




## Russ B. Altman

Kenneth Fong Professor and Professor of Bioengineering, of Genetics, of Medicine, of Biomedical Data Science, Senior Fellow at the Stanford Institute for Human-Centered AI and Professor, by courtesy, of Computer Science

 NIH Biosketch available Online

 Curriculum Vitae available Online

### CONTACT INFORMATION

#### • Alternate Contact

Tiffany Murray - Administrative Associate

**Email** [tiffany.murray@stanford.edu](mailto:tiffany.murray@stanford.edu)

**Tel** 650-725-0659

### Bio

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#### BIO

Russ Biagio Altman is the Kenneth Fong Professor of Bioengineering, Genetics, Medicine, Biomedical Data Science and (by courtesy) Computer Science) and past chairman of the Bioengineering Department at Stanford University. His primary research interests are in the application of computing (AI, data science and informatics) to problems relevant to medicine. He is particularly interested in methods for understanding drug action at molecular, cellular, organism and population levels. His lab studies how human genetic variation impacts drug response (e.g., <http://www.pharmgkb.org/>). Other work focuses on the analysis of biological molecules to understand the actions, interactions and adverse events of drugs (e.g., <http://helix.stanford.edu/>). He helps lead an FDA-supported Center of Excellence in Regulatory Science & Innovation.

Dr. Altman holds an AB from Harvard College, and an MD from Stanford Medical School, and a PhD in Medical Information Sciences from Stanford. He received the U.S. Presidential Early Career Award for Scientists and Engineers and a National Science Foundation CAREER Award. He is a fellow of the American College of Physicians (ACP), the American College of Medical Informatics (ACMI), the American Institute of Medical and Biological Engineering (AIMBE), and the American Association for the Advancement of Science (AAAS). He is a member of the National Academy of Medicine. He is a past-president, founding board member, and a fellow of the International Society for Computational Biology (ISCB), and a past-president of the American Society for Clinical Pharmacology & Therapeutics (ASCPT). He has chaired the Science Board advising the FDA commissioner, and has served on the NIH Director's Advisory Committee, and as cochair of the IOM Drug Forum. He is an organizer of the annual Pacific Symposium on Biocomputing, and a founder of Personalis (NASDAQ: PSNL). Dr. Altman is board certified in Internal Medicine and in Clinical Informatics. He received the Stanford Medical School graduate teaching award in 2000 and 2020, and the mentorship award in 2014. He is the founding editor of the Annual Reviews of Biomedical Data Science, and hosts a podcast entitled "The Future of Everything."

#### ACADEMIC APPOINTMENTS

- Professor, Bioengineering
- Professor, Genetics
- Professor, Computational Medicine
- Professor, Department of Biomedical Data Science

- Senior Fellow, Institute for Human-Centered Artificial Intelligence (HAI)
- Professor (By courtesy), Computer Science
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Wu Tsai Human Performance Alliance
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

## **ADMINISTRATIVE APPOINTMENTS**

- Faculty Director, SPADA (Stanford Predictives & Diagnostics Accelerator), (2016- present)
- Faculty Director, 100 Year Study of Artificial Intelligence, (2015- present)
- Associate Director, Human-Centered Artificial Intelligence Institute, (2018- present)
- Member, Biomedical Library and Informatics Research Committee Study Section (NIH), (2002-2005)
- President, International Society for Computational Biology, (2000-2001)
- President, American Society for Clinical Pharmacology and Therapeutics, (2013-2014)
- Director, Biomedical Informatics Training Program, (2000-2018)
- Chairman, Department of Bioengineering, (2007-2012)
- Chair, FDA Science Board, (2013-2014)
- Member, Advisory Committee to the Director (ACD), NIH, (2013-2016)

## **HONORS AND AWARDS**

- The Arthur Kornberg and Paul Berg Lifetime Achievement Award in Biomedical Sciences, Stanford Medical School (2023)
- Teaching Honor Roll, Tau Beta Pi (2020)
- Excellence in Graduate Teaching Award, Stanford Biosciences (2020)
- Fellow, American Association for the Advancement of Science (2014)
- Stanford Medical School Mentorship Award, Stanford Medical School (2014)
- Fellow, International Society for Computational Biology (2010)
- Member, Institute of Medicine of the National Academies (2009)
- Fellow, American Institute for Medical and Biological Engineering (2007)
- Award for Excellence in Graduate Teaching, Stanford Medical School (2000)
- Fellow, American College of Medical Informatics (1998)
- Fellow, American College of Physicians (1998)
- U.S. Presidential Early Career Award for Scientists & Engineers, NIH (1997)
- Post-Doctoral Fellowship, Howard Hughes Medical Institute (1991)

## **BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS**

- Global Health Faculty Fellow, Center for Innovation in Global Health (CIGH) (2024 - present)
- Co-Founder, Personalis.com (2013 - present)
- Editor-in-Chief, Annual Reviews of Biomedical Data Science (2016 - present)
- Board of Directors, YouScript.com (2018 - present)

- Advisor, Vanderbilt University Medical School (2014 - present)
- Advisor, NIH Advisory Committee to the Director (ACD) (2013 - 2017)
- Member, FDA Commissioner Science Board (2011 - 2014)
- Co-Organizer, Pacific Symposium on Biocomputing ([psb.stanford.edu](http://psb.stanford.edu)) (1995 - present)

### PROGRAM AFFILIATIONS

- Symbolic Systems Program

### PROFESSIONAL EDUCATION

- AB (summa cum laude), Harvard College , Biochemistry and Molecular Biology (1983)
- PhD, Stanford University , Medical Information Sciences (1989)
- MD, Stanford University , Medicine (1990)

### COMMUNITY AND INTERNATIONAL WORK

- Host, "The Future of Everything with Russ Altman" Podcast, <https://engineering.stanford.edu/magazine/collection/future-everything>
- Physician, Pharmacogenomics Consult Service, Stanford Clinics, CA

### PATENTS

- Nicholas Tatonetti, Russ B. Altman, Guy Haskin Fernald. "United States Patent 9305267 Signal detection algorithms to identify drug effects and drug interactions", The Board of Trustees of the Leland Stanford Junior University, Apr 5, 2016
- Kathleen A. Thompson, Russ B. Altman, Oliver M. Duschka. "United States Patent 6178416 Method and apparatus for knowledgebase searching", Jan 23, 2001
- Ramon M. Felciano, Russ B. Altman. "United States Patent 6052730 Method for monitoring and/or modifying web browsing sessions", The Board of Trustees of the Leland Stanford Junior University, Apr 18, 2000

### LINKS

- Helix Group Website: <http://helix.stanford.edu>
- Personal home page: <https://rbaltman.people.stanford.edu>

## Research & Scholarship

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### CURRENT RESEARCH AND SCHOLARLY INTERESTS

I am interested in the application of computational technologies to problems in molecular biology of relevance to medicine. In particular, my laboratory focuses on drug response at the molecular level, working in three areas. First, we are building a comprehensive pharmacogenomics knowledge base (<http://www.pharmgkb.org/>) that provides access to information relating genotype to phenotype (in particular, how variation in genetics leads to variation in response to drugs). We are interested in collaboratively discovering and applying new pharmacogenomics knowledge. Second, we are interested in the analysis of three dimensional biological structures. We have methods for analyzing protein structures to recognize and annotate active sites and binding sites, particularly in the context of interactions with small molecule drugs. We are also interested in physics-based simulation of biological structures to understand how their dynamics impact their function (<http://simbios.stanford.edu/>). Finally, we are interested in computational methods for analyzing functional genomics information. We use natural language processing techniques for extracting and summarizing information in the literature, chemoinformatics methods for understanding small molecule function, and machine learning & data mining techniques to understand the molecular responses to drugs.

