Indra Neil Sarkar

List of Publications by Year
in descending order

90 papers	1,864 citations	279798 23 h-index	289244 40 g-index
95 all docs	95 docs citations	95 times ranked	3164 citing authors

#	Article	IF	Citations
1	The effect of levetiracetam treatment on survival in patients with glioblastoma: a systematic review and meta-analysis. Journal of Neuro-Oncology, 2022, 156, 257-267.	2.9	9
2	Access to community-based reproductive health services and incidence of low birthweight delivery among refugee and displaced mothers: a retrospective study in the Thailand-Myanmar border region. BMJ Open, 2022, 12, e052571.	1.9	1
3	LYRUS: a machine learning model for predicting the pathogenicity of missense variants. Bioinformatics Advances, 2022, 2, vbab045.	2.4	4
4	Using the Montreal cognitive assessment to identify individuals with subtle cognitive decline.. Neuropsychology, 2022, 36, 373-383.	1.3	4
5	Statewide evaluation of COVID-19 vaccine hesitancy in Rhode Island. PLoS ONE, 2022, 17, e0268587.	2.5	3
6	Predicting open wound mortality in the ICU using machine learning. Journal of Emergency and Critical Care Medicine, 2021, 5, 13-13.	0.7	2
7	Adverse events following mRNA SARS-CoV-2 vaccination among U.S. nursing home residents. Vaccine, 2021, 39, 3844-3851.	3.8	42
8	Adverse Events Following One Dose of mRNA COVID-19 Vaccination Among US Nursing Home Residents With and Without a Previous SARS-CoV-2 Infection. Journal of the American Medical Directors Association, 2021, 22, 2228-2232.	2.5	18
9	A changed world built on informatics innovation. JAMIA Open, 2021, 3, 487-487.	2.0	0
10	Achieving A Certain Major Achievement During Uncertain Times. JAMIA Open, 2020, 3, 1-1.	2.0	0
11	#BlackLivesMatter. JAMIA Open, 2020, 3, 141-141.	2.0	0
12	Curated multiple sequence alignment for the Adenomatous Polyposis Coli (APC) gene and accuracy of in silico pathogenicity predictions. PLoS ONE, 2020, 15, e0233673.	2.5	1
13	Identifying Herbal Adverse Events From Spontaneous Reporting Systems Using Taxonomic Name Resolution Approach. Bioinformatics and Biology Insights, 2020, 14, 117793222092135.	2.0	7
14	A Phylogenetic Approach to Analyze the Conservativeness of BRCA1 and BRCA2 Mutations. AMIA ... Annual Symposium proceedings, 2020, 2020, 677-686.	0.2	1
15	Supporting rigor through reproducibility. JAMIA Open, 2020, 3, 319-320.	2.0	0
16	Harnessing electronic data to inform health decisions. JAMIA Open, 2019, 2, 215-216.	2.0	0
17	Solr-Plant: efficient extraction of plant names from text. BMC Bioinformatics, 2019, 20, 263.	2.6	6
18	Today's data for tomorrow's knowledge. JAMIA Open, 2019, 2, 1-1.	2.0	2

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19	Reimagining the research-practice relationship: policy recommendations for informatics-enabled evidence-generation across the US health system. JAMIA Open, 2019, 2, 2-9.	2.0	8
20	Community abstracts: coming soon!. JAMIA Open, 2019, 2, 399-399.	2.0	0
21	Quality Informatics: The Convergence of Healthcare Data, Analytics, and Clinical Excellence. Applied Clinical Informatics, 2019, 10, 272-277.	1.7	9
22	Enabling open access to support biomedical research. JAMIA Open, 2019, 2, 281-281.	2.0	0
23	Machine learning approach to literature mining for the genetics of complex diseases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	1
24	Using Self Organizing Maps to Compare Sepsis Patients from the Neonatal and Adult Intensive Care Unit. AMIA Summits on Translational Science Proceedings, 2019, 2019, 127-135.	0.4	0
25	Using Unsupervised Clustering to Identify Pregnancy Co-Morbidities. AMIA Summits on Translational Science Proceedings, 2019, 2019, 305-314.	0.4	1
26	Finding the patient in informatics. JAMIA Open, 2018, 1, 129-129.	2.0	0
27	Health Information Exchange in Emergency Medical Services. Applied Clinical Informatics, 2018, 09, 884-891.	1.7	14
28	A new journal for sharing informatics innovations: introducing JAMIA Open. JAMIA Open, 2018, 1, 1-2.	2.0	3
29	Predicting Mortality in Diabetic ICU Patients Using Machine Learning and Severity Indices. AMIA Summits on Translational Science Proceedings, 2018, 2017, 310-319.	0.4	7
30	Identifying Supplement Use Within Clinical Notes: An Applicationof Natural Language Processing. AMIA Summits on Translational Science Proceedings, 2018, 2017, 196-205.	0.4	3
31	Crossing the health IT chasm: considerations and policy recommendations to overcome current challenges and enable value-based care. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 1036-1043.	4.4	41
32	Identifying Complementary and Alternative Medicine Usage Information from Internet Resources. Methods of Information in Medicine, 2016, 55, 322-332.	1.2	22
33	Developing new pathways into the biomedical informatics field: the AMIA High School Scholars Program. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 819-823.	4.4	8
34	Prevention of treatment-related fluid overload reduces estimated effective cost of prothrombin complex concentrate in patients requiring rapid vitamin K antagonist reversal. Expert Review of Pharmacoeconomics and Outcomes Research, 2016, 16, 135-139.	1.4	9
35	A Cross-Species Analysis of Animal Models for the Investigation of Preterm Birth Mechanisms. Reproductive Sciences, 2016, 23, 482-491.	2.5	28
36	Identifying Family History and Substance Use Associations for Adult Epilepsy from the Electronic Health Record. AMIA Summits on Translational Science Proceedings, 2016, 2016, 250-9.	0.4	1

