Russ Altman

List of Publications by Year
in descending order

117 papers	7,483 citations	94433 37 h-index	62596 80 g-index
140 all docs	140 docs citations	140 times ranked	13962 citing authors

#	Article	IF	Citations
1	Guidelines for investigating causality of sequence variants in human disease. Nature, 2014, 508, 469-476.	27.8	1,130
2	Machine learning in chemoinformatics and drug discovery. Drug Discovery Today, 2018, 23, 1538-1546.	6.4	630
3	Data-Driven Prediction of Drug Effects and Interactions. Science Translational Medicine, 2012, 4, 125ra31.	12.4	610
4	Human induced pluripotent stem cell–derived cardiomyocytes recapitulate the predilection of breast cancer patients to doxorubicin-induced cardiotoxicity. Nature Medicine, 2016, 22, 547-556.	30.7	573
5	Clinical Interpretation and Implications of Whole-Genome Sequencing. JAMA - Journal of the American Medical Association, 2014, 311, 1035.	7.4	398
6	Graph Convolutional Neural Networks for Predicting Drug-Target Interactions. Journal of Chemical Information and Modeling, 2019, 59, 4131-4149.	5.4	222
7	PharmGKB: A worldwide resource for pharmacogenomic information. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2018, 10, e1417.	6.6	205
8	Detecting Drug Interactions From Adverse-Event Reports: Interaction Between Paroxetine and Pravastatin Increases Blood Glucose Levels. Clinical Pharmacology and Therapeutics, 2011, 90, 133-142.	4.7	183
9	A novel signal detection algorithm for identifying hidden drug-drug interactions in adverse event reports. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 79-85.	4.4	165
10	The Pharmacogenomics Research Network Translational Pharmacogenetics Program: Outcomes and Metrics of Pharmacogenetic Implementations Across Diverse Healthcare Systems. Clinical Pharmacology and Therapeutics, 2017, 102, 502-510.	4.7	117
11	The International SSRI Pharmacogenomics Consortium (ISPC): a genome-wide association study of antidepressant treatment response. Translational Psychiatry, 2015, 5, e553-e553.	4.8	107
12	3D deep convolutional neural networks for amino acid environment similarity analysis. BMC Bioinformatics, 2017, 18, 302.	2.6	106
13	Examining the Use of Real–World Evidence in the Regulatory Process. Clinical Pharmacology and Therapeutics, 2020, 107, 843-852.	4.7	99
14	Challenges for Biomedical Informatics and Pharmacogenomics. Annual Review of Pharmacology and Toxicology, 2002, 42, 113-133.	9.4	93
15	Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research. Clinical Pharmacology and Therapeutics, 2019, 105, 1256-1262.	4.7	90
16	Robust recognition of zinc binding sites in proteins. Protein Science, 2008, 17, 54-65.	7.6	88
17	Pharmacogenomics: "Noninferiority" Is Sufficient for Initial Implementation. Clinical Pharmacology and Therapeutics, 2011, 89, 348-350.	4.7	85
18	Decaying relevance of clinical data towards future decisions in data-driven inpatient clinical order sets. International Journal of Medical Informatics, 2017, 102, 71-79.	3.3	80