## Teaching

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### COURSES

#### 2025-26

- Computational Applications of High-Throughput Protein Data for Machine Learning: BIOS 442 (Spr)
- Ethics in Bioengineering: BIOE 131, ETHICSOC 131X (Spr)
- Introduction to Biomedical Informatics Research Methodology: BIOE 212, BMDS 212, CS 272, GENE 212 (Spr)
- Principles of Pharmacogenomics: BMDS 224, GENE 224 (Aut, Spr)
- Representations and Algorithms for Computational Molecular Biology: BIOE 214, BMDS 214, CS 274, GENE 214 (Aut)
- Representations and Algorithms for Molecular Biology: Lectures: BMDS 216 (Aut)

#### 2024-25

- Ethics in Bioengineering: BIOE 131, ETHICSOC 131X (Spr)
- Introduction to Biomedical Informatics Research Methodology: BIOE 212, BIOMEDIN 212, CS 272, GENE 212 (Spr)
- Principles of Pharmacogenomics: BIOMEDIN 224, GENE 224 (Aut, Spr)
- Representations and Algorithms for Computational Molecular Biology: BIOE 214, BIOMEDIN 214, CS 274, GENE 214 (Aut)
- Representations and Algorithms for Molecular Biology: Lectures: BIOMEDIN 216 (Aut)

#### 2023-24

- Ethics in Bioengineering: BIOE 131, ETHICSOC 131X (Spr)
- Introduction to Biomedical Data Science Research Methodology: BIOE 212, BIOMEDIN 212, CS 272, GENE 212 (Spr)
- Principles of Pharmacogenomics: BIOMEDIN 224, GENE 224 (Aut, Spr)
- Representations and Algorithms for Computational Molecular Biology: BIOE 214, BIOMEDIN 214, CS 274, GENE 214 (Aut)
- Representations and Algorithms for Molecular Biology: Lectures: BIOMEDIN 216 (Aut)

#### 2022-23

- Ethics in Bioengineering: BIOE 131, ETHICSOC 131X (Spr)
- Introduction to Biomedical Data Science Research Methodology: BIOE 212, BIOMEDIN 212, CS 272, GENE 212 (Spr)
- Principles of Pharmacogenomics: BIOMEDIN 224, GENE 224 (Aut, Win, Spr, Sum)
- Representations and Algorithms for Computational Molecular Biology: BIOE 214, BIOMEDIN 214, CS 274, GENE 214 (Aut)
- Representations and Algorithms for Molecular Biology: Lectures: BIOMEDIN 216 (Aut)

### STANFORD ADVISEES

#### Med Scholar Project Advisor

Christine Lee, Johnny Powell, Helen Xu

#### Doctoral Dissertation Reader (AC)

Ibtihal Elfaki, EJ Fine, Jessica Kain, Jessica Karaguesian, Aviv Korman, Haim Krupkin, Louise Gabrielle Lima, Tianyu Lu, Holly McCann, Shuyu Shi, Elana Simon, Courtney Smith, Yixin Wang

#### Doctoral Dissertation Advisor (AC)

Vidal Arroyo, Stephanie Arteaga, Gowri Nayar, Issah Samori, Betty Xiong

#### Doctoral Dissertation Co-Advisor (AC)

Jeonghyeon Kim, Mohini Misra

### Master's Program Advisor

Emily Liu, Nikhil Lyles, Georgios Mikos, Sam Moghaddam, Janina Troper, Asmani Yamin, Bowen Zheng

### Doctoral (Program)

Sarah Arnold, Yasa Baig, Aviv Korman, Kara Liu, Janella Schwab Lizárraga, Emily Yemington

## GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Bioengineering (Phd Program)
- Biomedical Data Science (Masters Program)
- Biomedical Data Science (Phd Program)
- Biophysics (Phd Program)
- Genetics (Phd Program)

## Publications

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### PUBLICATIONS

- **TikTok is a valuable data source for tracking the opioid crisis.** *NPJ digital medicine*  
Samori, I. A., Carpenter, K. A., Smith, D. A., Humphreys, K., Lembke, A., Eichstaedt, J. C., Altman, R. B.  
2026
- **Interpreting PLMs for cancer discovery: High attention hotspots predict pathogenic mutation positions and novel drug binding sites**  
Pribus, S. J., Nayar, G., Altman, R.  
AMER ASSOC CANCER RESEARCH.2026
- **GATSBI: Improving context-aware protein embeddings through biologically motivated data splits.** *bioRxiv : the preprint server for biology*  
Nayar, G., Altman, R. B.  
2026
- **The Human Omnibus of Targetable Pockets.** *Journal of cheminformatics*  
Carpenter, K. A., Altman, R. B.  
2025; 17 (1): 180
- **Identifying DNA methylation sites affecting drug response using electronic health record-derived GWAS summary statistics.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Smith, D. A., Arteaga, S. A., Sadler, M. C., Altman, R. B.  
2025; 30: 457-472
- **Detecting clinician implicit biases in diagnoses using proximal causal inference.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Liu, K., Altman, R., Syrgkanis, V.  
2025; 30: 330-345
- **Paying attention to attention: High attention sites as indicators of protein family and function in language models.** *PLoS computational biology*  
Nayar, G., Tartici, A., Altman, R. B.  
2025; 21 (9): e1013424
- **Protein functional site annotation using local structure embeddings.** *Proceedings of the National Academy of Sciences of the United States of America*  
Derry, A., Tartici, A., Altman, R. B.  
2025; 122 (34): e2513219122
- **CRISPR-GPT for agentic automation of gene-editing experiments.** *Nature biomedical engineering*  
Qu, Y., Huang, K., Yin, M., Zhan, K., Liu, D., Yin, D., Cousins, H. C., Johnson, W. A., Wang, X., Shah, M., Altman, R. B., Zhou, D., Wang, et al  
2025

- **Unsupervised learning reveals landscape of local structural motifs across protein classes.** *Bioinformatics (Oxford, England)*  
Derry, A., Krupkin, H., Tartici, A., Altman, R. B.  
2025
- **Pool PaRTI: A PageRank-Based Pooling Method for Identifying Critical Residues and Enhancing Protein Sequence Representations.** *Bioinformatics (Oxford, England)*  
Tartici, A., Nayar, G., Altman, R. B.  
2025
- **Monitoring the opioid epidemic via social media discussions.** *NPJ digital medicine*  
Smith, D. A., Lavertu, A., Salecha, A., Hamamsy, T., Humphreys, K., Lembke, A., Kiang, M. V., Altman, R. B., Eichstaedt, J. C.  
2025; 8 (1): 284
- **Leveraging large-scale biobank EHRs to enhance pharmacogenetics of cardiometabolic disease medications.** *Nature communications*  
Sadler, M. C., Apostolov, A., Cevallos, C., Auwerx, C., Ribeiro, D. M., Altman, R. B., Kutalik, Z.  
2025; 16 (1): 2913
- **Genetic association studies using disease liabilities from deep neural networks.** *American journal of human genetics*  
Yang, L., Sadler, M. C., Altman, R. B.  
2025
- **Conditional Generative Models for Synthetic Tabular Data: Applications for Precision Medicine and Diverse Representations.** *Annual review of biomedical data science*  
Liu, K., Altman, R. B.  
2025
- **Toward a framework for risk mitigation of potential misuse of artificial intelligence in biomedical research.** *Nature machine intelligence*  
Trotsyuk, A. A., Waeiss, Q., Bhatia, R. T., Aponte, B. J., Heffernan, I. M., Madgavkar, D., Felder, R. M., Lehmann, L. S., Palmer, M. J., Greely, H., Wald, R., Goetz, L., Trengove, et al  
2024; 6 (12): 1435-1442
- **COLLAPSE: A representation learning framework for identification and characterization of protein structural sites.** *Protein science : a publication of the Protein Society*  
Derry, A., Altman, R. B.  
2022: e4541
- **POPDx: an automated framework for patient phenotyping across 392 246 individuals in the UK Biobank study.** *Journal of the American Medical Informatics Association : JAMIA*  
Yang, L., Wang, S., Altman, R. B.  
2022
- **Construction of disease-specific cytokine profiles by associating disease genes with immune responses.** *PLoS computational biology*  
Liu, T., Wang, S., Wornow, M., Altman, R. B.  
2022; 18 (4): e1009497
- **Quantifying the Severity of Adverse Drug Reactions Using Social Media: Network Analysis.** *Journal of medical Internet research*  
Lavertu, A., Hamamsy, T., Altman, R. B.  
2021; 23 (10): e27714
- **Leveraging the Cell Ontology to classify unseen cell types.** *Nature communications*  
Wang, S., Pisco, A. O., McGeever, A., Brbic, M., Zitnik, M., Darmanis, S., Leskovec, J., Karkania, J., Altman, R. B.  
2021; 12 (1): 5556
- **Drug Response Pharmacogenetics for 200,000 UK Biobank Participants.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
McInnes, G. n., Altman, R. B.  
2021; 26: 184–95
- **Analyzing the vast coronavirus literature with CoronaCentral.** *Proceedings of the National Academy of Sciences of the United States of America*  
Lever, J., Altman, R. B.

