# 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 | Challenges and opportunities in network-based solutions for biological questions. Briefings in Bioinformatics, 2022, 23, . | 6.5 | 10 |
| 2 | Construction of disease-specific cytokine profiles by associating disease genes with immune responses. PLoS Computational Biology, 2022, 18, e1009497. | 3.2 | 5 |
| 3 | Pharmacogenetics at Scale: An Analysis of the UK Biobank. Clinical Pharmacology and Therapeutics, 2021, 109, 1528-1537. | 4.7 | 78 |
| 4 | 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 |
| 5 | Large-scale labeling and assessment of sex bias in publicly available expression data. BMC Bioinformatics, 2021, 22, 168. | 2.6 | 12 |
| 6 | 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 |
| 7 | 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 |
| 8 | 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 |
| 9 | Genomewide Association Studies in Pharmacogenomics. Clinical Pharmacology and Therapeutics, 2021, 110, 637-648. | 4.7 | 38 |
| 10 | Leveraging the Cell Ontology to classify unseen cell types. Nature Communications, 2021, 12, 5556. | 12.8 | 21 |
| 11 | Quantifying the Severity of Adverse Drug Reactions Using Social Media: Network Analysis. Journal of Medical Internet Research, 2021, 23, e27714. | 4.3 | 6 |
| 12 | Pharmacogenomics Clinical Annotation Tool (Pharm<scp>CAT</scp>). Clinical Pharmacology and Therapeutics, 2020, 107, 203-210. | 4.7 | 65 |
| 13 | Examining the Use of Real‐World Evidence in the Regulatory Process. Clinical Pharmacology and Therapeutics, 2020, 107, 843-852. | 4.7 | 99 |
| 14 | Scientific considerations for global drug development. Science Translational Medicine, 2020, 12, . | 12.4 | 8 |
| 15 | Extracting chemical reactions from text using Snorkel. BMC Bioinformatics, 2020, 21, 217. | 2.6 | 10 |
| 16 | Gaussian embedding for large-scale gene set analysis. Nature Machine Intelligence, 2020, 2, 387-395. | 16.0 | 7 |
| 17 | Transfer learning enables prediction of CYP2D6 haplotype function. PLoS Computational Biology, 2020, 16, e1008399. | 3.2 | 32 |
| 18 | Extending TextAE for annotation of non-contiguous entities. Genomics and Informatics, 2020, 18, e15. | 0.8 | 0 |

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|---|---------|----|-----------|
| 19 | Graph Convolutional Neural Networks for Predicting Drug-Target Interactions. Journal of Chemical Information and Modeling, 2019, 59, 4131-4149. | 5.4 | 222 |
| 20 | Pocket similarity identifies selective estrogen receptor modulators as microtubule modulators at the taxane site. Nature Communications, 2019, 10, 1033. | 12.8 | 22 |
| 21 | 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 |
| 22 | Essential Characteristics of Pharmacogenomics Study Publications. Clinical Pharmacology and Therapeutics, 2019, 105, 86-91. | 4.7 | 9 |
| 23 | 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 |
| 24 | Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research. Clinical Pharmacology and Therapeutics, 2019, 105, 1256-1262. | 4.7 | 90 |
| 25 | Effect of <i><scp>CYP</scp>4F2</i>, <i><scp>VKORC</scp>1</i>, and <i><scp>CYP</scp>2C9</i> 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 |
| 26 | Pharmacogenomics in dermatology: tools for understanding gene-drug associations. Seminars in Cutaneous Medicine and Surgery, 2019, 38, E19-E24. | 1.6 | 3 |
| 27 | Mendelian Disease Associations Reveal Novel Insights into Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2018, 24, 471-481. | 1.9 | 5 |
| 28 | PharmGKB: A worldwide resource for pharmacogenomic information. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2018, 10, e1417. | 6.6 | 205 |