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37	Identifying Plant-Human Disease Associations in Biomedical Literature: A Case Study. AMIA Summits on Translational Science Proceedings, 2016, 2016, 84-93.	0.4	1
38	How to Prepare a Nursing Informatics Conference Submission. Studies in Health Technology and Informatics, 2016, 225, 703-4.	0.3	0
39	Adapting simultaneous analysis phylogenomic techniques to study complex disease gene relationships. Journal of Biomedical Informatics, 2015, 54, 10-38.	4.3	3
40	Geospatial and Temporal Analysis of Thyroid Cancer Incidence in a Rural Population. Thyroid, 2015, 25, 812-822.	4.5	35
41	Challenges in Identification of Potential Phytotherapies from Contemporary Biomedical Literature. , 2015, , 363-371.		3
42	Multi-source development of an integrated model for family health history. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, e67-e80.	4.4	10
43	Mining the Bibliome. Computers in Health Care, 2015, , 75-96.	0.3	1
44	Towards the Standardized Documentation of E-Cigarette Use in the Electronic Health Record for Population Health Surveillance and Research. AMIA Summits on Translational Science Proceedings, 2015, 2015, 199-203.	0.4	15
45	Mining and Visualizing Family History Associations in the Electronic Health Record: A Case Study for Pediatric Asthma. AMIA ... Annual Symposium proceedings, 2015, 2015, 396-405.	0.2	4
46	Automated Extraction of Substance Use Information from Clinical Texts. AMIA ... Annual Symposium proceedings, 2015, 2015, 2121-30.	0.2	25
47	Representation of Drug Use in Biomedical Standards, Clinical Text, and Research Measures. AMIA ... Annual Symposium proceedings, 2015, 2015, 376-85.	0.2	7
48	Putting Theory into Practice. , 2014, , 425-432.		1
49	Structural network analysis of biological networks for assessment of potential disease model organisms. Journal of Biomedical Informatics, 2014, 47, 178-191.	4.3	5
50	Drug repurposing: mining protozoan proteomes for targets of known bioactive compounds. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 238-244.	4.4	26
51	Mining the Electronic Health Record for Disease Knowledge. Methods in Molecular Biology, 2014, 1159, 269-286.	0.9	25
52	PubMedMiner: Mining and Visualizing MeSH-based Associations in PubMed. AMIA ... Annual Symposium proceedings, 2014, 2014, 1990-9.	0.2	6
53	Examining the use, contents, and quality of free-text tobacco use documentation in the Electronic Health Record. AMIA ... Annual Symposium proceedings, 2014, 2014, 366-74.	0.2	14
54	Bioinformatics opportunities for identification and study of medicinal plants. Briefings in Bioinformatics, 2013, 14, 238-250.	6.5	80