2021; 118 (23)

- **Analyzing the vast coronavirus literature with CoronaCentral.** *bioRxiv : the preprint server for biology*  
Lever, J., Altman, R. B.  
2020
- **RedMed: Extending drug lexicons for social media applications.** *Journal of biomedical informatics*  
Lavertu, A., Altman, R. B.  
2019: 103307
- **High precision protein functional site detection using 3D convolutional neural networks.** *Bioinformatics (Oxford, England)*  
Tornig, W., Altman, R. B.  
2019; 35 (9): 1503–12
- **Pocket similarity identifies selective estrogen receptor modulators as microtubule modulators at the taxane site.** *Nature communications*  
Lo, Y. C., Cormier, O. n., Liu, T. n., Nettles, K. W., Katzenellenbogen, J. A., Stearns, T. n., Altman, R. B.  
2019; 10 (1): 1033
- **Graph Convolutional Neural Networks for Predicting Drug-Target Interactions.** *Journal of chemical information and modeling*  
Tornig, W. n., Altman, R. B.  
2019
- **A global network of biomedical relationships derived from text** *BIOINFORMATICS*  
Percha, B., Altman, R. B.  
2018; 34 (15): 2614–24
- **Data-Driven Prediction of Drug Effects and Interactions** *SCIENCE TRANSLATIONAL MEDICINE*  
Tatonetti, N. P., Ye, P. P., Daneshjou, R., Altman, R. B.  
2012; 4 (125)
- **Clinical assessment incorporating a personal genome** *LANCET*  
Ashley, E. A., Butte, A. J., Wheeler, M. T., Chen, R., Klein, T. E., Dewey, F. E., Dudley, J. T., Ormond, K. E., Pavlovic, A., Morgan, A. A., Pushkarev, D., Neff, N. F., Hudgins, et al  
2010; 375 (9725): 1525-1535
- **Optimizing Enterprise Referral Processing through Automated Fax Triage** *NEJM CATALYST INNOVATIONS IN CARE DELIVERY*  
Mui, D., Tran, J. L. A., Onofre, S., Ramirez, S., Singh, V., Lago, A., Ng-Thow-Hing, J., Lavertu, A., Kaushal, A., Altman, R., Pallas, J., Boosi, S., Gohil, et al  
2026; 7 (5)
- **Drug-Target Interaction Prediction with PIGLET.** *bioRxiv : the preprint server for biology*  
Carpenter, K. A., Altman, R. B.  
2026
- **Biological data governance in an age of AI.** *Science (New York, N.Y.)*  
Bloomfield, D., Black, J. R., Crook, O., Brandes, N., Hanke, M. S., Inglesby, T. V., Cicero, A., Pollack, R., Hernandez-Boussard, T., Imperiale, M. J., Altman, R. B., Pannu, J.  
2026; 391 (6785): 558-561
- **Publisher Correction: CRISPR-GPT for agentic automation of gene-editing experiments.** *Nature biomedical engineering*  
Qu, Y., Huang, K., Yin, M., Zhan, K., Liu, D., Yin, D., Cousins, H. C., Johnson, W. A., Wang, X., Shah, M., Altman, R. B., Zhou, D., Wang, et al  
2025
- **Empirical Drug Dosage Validates Pharmacogenomic Associations in All of Us.** *Clinical and translational science*  
Matthias, J., Falaguera, M. J., Altman, R. B.  
2025; 18 (11): e70406
- **SubCell: Proteome-aware vision foundation models for microscopy capture single-cell biology.** *bioRxiv : the preprint server for biology*  
Gupta, A., Wefers, Z., Kahnert, K., Hansen, J. N., Misra, M. K., Leineweber, W., Cesnik, A., Lu, D., Axelsson, U., Ballillosera, F., Altman, R. B., Karaletsos, T., Lundberg, et al  
2025

- **Reframing Justice in Healthcare AI: An Ubuntu-Based Approach for Africa.** *Developing world bioethics*  
Ochasi, A., Mahamadou, A. J., Altman, R. B., Nkwocha, L. U.  
2025
- **Membrane-wide screening identifies potential tissue-specific determinants of SARS-CoV-2 tropism.** *PLoS pathogens*  
Dinesh, R. K., Wang, C., Qu, Y., Rustagi, A., Cousins, H., Zengel, J., Wang, X., Barnard, T. R., Johnson, W. A., Xu, G., Zhang, T., Magazine, N., Beck, et al  
2025; 21 (7): e1013157
- **A calcium-sensing receptor allelic series and underdiagnosis of genetically driven hypocalcemia.** *American journal of human genetics*  
Chang, J. B., Barnhill, C. P., Apostolov, A. M., Soliai, M. M., Hecker, J., Nierenberg, J. L., Stapleton Smith, L. M., Mathew, A. S., Zeng, X., Diao, J., Fernando, C. D., Chen, Q., Dulken, et al  
2025
- **Semi-supervised data-integrated feature importance enhances performance and interpretability of biological classification tasks.** *Bioinformatics (Oxford, England)*  
Kim, J. W., Altman, R. B.  
2025; 41 (Supplement\_1): i373-i381
- **Identifying DNA methylation sites affecting drug response using electronic health record-derived GWAS summary statistics.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Smith, D. A., Arteaga, S. A., Sadler, M. C., Altman, R. B.  
2025; 30: 457-472
- **Detecting clinician implicit biases in diagnoses using proximal causal inference.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Liu, K., Altman, R., Syrgkanis, V.  
2025; 30: 330-345
- **CRISPR-GPT: LLM Agents for Automated Design of Gene-Editing Experiments**  
Qu, Y., Huang, K., Yin, M., Zhan, K., Liu, D., Yin, D., Cousins, H., Johnson, W., Wang, X., Altman, R., Zhou, D., Wang, M., Cong, et al  
CELL PRESS.2025
- **Which social media platforms facilitate monitoring the opioid crisis?** *PLOS digital health*  
Carpenter, K. A., Nguyen, A. T., Smith, D. A., Samori, I. A., Humphreys, K., Lembke, A., Kiang, M. V., Eichstaedt, J. C., Altman, R. B.  
2025; 4 (4): e0000842
- **Pool PaRTI: A PageRank-Based Pooling Method for Identifying Critical Residues and Enhancing Protein Sequence Representations.** *bioRxiv : the preprint server for biology*  
Tartici, A., Nayar, G., Altman, R. B.  
2025
- **The E2F4 transcriptional repressor is a key mechanistic regulator of colon cancer resistance toirinotecan(CPT-11).** *bioRxiv : the preprint server for biology*  
Matsubara, J., Li, Y. F., Koul, S., Mukohyama, J., Valencia Salazar, L. E., Isobe, T., Qian, D., Clarke, M. F., Sahoo, D., Altman, R. B., Dalerba, P.  
2025
- **Databases of ligand-binding pockets and protein-ligand interactions.** *Computational and structural biotechnology journal*  
Carpenter, K. A., Altman, R. B.  
2024; 23: 1320-1338
- **Heterogeneous network approaches to protein pathway prediction.** *Computational and structural biotechnology journal*  
Nayar, G., Altman, R. B.  
2024; 23: 2727-2739
- **Heterogeneous network approaches to protein pathway prediction** *COMPUTATIONAL AND STRUCTURAL BIOTECHNOLOGY JOURNAL*  
Nayar, G., Altman, R. B.  
2024; 23: 2727-2739
- **Toward a framework for risk mitigation of potential misuse of artificial intelligence in biomedical research** *NATURE MACHINE INTELLIGENCE*