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19	WebFEATURE: an interactive web tool for identifying and visualizing functional sites on macromolecular structures. Nucleic Acids Research, 2003, 31, 3324-3327.	14.5	79
20	Pharmacogenetics at Scale: An Analysis of the UK Biobank. Clinical Pharmacology and Therapeutics, 2021, 109, 1528-1537.	4.7	78
21	Generating Genome-Scale Candidate Gene Lists for Pharmacogenomics. Clinical Pharmacology and Therapeutics, 2009, 86, 183-189.	4.7	75
22	Time to Organize the Bioinformatics Resourceome. PLoS Computational Biology, 2005, 1, e76.	3.2	70
23	Pharmacogenomicsâ€Based Pointâ€ofâ€Care Clinical Decision Support Significantly Alters Drug Prescribing. Clinical Pharmacology and Therapeutics, 2017, 102, 859-869.	4.7	68
24	Pharmacogenomics Clinical Annotation Tool (Pharm<scp>CAT</scp>). Clinical Pharmacology and Therapeutics, 2020, 107, 203-210.	4.7	65
25	Using Multiple Microenvironments to Find Similar Ligand-Binding Sites: Application to Kinase Inhibitor Binding. PLoS Computational Biology, 2011, 7, e1002326.	3.2	60
26	Chapter 7: Pharmacogenomics. PLoS Computational Biology, 2012, 8, e1002817.	3.2	57
27	Predicting inpatient clinical order patterns with probabilistic topic models vs conventional order sets. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 472-480.	4.4	54
28	Human Germline CRISPR-Cas Modification: Toward a Regulatory Framework. American Journal of Bioethics, 2015, 15, 25-29.	0.9	53
29	Environmental and State-Level Regulatory Factors Affect the Incidence of Autism and Intellectual Disability. PLoS Computational Biology, 2014, 10, e1003518.	3.2	48
30	Neurotoxicity of Generic Anesthesia Agents in Infants and Children. JAMA - Journal of the American Medical Association, 2015, 313, 1515.	7.4	48
31	Local Kinetic Measures of Macromolecular Structure Reveal Partitioning among Multiple Parallel Pathways from the Earliest Steps in the Folding of a Large RNA Molecule. Journal of Molecular Biology, 2006, 358, 1179-1190.	4.2	46
32	Artificial intelligence (AI) systems for interpreting complex medical datasets. Clinical Pharmacology and Therapeutics, 2017, 101, 585-586.	4.7	45
33	Evidence for Clinical Implementation of Pharmacogenomics in Cardiac Drugs. Mayo Clinic Proceedings, 2015, 90, 716-729.	3.0	44
34	Translational Bioinformatics: Linking the Molecular World to the Clinical World. Clinical Pharmacology and Therapeutics, 2012, 91, 994-1000.	4.7	43
35	A dynamic map for learning, communicating, navigating and improving therapeutic development. Nature Reviews Drug Discovery, 2018, 17, 150-150.	46.4	43
36	OrderRex: clinical order decision support and outcome predictions by data-mining electronic medical records. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 339-348.	4.4	42

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37	The Interactions Between Clinical Informatics and Bioinformatics: A Case Study. Journal of the American Medical Informatics Association: JAMIA, 2000, 7, 439-443.	4.4	41
38	Opportunities and challenges for the computational interpretation of rare variation in clinically important genes. American Journal of Human Genetics, 2021, 108, 535-548.	6.2	40
39	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	2.5	39
40	Association of the Polygenic Scores for Personality Traits and Response to Selective Serotonin Reuptake Inhibitors in Patients with Major Depressive Disorder. Frontiers in Psychiatry, 2018, 9, 65.	2.6	38
41	Genomewide Association Studies in Pharmacogenomics. Clinical Pharmacology and Therapeutics, 2021, 110, 637-648.	4.7	38
42	A research roadmap for next-generation sequencing informatics. Science Translational Medicine, 2016, 8, 335ps10.	12.4	37
43	Learning the Structure of Biomedical Relationships from Unstructured Text. PLoS Computational Biology, 2015, 11, e1004216.	3.2	36
44	Ranking Adverse Drug Reactions With Crowdsourcing. Journal of Medical Internet Research, 2015, 17, e80.	4.3	35
45	Relating Essential Proteins to Drug Side-Effects Using Canonical Component Analysis: A Structure-Based Approach. Journal of Chemical Information and Modeling, 2015, 55, 1483-1494.	5.4	34
46	Opportunities for developing therapies for rare genetic diseases: focus on gain-of-function and allostery. Orphanet Journal of Rare Diseases, 2017, 12, 61.	2.7	34
47	Knowledge-based Fragment Binding Prediction. PLoS Computational Biology, 2014, 10, e1003589.	3.2	32
48	Transfer learning enables prediction of CYP2D6 haplotype function. PLoS Computational Biology, 2020, 16, e1008399.	3.2	32
49	The Pioglitazone Trek via Human PPAR Gamma: From Discovery to a Medicine at the FDA and Beyond. Frontiers in Pharmacology, 2018, 9, 1093.	3.5	31
50	Pharmacogenomics: will the promise be fulfilled?. Nature Reviews Genetics, 2011, 12, 69-73.	16.3	29
51	Using â€œBig Dataâ€•to Dissect Clinical Heterogeneity. Circulation, 2015, 131, 232-233.	1.6	28
52	Pharmacogenomics and big genomic data: from lab to clinic and back again. Human Molecular Genetics, 2018, 27, R72-R78.	2.9	28
53	The association of obesity and coronary artery disease genes with response to SSRIs treatment in major depression. Journal of Neural Transmission, 2019, 126, 35-45.	2.8	27
54	Constraints on Biological Mechanism from Disease Comorbidity Using Electronic Medical Records and Database of Genetic Variants. PLoS Computational Biology, 2016, 12, e1004885.	3.2	27

