcomes, and Assess Guideline Adherence for Children With Cancer. JCO Clinical Cancer Informatics, 2021, 5, 1062-1075.	1.0	1
11	At-home testing to mitigate community transmission of SARS-CoV-2: protocol for a public health intervention with a nested prospective cohort study. BMC Public Health, 2021, 21, 2209.	1.2	17
12	The Molecular Analysis for Therapy Choice (NCI-MATCH) Trial: Lessons for Genomic Trial Design. Journal of the National Cancer Institute, 2020, 112, 1021-1029.	3.0	138
13	Cancer Informatics for Cancer Centers (CI4CC): Building a Community Focused on Sharing Ideas and Best Practices to Improve Cancer Care and Patient Outcomes. JCO Clinical Cancer Informatics, 2020, 4, 108-116.	1.0	3
14	Investigating sources of inaccuracy in wearable optical heart rate sensors. Npj Digital Medicine, 2020, 3, 18.	5.7	317
15	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	13.5	334
16	DNA methylation of individual repetitive elements in hepatitis C virus infection-induced hepatocellular carcinoma. Clinical Epigenetics, 2019, 11, 145.	1.8	31
17	Complexity of Delivering Precision Medicine: Opportunities and Challenges. American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting, 2018, 38, 998-1007.	1.8	22
18	Data Harmonization for a Molecularly Driven Health System. Cell, 2018, 174, 1045-1048.	13.5	11

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19	Cancer Moonshot Data and Technology Team: Enabling a National Learning Healthcare System for Cancer to Unleash the Power of Data. <i>Clinical Pharmacology and Therapeutics</i> , 2017, 101, 613-615.	2.3	18
20	Prediction of genome-wide DNA methylation in repetitive elements. <i>Nucleic Acids Research</i> , 2017, 45, 8697-8711.	6.5	106
21	Cancer Informatics: New Tools for a Data-Driven Age in Cancer Research. <i>Cancer Research</i> , 2017, 77, e1-e2.	0.4	11
22	A Comprehensive Infrastructure for Big Data in Cancer Research: Accelerating Cancer Research and Precision Medicine. <i>Frontiers in Cell and Developmental Biology</i> , 2017, 5, 83.	1.8	59
23	Toward a Shared Vision for Cancer Genomic Data. <i>New England Journal of Medicine</i> , 2016, 375, 1109-1112.	13.9	1,242
24	Linking short tandem repeat polymorphisms with cytosine modifications in human lymphoblastoid cell lines. <i>Human Genetics</i> , 2016, 135, 223-232.	1.8	2
25	Blood Epigenetic Age may Predict Cancer Incidence and Mortality. <i>EBioMedicine</i> , 2016, 5, 68-73.	2.7	162
26	Generating a focused view of disease ontology cancer terms for pan-cancer data integration and analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav032-bav032.	1.4	40
27	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. <i>American Journal of Human Genetics</i> , 2015, 97, 111-124.	2.6	203
28	Disease Ontology 2015 update: an expanded and updated database of human diseases for linking biomedical knowledge through disease data. <i>Nucleic Acids Research</i> , 2015, 43, D1071-D1078.	6.5	498
29	Review of Current Methods, Applications, and Data Management for the Bioinformatics Analysis of Whole Exome Sequencing. <i>Cancer Informatics</i> , 2014, 13s2, CIN.S13779.	0.9	113
30	A statistical method to estimate DNA copy number from Illumina high-density methylation arrays. <i>Systems Biomedicine (Austin, Tex)</i> , 2013, 1, 94-98.	0.7	1
31	The Gene Ontology: enhancements for 2011. <i>Nucleic Acids Research</i> , 2012, 40, D559-D564.	6.5	191
32	dictyBase 2013: integrating multiple Dictyostelid species. <i>Nucleic Acids Research</i> , 2012, 41, D676-D683.	6.5	107
33	Gene Ontology Annotations and Resources. <i>Nucleic Acids Research</i> , 2012, 41, D530-D535.	6.5	456
34	The disease and gene annotations (DGA): an annotation resource for human disease. <i>Nucleic Acids Research</i> , 2012, 41, D553-D560.	6.5	53
35	Disease Ontology: a backbone for disease semantic integration. <i>Nucleic Acids Research</i> , 2012, 40, D940-D946.	6.5	793
36	DNA methylation alterations in response to pesticide exposure <i>in vitro</i> . <i>Environmental and Molecular Mutagenesis</i> , 2012, 53, 542-549.	0.9	68