| 29 | Pharmacogenomics and big genomic data: from lab to clinic and back again. Human Molecular Genetics, 2018, 27, R72-R78. | 2.9 | 28 |
| 30 | 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 |
| 31 | A dynamic map for learning, communicating, navigating and improving therapeutic development. Nature Reviews Drug Discovery, 2018, 17, 150-150. | 46.4 | 43 |
| 32 | 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 |
| 33 | Biological and functional relevance of CASP predictions. Proteins: Structure, Function and Bioinformatics, 2018, 86, 374-386. | 2.6 | 12 |
| 34 | Biomarkers: Delivering on the expectation of molecularly driven, quantitative health. Experimental Biology and Medicine, 2018, 243, 313-322. | 2.4 | 13 |
| 35 | Challenges for Training Translational Researchers in the Era of Ubiquitous Data. Clinical Pharmacology and Therapeutics, 2018, 103, 171-173. | 4.7 | 6 |
| 36 | PathFX provides mechanistic insights into drug efficacy and safety for regulatory review and therapeutic development. PLoS Computational Biology, 2018, 14, e1006614. | 3.2 | 13 |

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| 37 | 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 |
| 38 | Data-driven human transcriptomic modules determined by independent component analysis. BMC Bioinformatics, 2018, 19, 327. | 2.6 | 25 |
| 39 | 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 |
| 40 | Machine learning in chemoinformatics and drug discovery. Drug Discovery Today, 2018, 23, 1538-1546. | 6.4 | 630 |
| 41 | Systematic target function annotation of human transcription factors. BMC Biology, 2018, 16, 4. | 3.8 | 12 |
| 42 | Reversals and limitations on high-intensity, life-sustaining treatments. PLoS ONE, 2018, 13, e0190569. | 2.5 | 7 |
| 43 | 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 |
| 44 | Artificial intelligence (AI) systems for interpreting complex medical datasets. Clinical Pharmacology and Therapeutics, 2017, 101, 585-586. | 4.7 | 45 |
| 45 | Pharmacogenomicsâ€Based Pointâ€ofâ€Care Clinical Decision Support Significantly Alters Drug Prescribing. Clinical Pharmacology and Therapeutics, 2017, 102, 859-869. | 4.7 | 68 |
| 46 | 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 |
| 47 | 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 |
| 48 | 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 |
| 49 | Shallow Representation Learning via Kernel PCA Improves QSAR Modelability. Journal of Chemical Information and Modeling, 2017, 57, 1859-1867. | 5.4 | 13 |
| 50 | 3D deep convolutional neural networks for amino acid environment similarity analysis. BMC Bioinformatics, 2017, 18, 302. | 2.6 | 106 |
| 51 | 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 |
| 52 | Flexible Analog Search with Kernel PCA Embedded Molecule Vectors. Computational and Structural Biotechnology Journal, 2017, 15, 320-327. | 4.1 | 4 |
| 53 | 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 |
| 54 | Towards Clinical Bioinformatics: Redux 2015. Yearbook of Medical Informatics, 2016, 25, S6-S7. | 1.0 | 1 |

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|---|---------|-----|-----------|
| 55 | 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 |
| 56 | Computing disease incidence, prevalence and comorbidity from electronic medical records. Journal of Biomedical Informatics, 2016, 63, 108-111. | 4.3 | 24 |
| 57 | Population-specific single-nucleotide polymorphism confers increased risk of venous thromboembolism in African Americans. Molecular Genetics &amp; Genomic Medicine, 2016, 4, 513-520. | 1.2 | 7 |
| 58 | 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 |
| 59 | Estimation of Maximum Recommended Therapeutic Dose Using Predicted Promiscuity and Potency. Clinical and Translational Science, 2016, 9, 311-320. | 3.1 | 7 |
