Stefano Ceri

List of Publications by Year
in descending order

77 papers	1,593 citations	393982 19 h-index	344852 36 g-index
83 all docs	83 docs citations	83 times ranked	1488 citing authors

#	Article	IF	Citations
1	META-BASE: A Novel Architecture for Large-Scale Genomic Metadata Integration. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 543-557.	1.9	19
2	Predicting Drug Synergism by Means of Non-Negative Matrix Tri-Factorization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1956-1967.	1.9	5
3	GeCoAgent: A Conversational Agent for Empowering Genomic Data Extraction and Analysis. ACM Transactions on Computing for Healthcare, 2022, 3, 1-29.	3.3	5
4	ViruClust: direct comparison of SARS-CoV-2 genomes and genetic variants in space and time. Bioinformatics, 2022, 38, 1988-1994.	1.8	9
5	Interoperability of COVID-19 Clinical Phenotype Data with Host and Viral Genetics Data. BioMed, 2022, 2, 69-81.	0.6	3
6	Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity. Human Genetics, 2022, 141, 147-173.	1.8	22
7	CoV2K model, a comprehensive representation of SARS-CoV-2 knowledge and data interplay. Scientific Data, 2022, 9, .	2.4	6
8	The road towards data integration in human genomics: players, steps and interactions. Briefings in Bioinformatics, 2021, 22, 30-44.	3.2	22
9	ViruSurf: an integrated database to investigate viral sequences. Nucleic Acids Research, 2021, 49, D817-D824.	6.5	36
10	Federated sharing and processing of genomic datasets for tertiary data analysis. Briefings in Bioinformatics, 2021, 22, .	3.2	7
11	EpiSurf: metadata-driven search server for analyzing amino acid changes within epitopes of SARS-CoV-2 and other viral species. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	6
12	Show, Donâ€™t Tell. Reflections on the Design of Multi-modal Conversational Interfaces. Lecture Notes in Computer Science, 2021, , 64-77.	1.0	2
13	Employing a systematic approach to biobanking and analyzing clinical and genetic data for advancing COVID-19 research. European Journal of Human Genetics, 2021, 29, 745-759.	1.4	35
14	Systematic inference and comparison of multi-scale chromatin sub-compartments connects spatial organization to cell phenotypes. Nature Communications, 2021, 12, 2439.	5.8	50
15	Identifying collateral and synthetic lethal vulnerabilities within the DNA-damage response. BMC Bioinformatics, 2021, 22, 250.	1.2	2
16	VirusViz: comparative analysis and effective visualization of viral nucleotide and amino acid variants. Nucleic Acids Research, 2021, 49, e90-e90.	6.5	18
17	CoV2K: A Knowledge Base of SARS-CoV-2 Variant Impacts. Lecture Notes in Business Information Processing, 2021, , 274-282.	0.8	9
18	A review on viral data sources and search systems for perspective mitigation of COVID-19. Briefings in Bioinformatics, 2021, 22, 664-675.	3.2	22

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19	Socioeconomic differences and persistent segregation of Italian territories during COVID-19 pandemic. Scientific Reports, 2021, 11, 21174.	1.6	18
20	Data-driven analysis of amino acid change dynamics timely reveals SARS-CoV-2 variant emergence. Scientific Reports, 2021, 11, 21068.	1.6	15
21	VirusLab: A Tool for Customized SARS-CoV-2 Data Analysis. BioTech, 2021, 10, 27.	1.3	4
22	Data Science for Genomic Data Management: Challenges, Resources, Experiences. SN Computer Science, 2020, 1, 1.	2.3	5
23	Content-based characterization of online social communities. Information Processing and Management, 2020, 57, 102133.	5.4	6
24	OpenGDC: Unifying, Modeling, Integrating Cancer Genomic Data and Clinical Metadata. Applied Sciences (Switzerland), 2020, 10, 6367.	1.3	12
25	Spatial patterns of CTCF sites define the anatomy of TADs and their boundaries. Genome Biology, 2020, 21, 197.	3.8	45
26	NAUTICA: classifying transcription factor interactions by positional and protein-protein interaction information. Biology Direct, 2020, 15, 13.	1.9	6
27	Matrix Factorization-based Technique for Drug Repurposing Predictions. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 3162-3172.	3.9	24
28	Array-based Data Management for Genomics. , 2020, , .		1
29	Investigating Italian disinformation spreading on Twitter in the context of 2019 European elections. PLoS ONE, 2020, 15, e0227821.	1.1	53
30	Designing and Evaluating Deep Learning Models for Cancer Detection on Gene Expression Data. Lecture Notes in Computer Science, 2020, , 249-261.	1.0	3
31	Empowering Virus Sequence Research Through Conceptual Modeling. Lecture Notes in Computer Science, 2020, , 388-402.	1.0	15
32	Topology comparison of Twitter diffusion networks effectively reveals misleading information. Scientific Reports, 2020, 10, 1372.	1.6	53
33	A multi-layer approach to disinformation detection in US and Italian news spreading on Twitter. EPJ Data Science, 2020, 9, .	1.5	20
34	OK, DNA!. , 2020, , .		3
35	Exploring chromatin conformation and gene co-expression through graph embedding. Bioinformatics, 2020, 36, i700-i708.	1.8	5
36	Performance Prediction for Data-driven Workflows on Apache Spark. , 2020, , .		3