- Trotsyuk, A. A., Waeiss, Q., Bhatia, R., Aponte, B. J., Heffernan, I. M. L., Madgavkar, D., Felder, R., Lehmann, L., Palmer, M. J., Greely, H., Wald, R., Goetz, L., Trengove, et al  
2024
- **Which social media platforms facilitate monitoring the opioid crisis?** *medRxiv : the preprint server for health sciences*  
Carpenter, K. A., Nguyen, A. T., Smith, D. A., Samori, I. A., Humphreys, K., Lembke, A., Kiang, M. V., Eichstaedt, J. C., Altman, R. B.  
2024
  - **Prospector Heads: Generalized Feature Attribution for Large Models & Data.** *ArXiv*  
Machiraju, G., Derry, A., Desai, A., Guha, N., Karimi, A. H., Zou, J., Altman, R. B., Ré, C., Mallick, P.  
2024
  - **Unsupervised network learning enables systematic characterization of genetic risk pathways for primary open-angle glaucoma**  
Cousins, H., Altman, R. B., Pasquale, L. R.  
ASSOC RESEARCH VISION OPHTHALMOLOGY INC.2024
  - **Elucidating the semantics-topology trade-off for knowledge inference-based pharmacological discovery.** *Journal of biomedical semantics*  
Sosa, D. N., Neculae, G., Fauqueur, J., Altman, R. B.  
2024; 15 (1): 5
  - **Computational Approaches to Drug Repurposing: Methods, Challenges, and Opportunities.** *Annual review of biomedical data science*  
Cousins, H. C., Nayar, G., Altman, R. B.  
2024
  - **Leveraging large-scale biobank EHRs to enhance pharmacogenetics of cardiometabolic disease medications.** *medRxiv : the preprint server for health sciences*  
Sadler, M. C., Apostolov, A., Cevallos, C., Ribeiro, D. M., Altman, R. B., Kutalik, Z.  
2024
  - **CAGI, the Critical Assessment of Genome Interpretation, establishes progress and prospects for computational genetic variant interpretation methods** *GENOME BIOLOGY*  
Jain, S., Bakolitsa, C., Brenner, S. E., Radivojac, P., Moul, J., Repo, S., Hoskins, R. A., Andreoletti, G., Barsky, D., Chellapan, A., Chu, H., Dabburu, N., Kollipara, et al  
2024; 25 (1): 53
  - **CRISPR-GPT: an LLM agent for automated design of gene-editing experiments** *bioRxiv: the preprint server for biology*  
Qu, Y., Huang, K., Cousins, H., Johnson, W., Yin, D., Shah, M., Zhou, D., Altman, R., Wang, M., Cong, L.  
2024
  - **DEEP LEARNING FOR LOCALIZED DETECTION OF OPTIC DISC HEMORRHAGES (vol 255, pg 161, 2023)** *AMERICAN JOURNAL OF OPHTHALMOLOGY*  
Brown, A. C., Cousins, H., Cousins, C. C., Esquenazi, K., Filipowicz, A., Barna, L., Kim, Y., Vinod, K., Chadha, N., Altman, R. B., Coote, M., Elze, T., Topouzis, et al  
2024; 257
  - **A mitochondrial inside-out iron-calcium signal reveals drug targets for Parkinson's disease.** *Cell reports*  
Bharat, V., Durairaj, A. S., Vanhauwaert, R., Li, L., Muir, C. M., Chandra, S., Kwak, C. S., Le Guen, Y., Nandakishore, P., Hsieh, C. H., Rensi, S. E., Altman, R. B., Greicius, et al  
2023; 42 (12): 113544
  - **Integrative analyses highlight functional regulatory variants associated with neuropsychiatric diseases.** *Nature genetics*  
Guo, M. G., Reynolds, D. L., Ang, C. E., Liu, Y., Zhao, Y., Donohue, L. K., Siprashvili, Z., Yang, X., Yoo, Y., Mondal, S., Hong, A., Kain, J., Meservey, et al  
2023
  - **Explainable protein function annotation using local structure embeddings.** *bioRxiv : the preprint server for biology*  
Derry, A., Altman, R. B.  
2023
  - **A Holy Grail - The Prediction of Protein Structure.** *The New England journal of medicine*  
Altman, R. B.

2023

- **Stronger regulation of AI in biomedicine.** *Science translational medicine*  
Trotskyuk, A. A., Federico, C. A., Cho, M. K., Altman, R. B., Magnus, D.  
2023; 15 (713): eadi0336
- **The phenotype-genotype reference map: Improving biobank data science through replication.** *American journal of human genetics*  
Bastarache, L., Delozier, S., Pandit, A., He, J., Lewis, A., Annis, A. C., LeFaive, J., Denny, J. C., Carroll, R. J., Altman, R. B., Hughey, J. J., Zawistowski, M., Peterson, et al  
2023
- **Associating biological context with protein-protein interactions through text mining at PubMed scale.** *Journal of biomedical informatics*  
Sosa, D. N., Hintzen, R., Xiong, B., de Giorgio, A., Fauqueur, J., Davies, M., Lever, J., Altman, R. B.  
2023: 104474
- **Genetic Correlations Among Corneal Biophysical Parameters and Anthropometric Traits.** *Translational vision science & technology*  
Cousins, H. C., Cousins, C. C., Valluru, G., Altman, R. B., Liu, Y., Pasquale, L. R., Ahmad, S.  
2023; 12 (8): 8
- **Integrative analysis of functional genomic screening and clinical data identifies a protective role for spironolactone in severe COVID-19.** *Cell reports methods*  
Cousins, H. C., Kline, A. S., Wang, C., Qu, Y., Zengel, J., Carette, J., Wang, M., Altman, R. B., Luo, Y., Cong, L.  
2023; 3 (7): 100503
- **Deep learning for localized detection of optic disc hemorrhages.** *American journal of ophthalmology*  
Brown, A., Cousins, H., Cousins, C., Esquenazi, K., Elze, T., Harris, A., Filipowicz, A., Barna, L., Yonwook, K., Vinod, K., Chadha, N., Altman, R. B., Coote, et al  
2023
- **Network-based machine learning for gene prioritization in primary open-angle glaucoma**  
Cousins, H., Altman, R. B., Pasquale, L. R.  
ASSOC RESEARCH VISION OPHTHALMOLOGY INC.2023
- **Association between spironolactone use and COVID-19 outcomes in population-scale claims data: a retrospective cohort study.** *medRxiv : the preprint server for health sciences*  
Cousins, H. C., Altman, R. B.  
2023
- **Using GPT-3 to Build a Lexicon of Drugs of Abuse Synonyms for Social Media Pharmacovigilance.** *Biomolecules*  
Carpenter, K. A., Altman, R. B.  
2023; 13 (2)
- **Multilingual translation for zero-shot biomedical classification using BioTranslator.** *Nature communications*  
Xu, H., Woicik, A., Poon, H., Altman, R. B., Wang, S.  
2023; 14 (1): 738
- **Mapping transcriptional heterogeneity and metabolic networks in fatty livers at single-cell resolution.** *iScience*  
Coassolo, L., Liu, T., Jung, Y., Taylor, N. P., Zhao, M., Charville, G. W., Nissen, S. B., Yki-Jarvinen, H., Altman, R. B., Svensson, K. J.  
2023; 26 (1): 105802
- **Genetic association studies using disease liabilities from deep neural networks.** *medRxiv : the preprint server for health sciences*  
Yang, L., Sadler, M. C., Altman, R. B.  
2023
- **Promises and challenges in pharmacoepigenetics.** *Cambridge prisms, Precision medicine*  
Smith, D. A., Sadler, M. C., Altman, R. B.  
2023; 1: e18
- **Detecting Contradictory COVID-19 Drug Efficacy Claims from Biomedical Literature**  
Sosa, D. N., Suresh, M., Potts, C., Altman, R. B.  
edited by Boyd-Graber, J., Okazaki, N., Rogers, A.