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55	Personal Genomic Measurements: The Opportunity for Information Integration. Clinical Pharmacology and Therapeutics, 2013, 93, 21-23.	4.7	26
56	Development of an automated assessment tool for MedWatch reports in the FDA adverse event reporting system. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 913-920.	4.4	26
57	Data-driven human transcriptomic modules determined by independent component analysis. BMC Bioinformatics, 2018, 19, 327.	2.6	25
58	Structural characterization of proteins using residue environments. Proteins: Structure, Function and Bioinformatics, 2005, 61, 741-747.	2.6	24
59	Direct-to-Consumer Genetic Testing: Failure Is Not an Option. Clinical Pharmacology and Therapeutics, 2009, 86, 15-17.	4.7	24
60	Computing disease incidence, prevalence and comorbidity from electronic medical records. Journal of Biomedical Informatics, 2016, 63, 108-111.	4.3	24
61	Genome-wide and candidate gene approaches of clopidogrel efficacy using pharmacodynamic and clinical end pointsâ€"Rationale and design of the International Clopidogrel Pharmacogenomics Consortium (ICPC). American Heart Journal, 2018, 198, 152-159.	2.7	24
62	Challenges in the Pharmacogenomic Annotation of Whole Genomes. Clinical Pharmacology and Therapeutics, 2013, 94, 211-213.	4.7	23
63	Sequence to Medical Phenotypes: A Framework for Interpretation of Human Whole Genome DNA Sequence Data. PLoS Genetics, 2015, 11, e1005496.	3.5	23
64	Effect of $CYP4F2$, $VKORC1$, and $CYP2C9$ in Influencing Coumarin Dose: A Singleâ€Patient Data Metaâ€Analysis in More Than 15,000 Individuals. Clinical Pharmacology and Therapeutics, 2019, 105, 1477-1491.	4.7	23
65	Pocket similarity identifies selective estrogen receptor modulators as microtubule modulators at the taxane site. Nature Communications, 2019, 10, 1033.	12.8	22
66	Analyzing the vast coronavirus literature with CoronaCentral. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	22
67	Variations in the Binding Pocket of an Inhibitor of the Bacterial Division Protein FtsZ across Genotypes and Species. PLoS Computational Biology, 2015, 11, e1004117.	3.2	21
68	Leveraging the Cell Ontology to classify unseen cell types. Nature Communications, 2021, 12, 5556.	12.8	21
69	Personalization in practice. Science, 2015, 350, 282-283.	12.6	20
70	Expanding a radiology lexicon using contextual patterns in radiology reports. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 679-685.	4.4	20
71	The Education Potential of the Pharmacogenetics and Pharmacogenomics Knowledge Base (PharmGKB). Clinical Pharmacology and Therapeutics, 2007, 82, 472-475.	4.7	16
72	High Precision Prediction of Functional Sites in Protein Structures. PLoS ONE, 2014, 9, e91240.	2.5	15

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73	Unmet needs: Research helps regulators do their jobs. Science Translational Medicine, 2015, 7, 315ps22.	12.4	15
74	Interpreting the CYP2D6 Results From the International Tamoxifen Pharmacogenetics Consortium. Clinical Pharmacology and Therapeutics, 2014, 96, 144-146.	4.7	14
75	High Resolution Prediction of Calcium-Binding Sites in 3D Protein Structures Using FEATURE. Journal of Chemical Information and Modeling, 2015, 55, 1663-1672.	5.4	13
76	Shallow Representation Learning via Kernel PCA Improves QSAR Modelability. Journal of Chemical Information and Modeling, 2017, 57, 1859-1867.	5.4	13
77	Biomarkers: Delivering on the expectation of molecularly driven, quantitative health. Experimental Biology and Medicine, 2018, 243, 313-322.	2.4	13
78	PathFX provides mechanistic insights into drug efficacy and safety for regulatory review and therapeutic development. PLoS Computational Biology, 2018, 14, e1006614.	3.2	13
79	Introduction to Translational Bioinformatics Collection. PLoS Computational Biology, 2012, 8, e1002796.	3.2	12
80	Biological and functional relevance of CASP predictions. Proteins: Structure, Function and Bioinformatics, 2018, 86, 374-386.	2.6	12
81	Systematic target function annotation of human transcription factors. BMC Biology, 2018, 16, 4.	3.8	12
82	Large-scale labeling and assessment of sex bias in publicly available expression data. BMC Bioinformatics, 2021, 22, 168.	2.6	12
83	Using Pre-existing Microarray Datasets to Increase Experimental Power: Application to Insulin Resistance. PLoS Computational Biology, 2010, 6, e1000718.	3.2	11
84	Predicting Cancer Drug Response: Advancing the DREAM. Cancer Discovery, 2015, 5, 237-238.	9.4	11
85	2010 Translational bioinformatics year in review. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 358-366.	4.4	10
86	Extracting chemical reactions from text using Snorkel. BMC Bioinformatics, 2020, 21, 217.	2.6	10
87	Challenges and opportunities in network-based solutions for biological questions. Briefings in Bioinformatics, 2022, 23, .	6.5	10
88	Genetic nondiscrimination legislation: a critical prerequisite for pharmacogenomics data sharing. Pharmacogenomics, 2007, 8, 519-519.	1.3	9
89	Essential Characteristics of Pharmacogenomics Study Publications. Clinical Pharmacology and Therapeutics, 2019, 105, 86-91.	4.7	9
90	An ?Omics? view of drug development. Drug Development Research, 2004, 62, 81-85.	2.9	8