| 60 | A research roadmap for next-generation sequencing informatics. Science Translational Medicine, 2016, 8, 335ps10. | 12.4 | 37 |
| 61 | 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 |
| 62 | 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 |
| 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 | Evidence for Clinical Implementation of Pharmacogenomics in Cardiac Drugs. Mayo Clinic Proceedings, 2015, 90, 716-729. | 3.0 | 44 |
| 65 | Neurotoxicity of Generic Anesthesia Agents in Infants and Children. JAMA - Journal of the American Medical Association, 2015, 313, 1515. | 7.4 | 48 |
| 66 | Human Germline CRISPR-Cas Modification: Toward a Regulatory Framework. American Journal of Bioethics, 2015, 15, 25-29. | 0.9 | 53 |
| 67 | Unmet needs: Research helps regulators do their jobs. Science Translational Medicine, 2015, 7, 315ps22. | 12.4 | 15 |
| 68 | Enabling the Curation of Your Pharmacogenetic Study. Clinical Pharmacology and Therapeutics, 2015, 97, 116-119. | 4.7 | 6 |
| 69 | Using "Big Data" to Dissect Clinical Heterogeneity. Circulation, 2015, 131, 232-233. | 1.6 | 28 |
| 70 | Predicting Cancer Drug Response: Advancing the DREAM. Cancer Discovery, 2015, 5, 237-238. | 9.4 | 11 |
| 71 | 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 |
| 72 | 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 |

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|---|---------|-----|-----------|
| 73 | The International SSRI Pharmacogenomics Consortium (ISPC): a genome-wide association study of antidepressant treatment response. Translational Psychiatry, 2015, 5, e553-e553. | 4.8 | 107 |
| 74 | Potential Adverse Effects of Anesthesia in Children—Reply. JAMA - Journal of the American Medical Association, 2015, 314, 409. | 7.4 | 2 |
| 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 | Personalization in practice. Science, 2015, 350, 282-283. | 12.6 | 20 |
| 77 | 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 |
| 78 | Learning the Structure of Biomedical Relationships from Unstructured Text. PLoS Computational Biology, 2015, 11, e1004216. | 3.2 | 36 |
| 79 | Ranking Adverse Drug Reactions With Crowdsourcing. Journal of Medical Internet Research, 2015, 17, e80. | 4.3 | 35 |
| 80 | High Precision Prediction of Functional Sites in Protein Structures. PLoS ONE, 2014, 9, e91240. | 2.5 | 15 |
| 81 | Environmental and State-Level Regulatory Factors Affect the Incidence of Autism and Intellectual Disability. PLoS Computational Biology, 2014, 10, e1003518. | 3.2 | 48 |
| 82 | Knowledge-based Fragment Binding Prediction. PLoS Computational Biology, 2014, 10, e1003589. | 3.2 | 32 |
| 83 | Clinical Interpretation and Implications of Whole-Genome Sequencing. JAMA - Journal of the American Medical Association, 2014, 311, 1035. | 7.4 | 398 |
| 84 | Guidelines for investigating causality of sequence variants in human disease. Nature, 2014, 508, 469-476. | 27.8 | 1,130 |
| 85 | Interpreting the CYP2D6 Results From the International Tamoxifen Pharmacogenetics Consortium. Clinical Pharmacology and Therapeutics, 2014, 96, 144-146. | 4.7 | 14 |
| 86 | Personal Genomic Measurements: The Opportunity for Information Integration. Clinical Pharmacology and Therapeutics, 2013, 93, 21-23. | 4.7 | 26 |
| 87 | Challenges in the Pharmacogenomic Annotation of Whole Genomes. Clinical Pharmacology and Therapeutics, 2013, 94, 211-213. | 4.7 | 23 |
| 88 | Chapter 7: Pharmacogenomics. PLoS Computational Biology, 2012, 8, e1002817. | 3.2 | 57 |
| 89 | Data-Driven Prediction of Drug Effects and Interactions. Science Translational Medicine, 2012, 4, 125ra31. | 12.4 | 610 |