ASSOC COMPUTATIONAL LINGUISTICS-ACL.2023: 694-713

- **Gene set proximity analysis: expanding gene set enrichment analysis through learned geometric embeddings, with drug-repurposing applications in COVID-19.** *Bioinformatics (Oxford, England)*  
Cousins, H., Hall, T., Guo, Y., Tso, L., Tzeng, K. T., Cong, L., Altman, R. B.  
2022
- **Functional genomics of OCTN2 variants informs protein-specific variant effect predictor for Carnitine Transporter Deficiency.** *Proceedings of the National Academy of Sciences of the United States of America*  
Koleske, M. L., McInnes, G., Brown, J. E., Thomas, N., Hutchinson, K., Chin, M. Y., Koehl, A., Arkin, M. R., Schlessinger, A., Gallagher, R. C., Song, Y. S., Altman, R. B., Giacomini, et al  
2022; 119 (46): e2210247119
- **A cis-regulatory lexicon of DNA motif combinations mediating cell-type-specific gene regulation.** *Cell genomics*  
Donohue, L. K., Guo, M. G., Zhao, Y., Jung, N., Bussat, R. T., Kim, D. S., Neela, P. H., Kellman, L. N., Garcia, O. S., Meyers, R. M., Altman, R. B., Khavari, P. A.  
2022; 2 (11)
- **A network paradigm predicts drug synergistic effects using downstream protein-protein interactions.** *CPT: pharmacometrics & systems pharmacology*  
Wilson, J. L., Steinberg, E., Racz, R., Altman, R. B., Shah, N., Grimes, K.  
2022
- **Contexts and contradictions: a roadmap for computational drug repurposing with knowledge inference.** *Briefings in bioinformatics*  
Sosa, D. N., Altman, R. B.  
2022
- **Genetic Correlations between Corneal Biophysical Parameters and Anthropomorphic Traits**  
Cousins, H., Cousins, C., Valluru, G., Liu, Y., Ahmad, S., Altman, R. B., Pasquale, L. R.  
ASSOC RESEARCH VISION OPHTHALMOLOGY INC.2022
- **Protein sequence design with a learned potential.** *Nature communications*  
Anand, N., Eguchi, R., Mathews, I. I., Perez, C. P., Derry, A., Altman, R. B., Huang, P.  
2022; 13 (1): 746
- **Training data composition affects performance of protein structure analysis algorithms.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Derry, A., Carpenter, K. A., Altman, R. B.  
2022; 27: 10-21
- **Recommendations for achieving interoperable and shareable medical data in the USA.** *Communications medicine*  
Szarfman, A., Levine, J. G., Tønning, J. M., Weichold, F., Bloom, J. C., Soreth, J. M., Geanacopoulos, M., Callahan, L., Spotnitz, M., Ryan, Q., Pease-Fye, M., Brownstein, J. S., Ed Hammond, et al  
2022; 2: 86
- **Challenges and opportunities in network-based solutions for biological questions.** *Briefings in bioinformatics*  
Guo, M. G., Sosa, D. N., Altman, R. B.  
2021
- **PhenClust, a standalone tool for identifying trends within sets of biological phenotypes using semantic similarity and the Unified Medical Language System metathesaurus.** *JAMIA open*  
Wilson, J. L., Wong, M., Stepanov, N., Petkovic, D., Altman, R.  
2021; 4 (3): oaab079
- **Genome-wide Association Studies in Pharmacogenomics.** *Clinical pharmacology and therapeutics*  
McInnes, G., Yee, S. W., Pershad, Y., Altman, R. B.  
2021
- **Distinct clinical phenotypes for Crohn's disease derived from patient surveys.** *BMC gastroenterology*  
Liu, T., Han, L., Tilley, M., Afzelius, L., Maciejewski, M., Jelinsky, S., Tian, C., McIntyre, M., 23andMe Research Team, Bing, N., Hung, K., Altman, R. B., Agee, M., et al

2021; 21 (1): 160

- **Opportunities and challenges for the computational interpretation of rare variation in clinically important genes.** *American journal of human genetics*  
McInnes, G., Sharo, A. G., Koleske, M. L., Brown, J. E., Norstad, M., Adhikari, A. N., Wang, S., Brenner, S. E., Halpern, J., Koenig, B. A., Magnus, D. C., Gallagher, R. C., Giacomini, et al  
2021; 108 (4): 535–48
- **Large-scale labeling and assessment of sex bias in publicly available expression data.** *BMC bioinformatics*  
Flynn, E., Chang, A., Altman, R. B.  
2021; 22 (1): 168
- **Search and visualization of gene-drug-disease interactions for pharmacogenomics and precision medicine research using GeneDive.** *Journal of biomedical informatics*  
Wong, M., Previde, P., Cole, J., Thomas, B., Laxmeshwar, N., Mallory, E., Lever, J., Petkovic, D., Altman, R. B., Kulkarni, A.  
2021: 103732
- **Modeling drug response using network-based personalized treatment prediction (NetPTP) with applications to inflammatory bowel disease.** *PLoS computational biology*  
Han, L., Sayyid, Z. N., Altman, R. B.  
2021; 17 (2): e1008631
- **A New Era in Pharmacovigilance: Towards real world data and digital monitoring.** *Clinical pharmacology and therapeutics*  
Lavertu, A., Vora, B., Giacomini, K. M., Altman, R., Rensi, S.  
2021
- **Repurposing Biomedical Informaticians for COVID-19.** *Journal of biomedical informatics*  
Sosa, D. N., Chen, B., Kaushal, A., Lavertu, A., Lever, J., Rensi, S., Altman, R.  
2021: 103673
- **Drug Response Pharmacogenetics for 200,000 UK Biobank Participants**  
McInnes, G., Altman, R. B.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2021: 184-195
- **Pharmacogenetics at Scale: An Analysis of the UK Biobank.** *Clinical pharmacology and therapeutics*  
McInnes, G., Lavertu, A., Sangkuhl, K., Klein, T. E., Whirl-Carrillo, M., Altman, R. B.  
2020
- **Transfer learning enables prediction of CYP2D6 haplotype function.** *PLoS computational biology*  
McInnes, G., Dalton, R., Sangkuhl, K., Whirl-Carrillo, M., Lee, S., Tsao, P. S., Gaedigk, A., Altman, R. B., Woodahl, E. L.  
2020; 16 (11): e1008399
- **OrderRex clinical user testing: a randomized trial of recommender system decision support on simulated cases.** *Journal of the American Medical Informatics Association : JAMIA*  
Kumar, A., Aikens, R. C., Hom, J., Shieh, L., Chiang, J., Morales, D., Saini, D., Musen, M., Baiocchi, M., Altman, R., Goldstein, M. K., Asch, S., Chen, et al  
2020
- **MARS: discovering novel cell types across heterogeneous single-cell experiments.** *Nature methods*  
Brbic, M., Zitnik, M., Wang, S., Pisco, A. O., Altman, R. B., Darmanis, S., Leskovec, J.  
2020
- **PharmGKB tutorial for pharmacogenomics of drugs potentially used in the context of COVID-19.** *Clinical pharmacology and therapeutics*  
Huddart, R., Whirl-Carrillo, M., Altman, R. B., Klein, T. E.  
2020
- **Sex-specific genetic effects across biomarkers.** *European journal of human genetics : EJHG*  
Flynn, E., Tanigawa, Y., Rodriguez, F., Altman, R. B., Sinnott-Armstrong, N., Rivas, M. A.  
2020