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37	Text data extraction for a prospective, research-focused data mart: implementation and validation. BMC Medical Informatics and Decision Making, 2012, 12, 106.	1.5	13
38	Using the Bioconductor GeneAnswers Package to Interpret Gene Lists. Methods in Molecular Biology, 2012, 802, 101-112.	0.4	22
39	Genome-wide study of DNA methylation alterations in response to diazinon exposure in vitro. Environmental Toxicology and Pharmacology, 2012, 34, 959-968.	2.0	47
40	A Framework for Annotating Human Genome in Disease Context. PLoS ONE, 2012, 7, e49686.	1.1	13
41	The eMERGE Network: A consortium of biorepositories linked to electronic medical records data for conducting genomic studies. BMC Medical Genomics, 2011, 4, 13.	0.7	618
42	Mining the Gene Wiki for functional genomic knowledge. BMC Genomics, 2011, 12, 603.	1.2	8
43	Direct2Experts: a pilot national network to demonstrate interoperability among research-networking platforms. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, i157-i160.	2.2	25
44	dictyBase update 2011: web 2.0 functionality and the initial steps towards a genome portal for the Amoebozoa. Nucleic Acids Research, 2011, 39, D620-D624.	6.5	39
45	Comparison of Beta-value and M-value methods for quantifying methylation levels by microarray analysis. BMC Bioinformatics, 2010, 11, 587.	1.2	1,597
46	A collection of bioconductor methods to visualize gene-list annotations. BMC Research Notes, 2010, 3, 10.	0.6	47
47	The Gene Ontology in 2010: extensions and refinements. Nucleic Acids Research, 2010, 38, D331-D335.	6.5	450
48	Visual Presentation as a Welcome Alternative to Textual Presentation of Gene Annotation Information. Advances in Experimental Medicine and Biology, 2010, 680, 709-715.	0.8	5
49	From disease ontology to disease-ontology lite: statistical methods to adapt a general-purpose ontology for the test of gene-ontology associations. Bioinformatics, 2009, 25, i63-i68.	1.8	99
50	Visual annotation of the gene database. , 2009, 2009, 4175-7.		0
51	dictyBase—a Dictyostelium bioinformatics resource update. Nucleic Acids Research, 2009, 37, D515-D519.	6.5	71
52	Annotating the human genome with Disease Ontology. BMC Genomics, 2009, 10, S6.	1.2	204
53	The Gene Ontology project in 2008. Nucleic Acids Research, 2008, 36, D440-D444.	6.5	699
54	Model-based variance-stabilizing transformation for Illumina microarray data. Nucleic Acids Research, 2008, 36, e11-e11.	6.5	447

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55	<i>lumi</i>: a pipeline for processing Illumina microarray. <i>Bioinformatics</i> , 2008, 24, 1547-1548.	1.8	1,954
56	A divide-and-conquer strategy to solve the out-of-memory problem of processing thousands of Affymetrix microarrays. <i>International Journal of Computational Biology and Drug Design</i> , 2008, 1, 396.	0.3	0
57	Xanthusbase: adapting wikipedia principles to a model organism database. <i>Nucleic Acids Research</i> , 2007, 35, D422-D426.	6.5	13
58	OligoCalc: an online oligonucleotide properties calculator. <i>Nucleic Acids Research</i> , 2007, 35, W43-W46.	6.5	1,035
59	Mining Biomedical Data Using MetaMap Transfer (MMTx) and the Unified Medical Language System (UMLS). <i>Methods in Molecular Biology</i> , 2007, 408, 153-169.	0.4	22
60	Application of Wavelet Transform to the MS-based Proteomics Data Preprocessing. , 2007, , .		6
61	nulD: A universal naming schema of oligonucleotides for Illumina, Affymetrix, and other microarrays. <i>Biology Direct</i> , 2007, 2, 16.	1.9	75
62	Other riffs on cooperation are already showing how well a wiki could work. <i>Nature</i> , 2007, 446, 856-856.	13.7	6
63	Interpreting Microarray Results With Gene Ontology and MeSH. <i>Methods in Molecular Biology</i> , 2007, 377, 223-241.	0.4	24
64	Improved peak detection in mass spectrum by incorporating continuous wavelet transform-based pattern matching. <i>Bioinformatics</i> , 2006, 22, 2059-2065.	1.8	613
65	Annotating nonspecific SAGE tags with microarray data. <i>Genomics</i> , 2006, 87, 173-180.	1.3	7
66	The Informatics and Bioinformatics Infrastructure of a Nutrigenomics Biobank. , 2006, , 353-374.		0
67	The Gene Ontology (GO) project in 2006. <i>Nucleic Acids Research</i> , 2006, 34, D322-D326.	6.5	923
68	dictyBase, the model organism database for <i>Dictyostelium discoideum</i> . <i>Nucleic Acids Research</i> , 2006, 34, D423-D427.	6.5	101
69	Improved prediction of treatment response using microarrays and existing biological knowledge. <i>Pharmacogenomics</i> , 2006, 7, 495-501.	0.6	7
70	Irrational Exuberance in Clinical Proteomics. <i>Clinical Cancer Research</i> , 2005, 11, 7963-7964.	3.2	2
71	The case for strategic international alliances to harness nutritional genomics for public and personal health. <i>British Journal of Nutrition</i> , 2005, 94, 623-632.	1.2	137
72	What is mzXML good for?. <i>Expert Review of Proteomics</i> , 2005, 2, 839-845.	1.3	47

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73	dictyBase: a new Dictyostelium discoideum genome database. Nucleic Acids Research, 2004, 32, 332D-333.	6.5	98
74	A genome end-game: understanding gene function in the nervous system. Nature Neuroscience, 2004, 7, 484-485.	7.1	9
75	The Gene Ontology (GO) database and informatics resource. Nucleic Acids Research, 2004, 32, 258D-261.	6.5	3,462
76	Large-scale mutagenesis of the mouse to understand the genetic bases of nervous system structure and function. Molecular Brain Research, 2004, 132, 105-115.	2.5	77
77	Identification of genes contributing to the obese yellowAvyphenotype: caloric restriction, genotype, diet Å— genotype interactions. Physiological Genomics, 2004, 18, 316-324.	1.0	32
78	Chemically Induced Mutations in the Mouse that Affect the Fundus and Electroretinogram. , 2003, , 188-189.		0
79	Some Aspects of Analysis of Gene Array Data. Cancer Treatment and Research, 2002, 113, 71-89.	0.2	4
80	The SV40 core sequence functions as a repressor element in yeast. Journal of Biological Chemistry, 1991, 266, 21362-7.	1.6	4
81	The saccharomyces and Drosophila heat shock transcription factors are identical in size and DNA binding properties. Cell, 1987, 48, 507-515.	13.5	234
82	Interpreting Microarray Results With Gene Ontology and MeSH. , 0, , 223-242.		0