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91	Scientific considerations for global drug development. Science Translational Medicine, 2020, 12, .	12.4	8
92	Populationâ€specific singleâ€nucleotide polymorphism confersÂincreased risk of venous thromboembolism in African Americans. Molecular Genetics & Genomic Medicine, 2016, 4, 513-520.	1.2	7
93	Estimation of Maximum Recommended Therapeutic Dose Using Predicted Promiscuity and Potency. Clinical and Translational Science, 2016, 9, 311-320.	3.1	7
94	Reversals and limitations on high-intensity, life-sustaining treatments. PLoS ONE, 2018, 13, e0190569.	2.5	7
95	Gaussian embedding for large-scale gene set analysis. Nature Machine Intelligence, 2020, 2, 387-395.	16.0	7
96	Title is missing!. Machine Learning, 2003, 52, 119-145.	5.4	6
97	An XML-based interchange format for genotype-phenotype data. Human Mutation, 2008, 29, 212-219.	2.5	6
98	Enabling the Curation of Your Pharmacogenetic Study. Clinical Pharmacology and Therapeutics, 2015, 97, 116-119.	4.7	6
99	Challenges for Training Translational Researchers in the Era of Ubiquitous Data. Clinical Pharmacology and Therapeutics, 2018, 103, 171-173.	4.7	6
100	Research Projects Supported by the <scp>University of California, San Francisco</scp>â€Stanford Center of Excellence in Regulatory Science and Innovation. Clinical Pharmacology and Therapeutics, 2019, 105, 815-818.	4.7	6
101	Quantifying the Severity of Adverse Drug Reactions Using Social Media: Network Analysis. Journal of Medical Internet Research, 2021, 23, e27714.	4.3	6
102	Using surface envelopes for discrimination of molecular models. Protein Science, 2004, 13, 15-24.	7.6	5
103	Mendelian Disease Associations Reveal Novel Insights into Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2018, 24, 471-481.	1.9	5
104	Modeling drug response using network-based personalized treatment prediction (NetPTP) with applications to inflammatory bowel disease. PLoS Computational Biology, 2021, 17, e1008631.	3.2	5
105	Construction of disease-specific cytokine profiles by associating disease genes with immune responses. PLoS Computational Biology, 2022, 18, e1009497.	3.2	5
106	Flexible Analog Search with Kernel PCA Embedded Molecule Vectors. Computational and Structural Biotechnology Journal, 2017, 15, 320-327.	4.1	4
107	Commentaries on "Informatics and medicine: from molecules to populations". Methods of Information in Medicine, 2008, 47, 296-317.	1.2	4
108	Genomics in the clinic: ethical and policy challenges in clinical next-generation sequencing programs at early adopter USA institutions. Personalized Medicine, 2015, 12, 269-282.	1.5	3

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109	PhenClust, a standalone tool for identifying trends within sets of biological phenotypes using semantic similarity and the Unified Medical Language System metathesaurus. JAMIA Open, 2021, 4, ooab079.	2.0	3
110	Pharmacogenomics in dermatology: tools for understanding gene-drug associations. Seminars in Cutaneous Medicine and Surgery, 2019, 38, E19-E24.	1.6	3
111	Potential Adverse Effects of Anesthesia in Children—Reply. JAMA - Journal of the American Medical Association, 2015, 314, 409.	7.4	2
112	Genetic sequence data for pharmacogenomics. Current Opinion in Drug Discovery & Development, 2003, 6, 297-303.	1.9	2
113	Complexities of Managing Biomedical Information. OMICS A Journal of Integrative Biology, 2003, 7, 127-129.	2.0	1
114	Towards Clinical Bioinformatics: Redux 2015. Yearbook of Medical Informatics, 2016, 25, S6-S7.	1.0	1
115	Response to Open Peer Commentaries on "Human Germline CRISPR-Cas Modification: Toward a Regulatory Framework". American Journal of Bioethics, 2016, 16, W1-W2.	0.9	1
116	Using surface envelopes to constrain molecular modeling. Protein Science, 2007, 16, 1266-1273.	7.6	0
117	Extending TextAE for annotation of non-contiguous entities. Genomics and Informatics, 2020, 18, e15.	0.8	0