- **Scientific considerations for global drug development.** *Science translational medicine*  
Wilson, J. L., Cheung, K. W., Lin, L., Green, E. A., Porras, A. I., Zou, L., Mukanga, D., Akpa, P. A., Darko, D. M., Yuan, R., Ding, S., Johnson, W. C., Lee, et al  
2020; 12 (554)
- **Gaussian embedding for large-scale gene set analysis** *NATURE MACHINE INTELLIGENCE*  
Wang, S., Flynn, E. R., Altman, R. B.  
2020; 2 (7): 387–95
- **Gaussian Embedding for Large-scale Gene Set Analysis.** *Nature machine intelligence*  
Wang, S., Flynn, E. R., Altman, R. B.  
2020; 2 (7): 387-395
- **Homology modeling of TMPRSS2 yields candidate drugs that may inhibit entry of SARS-CoV-2 into human cells.** *ChemRxiv : the preprint server for chemistry*  
Rensi, S., Keys, A., Lo, Y. C., Derry, A., McInnes, G., Liu, T., Altman, R.  
2020
- **PharmGKB summary: lamotrigine pathway, pharmacokinetics and pharmacodynamics.** *Pharmacogenetics and genomics*  
Mitra-Ghosh, T., Callisto, S. P., Lamba, J. K., Rimmel, R. P., Birnbaum, A. K., Barbarino, J. M., Klein, T. E., Altman, R. B.  
2020
- **Pathway and network embedding methods for prioritizing psychiatric drugs.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Pershad, Y. n., Guo, M. n., Altman, R. B.  
2020; 25: 671–82
- **Pathway and network embedding methods for prioritizing psychiatric drugs**  
Pershad, Y., Guo, M., Altman, R. B.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2020: 671-682
- **A Literature-Based Knowledge Graph Embedding Method for Identifying Drug Repurposing Opportunities in Rare Diseases**  
Sosa, D. N., Derry, A., Guo, M., Wei, E., Brinton, C., Altman, R. B.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2020: 463-474
- **PGxMine: Text mining for curation of PharmGKB**  
Lever, J., Barbarino, J. M., Gong, L., Huddart, R., Sangkuhl, K., Whaley, R., Whirl-Carrillo, M., Woon, M., Klein, T. E., Altman, R. B.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2020: 611-622
- **Variant Interpretation in Current Pharmacogenetic Testing.** *Journal of personalized medicine*  
Luvsantseren, S. n., Whirl-Carrillo, M. n., Sangkuhl, K. n., Shin, N. n., Wen, A. n., Empey, P. n., Alam, B. n., David, S. n., Dunnenberger, H. M., Orlando, L. n., Altman, R. n., Palaniappan, L. n.  
2020; 10 (4)
- **Geographic Distribution of US Cohorts Used to Train Deep Learning Algorithms.** *JAMA*  
Kaushal, A. n., Altman, R. n., Langlotz, C. n.  
2020; 324 (12): 1212–13
- **Extending TextAE for annotation of non-contiguous entities.** *Genomics & informatics*  
Lever, J. n., Altman, R. n., Kim, J. D.  
2020; 18 (2): e15
- **Genome-wide association study of platelet reactivity and cardiovascular response in patients treated with clopidogrel: a study by the International Clopidogrel Pharmacogenomics Consortium (ICPC).** *Clinical pharmacology and therapeutics*  
Verma, S. S., Bergmeijer, T. O., Gong, L. n., Reny, J. L., Lewis, J. P., Mitchell, B. D., Alexopoulos, D. n., Aradi, D. n., Altman, R. B., Bliden, K. n., Bradford, Y. n., Campo, G. n., Chang, et al  
2020

- **Extracting chemical reactions from text using Snorkel.** *BMC bioinformatics*  
Mallory, E. K., de Rochemonteix, M. n., Ratner, A. n., Acharya, A. n., Re, C. n., Bright, R. A., Altman, R. B.  
2020; 21 (1): 217
- **Classifying non-small cell lung cancer types and transcriptomic subtypes using convolutional neural networks.** *Journal of the American Medical Informatics Association : JAMIA*  
Yu, K. H., Wang, F. n., Berry, G. J., Ré, C. n., Altman, R. B., Snyder, M. n., Kohane, I. S.  
2020; 27 (5): 757–69
- **Pharmacogenomics in Asian subpopulations and impacts on commonly prescribed medications.** *Clinical and translational science*  
Lo, C. n., Nguyen, S. n., Yang, C. n., Witt, L. n., Wen, A. n., Liao, T. V., Nguyen, J. n., Lin, B. n., Altman, R. B., Palaniappan, L. n.  
2020
- **A Literature-Based Knowledge Graph Embedding Method for Identifying Drug Repurposing Opportunities in Rare Diseases.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Sosa, D. N., Derry, A. n., Guo, M. n., Wei, E. n., Brinton, C. n., Altman, R. B.  
2020; 25: 463–74
- **PGxMine: Text mining for curation of PharmGKB.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Lever, J. n., Barbarino, J. M., Gong, L. n., Huddart, R. n., Sangkuhl, K. n., Whaley, R. n., Whirl-Carrillo, M. n., Woon, M. n., Klein, T. E., Altman, R. B.  
2020; 25: 611–22
- **Wiring Minds Successfully applying AI to biomedicine requires innovators trained in contrasting cultures** *NATURE*  
Kaushal, A., Altman, R. B.  
2019; 576 (7787): S62–S63
- **PharmGKB summary: very important pharmacogene information for CACNA1S.** *Pharmacogenetics and genomics*  
Sangkuhl, K., Dirksen, R. T., Alvarellos, M. L., Altman, R. B., Klein, T. E.  
2019
- **PharmGKB summary: sertraline pathway, pharmacokinetics.** *Pharmacogenetics and genomics*  
Huddart, R., Hicks, J. K., Ramsey, L. B., Strawn, J. R., Smith, D. M., Bobonis Babilonia, M., Altman, R. B., Klein, T. E.  
2019
- **Maria-I: A Deep-Learning Approach for Accurate Prediction of MHC Class I Tumor Neoantigen Presentation**  
Kathuria, K. R., Chen, B., Khodadoust, M. S., Olsson, N., Davis, M. M., Elias, J. E., Levy, R., Altman, R. B., Alizadeh, A. A.  
AMER SOC HEMATOLOGY.2019
- **Retro-2 protects cells from ricin toxicity by inhibiting ASNA1-mediated ER targeting and insertion of tail-anchored proteins.** *eLife*  
Morgens, D. W., Chan, C., Kane, A. J., Weir, N. R., Li, A., Dubreuil, M. M., Tsui, C. K., Hess, G. T., Lavertu, A., Han, K., Polyakov, N., Zhou, J., Handy, et al  
2019; 8
- **Successfully applying AI to biomedicine requires innovators trained in contrasting cultures** *NATURE*  
Kaushal, A., Altman, R. B.  
2019; 574 (7779): S62–S63
- **Atrial Fibrillation Burden Signature and Near-Term Prediction of Stroke: A Machine Learning Analysis.** *Circulation. Cardiovascular quality and outcomes*  
Han, L., Askari, M., Altman, R. B., Schmitt, S. K., Fan, J., Bentley, J. P., Narayan, S. M., Turakhia, M. P.  
2019; 12 (10): e005595
- **Pharmacogenomic Polygenic Response Score Predicts Ischemic Events and Cardiovascular Mortality in Clopidogrel-Treated Patients.** *European heart journal. Cardiovascular pharmacotherapy*  
Lewis, J. P., Backman, J. D., Reny, J., Bergmeijer, T. O., Mitchell, B. D., Ritchie, M. D., Dery, J., Pakyz, R. E., Gong, L., Ryan, K., Kim, E., Aradi, D., Fernandez-Cadenas, et al  
2019
- **PharmGKB summary: methylphenidate pathway, pharmacokinetics/pharmacodynamics** *PHARMACOGENETICS AND GENOMICS*  
Stevens, T., Sangkuhl, K., Brown, J. T., Altman, R. B., Klein, T. E.

2019; 29 (6): 136–54

- **Pharmacogenomics Clinical Annotation Tool (PharmCAT).** *Clinical pharmacology and therapeutics*  
Sangkuhl, K., Whirl-Carrillo, M., Whaley, R. M., Woon, M., Lavertu, A., Altman, R. B., Carter, L., Verma, A., Ritchie, M. D., Klein, T. E.  
2019
- **PharmGKB summary: Ondansetron and tropisetron pathways, pharmacokinetics and pharmacodynamics** *PHARMACOGENETICS AND GENOMICS*  
Huddart, R., Altman, R. B., Klein, T. E.  
2019; 29 (4): 91–97
- **Effect of CYP4F2, VKORC1, and CYP2C9 in Influencing Coumarin Dose: A Single-Patient Data Meta-Analysis in More Than 15,000 Individuals** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Danese, E., Raimondi, S., Montagnana, M., Tagetti, A., Langae, T., Borgiani, P., Ciccacci, C., Carcas, A. J., Borobia, A. M., Tong, H. Y., Davila-Fajardo, C., Botton, M., Bourgeois, et al  
2019; 105 (6): 1477–91
- **Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges.** *Human mutation*  
McInnes, G., Daneshjou, R., Katsonis, P., Lichtarge, O., Srinivasan, R. G., Rana, S., Radivojac, P., Mooney, S. D., Pagel, K. A., Stamboulian, M., Jiang, Y., Capriotti, E., Wang, et al  
2019
- **Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Huddart, R., Fohner, A. E., Whirl-Carrillo, M., Wojcik, G. L., Gignoux, C. R., Popejoy, A. B., Bustamante, C. D., Altman, R. B., Klein, T. E.  
2019; 105 (5): 1256–62
- **PharmGKB summary: methylphenidate pathway, pharmacokinetics/pharmacodynamics.** *Pharmacogenetics and genomics*  
Stevens, T., Sangkuhl, K., Brown, J. T., Altman, R. B., Klein, T. E.  
2019
- **Research Projects Supported by the University of California, San Francisco-Stanford Center of Excellence in Regulatory Science and Innovation** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Giacomini, K. M., Lin, L., Altman, R. B.  
2019; 105 (4): 815–18
- **Pocket similarity identifies selective estrogen receptor modulators as microtubule modulators at the taxane site** *NATURE COMMUNICATIONS*  
Lo, Y., Cormier, O., Liu, T., Nettles, K. W., Katzenellenbogen, J. A., Stearns, T., Altman, R. B.  
2019; 10
- **Pharmacogenomics in dermatology: tools for understanding gene-drug associations.** *Seminars in cutaneous medicine and surgery*  
Daneshjou, R., Huddart, R., Klein, T. E., Altman, R. B.  
2019; 38 (1): E19–E24
- **Research Projects Supported by the University of California, San Francisco-Stanford Center of Excellence in Regulatory Science and Innovation.** *Clinical pharmacology and therapeutics*  
Giacomini, K. M., Lin, L., Altman, R. B.  
2019
- **PharmGKB summary: Ondansetron and tropisetron pathways, pharmacokinetics and pharmacodynamics.** *Pharmacogenetics and genomics*  
Huddart, R., Altman, R. B., Klein, T. E.  
2019
- **Computational analysis of kinase inhibitor selectivity using structural knowledge** *BIOINFORMATICS*  
Lo, Y., Liu, T., Morrissey, K. M., Kakiuchi-Kiyota, S., Johnson, A. R., Broccatelli, F., Zhong, Y., Joshi, A., Altman, R. B.  
2019; 35 (2): 235–42
- **The association of obesity and coronary artery disease genes with response to SSRIs treatment in major depression.** *Journal of neural transmission (Vienna, Austria : 1996)*