#	ARTICLE	IF	CITATIONS
37	Investigating Italian disinformation spreading on Twitter in the context of 2019 European elections. , 2020, 15, e0227821.		0
38	Investigating Italian disinformation spreading on Twitter in the context of 2019 European elections. , 2020, 15, e0227821.		0
39	Investigating Italian disinformation spreading on Twitter in the context of 2019 European elections. , 2020, 15, e0227821.		0
40	Investigating Italian disinformation spreading on Twitter in the context of 2019 European elections. , 2020, 15, e0227821.		0
41	Investigating Italian disinformation spreading on Twitter in the context of 2019 European elections. , 2020, 15, e0227821.		0
42	Investigating Italian disinformation spreading on Twitter in the context of 2019 European elections. , 2020, 15, e0227821.		0
43	Investigating Italian disinformation spreading on Twitter in the context of 2019 European elections. , 2020, 15, e0227821.		0
44	Investigating Italian disinformation spreading on Twitter in the context of 2019 European elections. , 2020, 15, e0227821.		0
45	Processing of big heterogeneous genomic datasets for tertiary analysis of Next Generation Sequencing data. Bioinformatics, 2019, 35, 729-736.	1.8	47
46	Optimal Binning for Genomics. IEEE Transactions on Computers, 2019, 68, 125-138.	2.4	4
47	Non-negative Matrix Tri-Factorization for Data Integration and Network-based Drug Repositioning. , 2019, , .		6
48	PyGMQL: scalable data extraction and analysis for heterogeneous genomic datasets. BMC Bioinformatics, 2019, 20, 560.	1.2	15
49	Extensive epigenomic integration of the glucocorticoid response in primary human monocytes and in vitro derived macrophages. Scientific Reports, 2019, 9, 2772.	1.6	27
50	GenoSurf: metadata driven semantic search system for integrated genomic datasets. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	35
51	Drug Repositioning Predictions by Non-Negative Matrix Tri-Factorization of Integrated Association Data. , 2019, , .		6
52	Metadata management for scientific databases. Information Systems, 2019, 81, 1-20.	2.4	15
53	Next Generation Indexing for Genomic Intervals. IEEE Transactions on Knowledge and Data Engineering, 2019, 31, 2008-2021.	4.0	11
54	From a Conceptual Model to a Knowledge Graph for Genomic Datasets. Lecture Notes in Computer Science, 2019, , 352-360.	1.0	8

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55	Exploiting Conceptual Modeling for Searching Genomic Metadata: A Quantitative and Qualitative Empirical Study. Lecture Notes in Computer Science, 2019, , 83-94.	1.0	7
56	False News On Social Media. SIGMOD Record, 2019, 48, 18-27.	0.7	80
57	On the role of statistics in the era of big data: A computer science perspective. Statistics and Probability Letters, 2018, 136, 68-72.	0.4	10
58	Ratiometric sweat secretion optical test in cystic fibrosis, carriers and healthy subjects. Journal of Cystic Fibrosis, 2018, 17, 186-189.	0.3	17
59	TICA: Transcriptional Interaction and Coregulation Analyzer. Genomics, Proteomics and Bioinformatics, 2018, 16, 342-353.	3.0	6
60	Exploring Genomic Datasets. , 2018, , .		5
61	Implementing a Transcription Factor Interaction Prediction System Using the GenoMetric Query Language. Methods in Molecular Biology, 2018, 1807, 63-81.	0.4	1
62	Overview of GeCo: A Project for Exploring and Integrating Signals from the Genome. Communications in Computer and Information Science, 2018, , 46-57.	0.4	6
63	Data Management for Heterogeneous Genomic Datasets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1251-1264.	1.9	12
64	TCGA2BED: extracting, extending, integrating, and querying The Cancer Genome Atlas. BMC Bioinformatics, 2017, 18, 6.	1.2	33
65	Indexing Next-Generation Sequencing data. Information Sciences, 2017, 384, 90-109.	4.0	7
66	Framework for Supporting Genomic Operations. IEEE Transactions on Computers, 2017, 66, 443-457.	2.4	22
67	Explorative visual analytics on interval-based genomic data and their metadata. BMC Bioinformatics, 2017, 18, 536.	1.2	4
68	Evaluating Genomic Big Data Operations on SciDB and Spark. Lecture Notes in Computer Science, 2017, , 482-493.	1.0	5
69	Conceptual Modeling for Genomics: Building an Integrated Repository of Open Data. Lecture Notes in Computer Science, 2017, , 325-339.	1.0	31
70	The Early Days of Entity-Relationship Modeling Retrospective on Dataid Project and Beyond. , 2017, , 259-268.		1
71	Modeling and interoperability of heterogeneous genomic big data for integrative processing and querying. Methods, 2016, 111, 3-11.	1.9	41
72	Ontology-Based Search of Genomic Metadata. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 233-247.	1.9	13

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73	Evaluating cloud frameworks on genomic applications. , 2015, , .		17
74	GenoMetric Query Language: a novel approach to large-scale genomic data management. Bioinformatics, 2015, 31, 1881-1888.	1.8	79
75	Integrative warehousing of biomolecular information to support complex multi-topic queries for biomedical knowledge discovery. , 2013, , .		10
76	A Framework for Integrating, Exploring, and Searching Location-Based Web Data. IEEE Internet Computing, 2011, 15, 24-31.	3.2	8
77	What you always wanted to know about Datalog (and never dared to ask). IEEE Transactions on Knowledge and Data Engineering, 1989, 1, 146-166.	4.0	426