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55	Phylogeography of influenza A H5N1 clade 2.2.1.1 in Egypt. BMC Genomics, 2013, 14, 871.	2.8	20
56	Leveraging concept-based approaches to identify potential phyto-therapies. Journal of Biomedical Informatics, 2013, 46, 602-614.	4.3	7
57	Leveraging biodiversity knowledge for potential phyto-therapeutic applications. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 668-679.	4.4	19
58	A vector space model approach to identify genetically related diseases. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 249-254.	4.4	25
59	Building the Informatics Infrastructure for Comparative Effectiveness Research (CER). Medical Care, 2012, 50, S38-S48.	2.4	28
60	Translating standards into practice: Experiences and lessons learned in biomedicine and health care. Journal of Biomedical Informatics, 2012, 45, 609-612.	4.3	4
61	The impact of taxon sampling on phylogenetic inference: a review of two decades of controversy. Briefings in Bioinformatics, 2012, 13, 122-134.	6.5	203
62	Genome-wide search for leech antiplatelet proteins in the non-blood-feeding leechHelobdella robusta(Rhyncobdellida: Glossiphoniidae) reveals evidence of secreted anticoagulants. Invertebrate Biology, 2011, 130, 344-350.	0.9	20
63	Enhancing phylogeography by improving geographical information from GenBank. Journal of Biomedical Informatics, 2011, 44, S44-S47.	4.3	33
64	Selected Papers from the 2011 Summit on Translational Bioinformatics. Journal of Biomedical Informatics, 2011, 44, S3-S4.	4.3	0
65	Small-Molecule Inhibition of Choline Catabolism in Pseudomonas aeruginosa and Other Aerobic Choline-Catabolizing Bacteria. Applied and Environmental Microbiology, 2011, 77, 4383-4389.	3.1	16
66	Translational bioinformatics: linking knowledge across biological and clinical realms: Figure 1. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 354-357.	4.4	61
67	The Barcode of Life Data Portal: Bridging the Biodiversity Informatics Divide for DNA Barcoding. PLoS ONE, 2011, 6, e14689.	2.5	24
68	Towards Structuring Unstructured GenBank Metadata for Enhancing Comparative Biological Studies. AMIA Summits on Translational Science Proceedings, 2011, 2011, 6-10.	0.4	4
69	MeSHing molecular sequences and clinical trials: A feasibility study. Journal of Biomedical Informatics, 2010, 43, 442-450.	4.3	5
70	Genetic variation and phylogeny of the cosmopolitan marine genus Tubificoides (Annelida: Clitellata:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.7	32
71	Editorial: Bioinformatics education in the 21st century. Briefings in Bioinformatics, 2010, 11, 535-536.	6.5	6
72	Evaluation of family history information within clinical documents and adequacy of HL7 clinical statement and clinical genomics family history models for its representation: a case report. Journal of the American Medical Informatics Association: JAMIA, 2010, 17, 337-340.	4.4	30

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73	At the Intersection of Public-health Informatics and Bioinformatics. Epidemiology, 2010, 21, 764-768.	2.7	13
74	Biomedical informatics and translational medicine. Journal of Translational Medicine, 2010, 8, 22.	4.4	84
75	Salivary Transcriptome of the North American Medicinal Leech, Macrobdella decora. Journal of Parasitology, 2010, 96, 1211-1221.	0.7	59
76	Leveraging biomedical ontologies and annotation services to organize microbiome data from Mammalian hosts. AMIA ... Annual Symposium proceedings, 2010, 2010, 717-21.	0.2	8
77	GenBank and PubMed: How connected are they?. BMC Research Notes, 2009, 2, 101.	1.4	20
78	Appearance of new tetraspanin genes during vertebrate evolution. Genomics, 2008, 91, 326-334.	2.9	115
79	<scp>caos</scp> software for use in character–based DNA barcoding. Molecular Ecology Resources, 2008, 8, 1256-1259.	4.8	157
80	Biodiversity informatics: organizing and linking information across the spectrum of life. Briefings in Bioinformatics, 2007, 8, 347-357.	6.5	55
81	The phylogeny of rodent malaria parasites: Simultaneous analysis across three genomes. Infection, Genetics and Evolution, 2007, 7, 74-83.	2.3	71
82	DNA barcoding using chitons (genusMopalia). Molecular Ecology Notes, 2007, 7, 177-183.	1.7	74
83	Phylogenetics in the modern era. Journal of Biomedical Informatics, 2006, 39, 3-5.	4.3	1
84	OrthologID: automation of genome-scale ortholog identification within a parsimony framework. Bioinformatics, 2006, 22, 699-707.	4.1	89
85	BIODIVERSITY INFORMATICS: MANAGING KNOWLEDGE BEYOND HUMANS AND MODEL ORGANISMS â€" AN INTRODUCTION. , 2006, , .		0
86	Literature based discovery of gene clusters using phylogenetic methods. AMIA ... Annual Symposium proceedings, 2006, , 689-93.	0.2	1
87	Genestrace: phenomic knowledge discovery via structured terminology. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 103-14.	0.7	9
88	GENESTRACE: PHENOMIC KNOWLEDGE DISCOVERY VIA STRUCTURED TERMINOLOGY. , 2004, , .		9
89	Desiderata for Personal Electronic Communication in Clinical Systems. Journal of the American Medical Informatics Association: JAMIA, 2002, 9, 209-216.	4.4	6
90	Systematic Analysis of DNA Microarray Data: Ordering and Interpreting Patterns of Gene Expression. Genome Research, 2001, 11, 1149-1155.	5.5	31