- Amare, A. T., Schubert, K. O., Tekola-Ayele, F., Hsu, Y., Sangkuhl, K., Jenkins, G., Whaley, R. M., Barman, P., Batzler, A., Altman, R. B., Arolt, V., Brockmoller, J., Chen, et al  
2019
- **PathFXweb: a web application for identifying drug safety and efficacy phenotypes.** *Bioinformatics (Oxford, England)*  
Wilson, J. L., Wong, M. n., Chalke, A. n., Stepanov, N. n., Petkovic, D. n., Altman, R. B.  
2019
  - **GRep: Gene Set Representation via Gaussian Embedding**  
Wang, S., Flynn, E., Altman, R. B.  
edited by Cowen, L. J.  
SPRINGER INTERNATIONAL PUBLISHING AG.2019: 318-319
  - **A deep learning framework to predict binding preference of RNA constituents on protein surface.** *Nature communications*  
Lam, J. H., Li, Y. n., Zhu, L. n., Umarov, R. n., Jiang, H. n., Héliou, A. n., Sheong, F. K., Liu, T. n., Long, Y. n., Li, Y. n., Fang, L. n., Altman, R. B., Chen, et al  
2019; 10 (1): 4941
  - **Predicting HLA class II antigen presentation through integrated deep learning.** *Nature biotechnology*  
Chen, B. n., Khodadoust, M. S., Olsson, N. n., Wagar, L. E., Fast, E. n., Liu, C. L., Muftuoglu, Y. n., Sworder, B. J., Diehn, M. n., Levy, R. n., Davis, M. M., Elias, J. E., Altman, et al  
2019
  - **Examining the Use of Real-World Evidence in the Regulatory Process.** *Clinical pharmacology and therapeutics*  
Beaulieu-Jones, B. K., Finlayson, S. n., Yuan, W. n., Altman, R. B., Kohane, I. S., Prasad, V. n., Yu, K. H.  
2019
  - **#Science: The potential and the challenges of utilizing social media and other electronic communication platforms in health care.** *Clinical and translational science*  
Gijzen, V. n., Maddux, M. n., Lavertu, A. n., Gonzalez-Hernandez, G. n., Ram, N. n., Reeves, B. n., Robinson, T. n., Ziesenitz, V. n., Shakhnovich, V. n., Altman, R. n.  
2019
  - **Essential Characteristics of Pharmacogenomics Study Publications** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Thorn, C. F., Whirl-Carrillo, M., Hachad, H., Johnson, J. A., McDonagh, E. M., Ratain, M. J., Relling, M. V., Scott, S. A., Altman, R. B., Klein, T. E.  
2019; 105 (1): 86–91
  - **The association of obesity and coronary artery disease genes with response to SSRIs treatment in major depression** *JOURNAL OF NEURAL TRANSMISSION*  
Amare, A. T., Schubert, K., Tekola-Ayele, F., Hsu, Y., Sangkuhl, K., Jenkins, G., Whaley, R. M., Barman, P., Batzler, A., Altman, R. B., Arolt, V., Brockmoeller, J., Chen, et al  
2019; 126 (1): 35–45
  - **The effect of CYP4F2, VKORC1 and CYP2C9 in influencing coumarin dose. A single patient data meta-analysis in more than 15,000 individuals.** *Clinical pharmacology and therapeutics*  
Danese, E., Raimondi, S., Montagnana, M., Tagetti, A., Langae, T., Borgiani, P., Ciccacci, C., Carcas, A. J., Borobia, A. M., Tong, H. Y., Davila-Fajardo, C., Botton, M. R., Bourgeois, et al  
2018
  - **Standardized biogeographic grouping system for annotating populations in pharmacogenetic research.** *Clinical pharmacology and therapeutics*  
Huddart, R., Fohner, A. E., Whirl-Carrillo, M., Wojcik, G. L., Gignoux, C. R., Popejoy, A. B., Bustamante, C. D., Altman, R. B., Klein, T. E.  
2018
  - **PathFX provides mechanistic insights into drug efficacy and safety for regulatory review and therapeutic development** *PLOS COMPUTATIONAL BIOLOGY*  
Wilson, J. L., Racz, R., Liu, T., Adeniyi, O., Sun, J., Ramamoorthy, A., Pacanowski, M., Altman, R.  
2018; 14 (12)
  - **PathFX provides mechanistic insights into drug efficacy and safety for regulatory review and therapeutic development.** *PLoS computational biology*  
Wilson, J. L., Racz, R., Liu, T., Adeniyi, O., Sun, J., Ramamoorthy, A., Pacanowski, M., Altman, R.

2018; 14 (12): e1006614

- **Essential characteristics of pharmacogenomics study publications.** *Clinical pharmacology and therapeutics*  
Thorn, C. F., Whirl-Carrillo, M., Hachad, H., Johnson, J. A., McDonagh, E. M., Ratain, M. J., Relling, M. V., Scott, S. A., Altman, R. B., Klein, T. E.  
2018
- **The Pioglitazone Trek via Human PPAR Gamma: From Discovery to a Medicine at the FDA and Beyond** *FRONTIERS IN PHARMACOLOGY*  
Devchand, P. R., Liu, T., Altman, R. B., FitzGerald, G. A., Schadt, E. E.  
2018; 9
- **The Pioglitazone Trek via Human PPAR Gamma: From Discovery to a Medicine at the FDA and Beyond.** *Frontiers in pharmacology*  
Devchand, P. R., Liu, T., Altman, R. B., FitzGerald, G. A., Schadt, E. E.  
2018; 9: 1093
- **PharmGKB summary: oxycodone pathway, pharmacokinetics** *PHARMACOGENETICS AND GENOMICS*  
Huddart, R., Clarke, M., Altman, R. B., Klein, T. E.  
2018; 28 (10): 230–37
- **Data-driven human transcriptomic modules determined by independent component analysis.** *BMC bioinformatics*  
Zhou, W., Altman, R. B.  
2018; 19 (1): 327
- **Data-driven human transcriptomic module determined by independent component analysis** *BMC BIOINFORMATICS*  
Zhou, W., Altman, R. B.  
2018; 19
- **PharmGKB summary: clozapine pathway, pharmacokinetics** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Mueller, D. J., Altman, R. B., Klein, T. E.  
2018; 28 (9): 214–22
- **Machine learning in chemoinformatics and drug discovery** *DRUG DISCOVERY TODAY*  
Lo, Y., Rensi, S. E., Torng, W., Altman, R. B.  
2018; 23 (8): 1538–46
- **Computational Analysis of Kinase Inhibitor Selectivity using Structural Knowledge.** *Bioinformatics (Oxford, England)*  
Lo, Y., Liu, T., Morrissey, K. M., Kakiuchi-Kiyota, S., Johnson, A. R., Broccatelli, F., Zhong, Y., Joshi, A., Altman, R. B.  
2018
- **PharmGKB: A worldwide resource for pharmacogenomic information** *WILEY INTERDISCIPLINARY REVIEWS-SYSTEMS BIOLOGY AND MEDICINE*  
Barbarino, J. M., Whirl-Carrillo, M., Altman, R. B., Klein, T. E.  
2018; 10 (4)
- **Machine learning in chemoinformatics and drug discovery.** *Drug discovery today*  
Lo, Y., Rensi, S. E., Torng, W., Altman, R. B.  
2018
- **Pharmacogenomics and big genomic data: from lab to clinic and back again.** *Human molecular genetics*  
Lavertu, A., McInnes, G., Daneshjou, R., Whirl-Carrillo, M., Klein, T. E., Altman, R. B.  
2018; 27 (R1): R72–R78
- **Pharmacogenomics and big genomic data: from lab to clinic and back again** *HUMAN MOLECULAR GENETICS*  
Lavertu, A., McInnes, G., Daneshjou, R., Whirl-Carrillo, M., Klein, T. E., Altman, R. B.  
2018; 27 (R1): R72–R78
- **PharmGKB summary: atazanavir pathway, pharmacokinetics/pharmacodynamics** *PHARMACOGENETICS AND GENOMICS*  
Alvarellos, M., Guillemette, C., Altman, R. B., Klein, T. E.  
2018; 28 (5): 127–37
- **PharmGKB summary: clobazam pathway, pharmacokinetics** *PHARMACOGENETICS AND GENOMICS*  
Huddart, R., Leeder, J., Altman, R. B., Klein, T. E.