| 90 | Translational Bioinformatics: Linking the Molecular World to the Clinical World. Clinical Pharmacology and Therapeutics, 2012, 91, 994-1000. | 4.7 | 43 |

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|---|---------|----|-----------|
| 91 | Introduction to Translational Bioinformatics Collection. PLoS Computational Biology, 2012, 8, e1002796. | 3.2 | 12 |
| 92 | 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 |
| 93 | Pharmacogenomics: will the promise be fulfilled?. Nature Reviews Genetics, 2011, 12, 69-73. | 16.3 | 29 |
| 94 | Pharmacogenomics: â€œNoninferiorityâ€•Is Sufficient for Initial Implementation. Clinical Pharmacology and Therapeutics, 2011, 89, 348-350. | 4.7 | 85 |
| 95 | 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 |
| 96 | 2010 Translational bioinformatics year in review. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 358-366. | 4.4 | 10 |
| 97 | Using Multiple Microenvironments to Find Similar Ligand-Binding Sites: Application to Kinase Inhibitor Binding. PLoS Computational Biology, 2011, 7, e1002326. | 3.2 | 60 |
| 98 | Using Pre-existing Microarray Datasets to Increase Experimental Power: Application to Insulin Resistance. PLoS Computational Biology, 2010, 6, e1000718. | 3.2 | 11 |
| 99 | Generating Genome-Scale Candidate Gene Lists for Pharmacogenomics. Clinical Pharmacology and Therapeutics, 2009, 86, 183-189. | 4.7 | 75 |
| 100 | Direct-to-Consumer Genetic Testing: Failure Is Not an Option. Clinical Pharmacology and Therapeutics, 2009, 86, 15-17. | 4.7 | 24 |
| 101 | Robust recognition of zinc binding sites in proteins. Protein Science, 2008, 17, 54-65. | 7.6 | 88 |
| 102 | An XML-based interchange format for genotype-phenotype data. Human Mutation, 2008, 29, 212-219. | 2.5 | 6 |
| 103 | Commentaries on "Informatics and medicine: from molecules to populations". Methods of Information in Medicine, 2008, 47, 296-317. | 1.2 | 4 |
| 104 | Genetic nondiscrimination legislation: a critical prerequisite for pharmacogenomics data sharing. Pharmacogenomics, 2007, 8, 519-519. | 1.3 | 9 |
| 105 | The Education Potential of the Pharmacogenetics and Pharmacogenomics Knowledge Base (PharmGKB). Clinical Pharmacology and Therapeutics, 2007, 82, 472-475. | 4.7 | 16 |
| 106 | Using surface envelopes to constrain molecular modeling. Protein Science, 2007, 16, 1266-1273. | 7.6 | 0 |
| 107 | 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 |
| 108 | Structural characterization of proteins using residue environments. Proteins: Structure, Function and Bioinformatics, 2005, 61, 741-747. | 2.6 | 24 |

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|---|---------|-----|-----------|
| 109 | Time to Organize the Bioinformatics Resourceome. PLoS Computational Biology, 2005, 1, e76. | 3.2 | 70 |
| 110 | An ?Omics? view of drug development. Drug Development Research, 2004, 62, 81-85. | 2.9 | 8 |
| 111 | Using surface envelopes for discrimination of molecular models. Protein Science, 2004, 13, 15-24. | 7.6 | 5 |
| 112 | Title is missing!. Machine Learning, 2003, 52, 119-145. | 5.4 | 6 |
| 113 | WebFEATURE: an interactive web tool for identifying and visualizing functional sites on macromolecular structures. Nucleic Acids Research, 2003, 31, 3324-3327. | 14.5 | 79 |
| 114 | Complexities of Managing Biomedical Information. OMICS A Journal of Integrative Biology, 2003, 7, 127-129. | 2.0 | 1 |
| 115 | Genetic sequence data for pharmacogenomics. Current Opinion in Drug Discovery & Development, 2003, 6, 297-303. | 1.9 | 2 |
| 116 | Challenges for Biomedical Informatics and Pharmacogenomics. Annual Review of Pharmacology and Toxicology, 2002, 42, 113-133. | 9.4 | 93 |
| 117 | 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 |