2018; 28 (4): 110–15

- **Genome-wide and candidate gene approaches of clopidogrel efficacy using pharmacodynamic and clinical end points-Rationale and design of the International Clopidogrel Pharmacogenomics Consortium (ICPC)** *AMERICAN HEART JOURNAL*  
Bergmeijer, T. O., Reny, J., Pakyz, R. E., Gong, L., Lewis, J. P., Kim, E., Aradi, D., Fernandez-Cadenas, I., Horenstein, R. B., Lee, M., Whaley, R. M., Montaner, J., Franco Gensini, et al  
2018; 198: 152–59
- **A probabilistic pathway score (PROPS) for classification with applications to inflammatory bowel disease** *BIOINFORMATICS*  
Han, L., Maciejewski, M., Brockel, C., Gordon, W., Snapper, S. B., Korzenik, J. R., Afzelius, L., Altman, R. B.  
2018; 34 (6): 985–93
- **Association of the Polygenic Scores for Personality Traits and Response to Selective Serotonin Reuptake Inhibitors in Patients with Major Depressive Disorder** *FRONTIERS IN PSYCHIATRY*  
Amare, A. T., Schubert, K., Tekola-Ayele, F., Hsu, Y., Sangkuhl, K., Jenkins, G., Whaley, R. M., Barman, P., Batzler, A., Altman, R. B., Arolt, V., Brockmoeller, J., Chen, et al  
2018; 9: 65
- **Biological and functional relevance of CASP predictions** *PROTEINS-STRUCTURE FUNCTION AND BIOINFORMATICS*  
Liu, T., Ish-Shalom, S., Torng, W., Lafita, A., Bock, C., Mort, M., Cooper, D. N., Bliven, S., Capitani, G., Mooney, S. D., Altman, R. B.  
2018; 86: 374–86
- **Mendelian Disease Associations Reveal Novel Insights into Inflammatory Bowel Disease** *INFLAMMATORY BOWEL DISEASES*  
Han, L., Maciejewski, M., Brockel, C., Afzelius, L., Altman, R. B.  
2018; 24 (3): 471–81
- **Application of a Dynamic Map for Learning, Communicating, Navigating, and Improving Therapeutic Development** *CTS-CLINICAL AND TRANSLATIONAL SCIENCE*  
Wagner, J. A., Dahlem, A. M., Hudson, L. D., Terry, S. F., Altman, R. B., Gilliland, C., DeFeo, C., Austin, C. P.  
2018; 11 (2): 166–74
- **Reversals and limitations on high-intensity, life-sustaining treatments** *PLOS ONE*  
Chavez, G., Richman, I. B., Kaimal, R., Bentley, J., Yasukawa, L., Altman, R. B., Periyakoil, V. S., Chen, J. H.  
2018; 13 (2): e0190569
- **A global network of biomedical relationships derived from text.** *Bioinformatics (Oxford, England)*  
Percha, B., Altman, R. B.  
2018
- **PharmGKB: A worldwide resource for pharmacogenomic information.** *Wiley interdisciplinary reviews. Systems biology and medicine*  
Barbarino, J. M., Whirl-Carrillo, M., Altman, R. B., Klein, T. E.  
2018
- **Biomarkers: Delivering on the expectation of molecularly driven, quantitative health** *EXPERIMENTAL BIOLOGY AND MEDICINE*  
Wilson, J. L., Altman, R. B.  
2018; 243 (3): 313–22
- **A dynamic map for learning, communicating, navigating and improving therapeutic development.** *Nature reviews. Drug discovery*  
Wagner, J., Dahlem, A. M., Hudson, L. D., Terry, S. F., Altman, R. B., Gilliland, C. T., DeFeo, C., Austin, C. P.  
2018; 17 (2): 150
- **A dynamic map for learning, communicating, navigating and improving therapeutic development** *NATURE REVIEWS DRUG DISCOVERY*  
Wagner, J., Dahlem, A. M., Hudson, L. D., Terry, S. F., Altman, R. B., Gilliland, C., DeFeo, C., Austin, C. P.  
2018; 17 (2): 151–53
- **Challenges for Training Translational Researchers in the Era of Ubiquitous Data** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Altman, R. B.  
2018; 103 (2): 171–73
- **Systematic target function annotation of human transcription factors** *BMC BIOLOGY*  
Li, Y., Altman, R. B.

2018; 16: 4

- **Expanding a radiology lexicon using contextual patterns in radiology reports.** *Journal of the American Medical Informatics Association : JAMIA*  
Percha, B. n., Zhang, Y. n., Bozkurt, S. n., Rubin, D. n., Altman, R. B., Langlotz, C. P.  
2018
- **Chemical reaction vector embeddings: towards predicting drug metabolism in the human gut microbiome**  
Mallory, E. K., Acharya, A., Rensi, S. E., Turnbaugh, P. J., Bright, R. A., Altman, R. B.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2018: 56–67
- **GeneDive: A gene interaction search and visualization tool to facilitate precision medicine**  
Previde, P., Thomas, B., Wong, M., Mallory, E. K., Petkovic, D., Altman, R. B., Kulkarni, A.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2018: 590–601
- **Improving the explainability of Random Forest classifier - user centered approach**  
Petkovic, D., Altman, R., Wong, M., Vigil, A.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2018: 204–15
- **A E2F4/p107 complex regulates LDHA in the mechanism of chemotherapy resistance in human colorectal cancer stem cells**  
Matsubara, J., Li, Y. F., Dalerba, P., Sahoo, D., Altman, R. B., Clarke, M. F.  
WILEY.2018: 426
- **Chemical reaction vector embeddings: towards predicting drug metabolism in the human gut microbiome.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Mallory, E. K., Acharya, A., Rensi, S. E., Turnbaugh, P. J., Bright, R. A., Altman, R. B.  
2018; 23: 56–67
- **Association of Omics Features with Histopathology Patterns in Lung Adenocarcinoma** *CELL SYSTEMS*  
Yu, K., Berry, G. J., Rubin, D. L., Re, C., Altman, R. B., Snyder, M.  
2017; 5 (6): 620-+
- **Pharmacogenomics-Based Point-of-Care Clinical Decision Support Significantly Alters Drug Prescribing** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
O'Donnell, P. H., Wadhwa, N., Danahey, K., Borden, B. A., Lee, S. M., Hall, J. P., Klammer, C., Hussain, S., Siegler, M., Sorrentino, M. J., Davis, A. M., Sacro, Y. A., Nanda, et al  
2017; 102 (5): 859–69
- **PharmGKB summary: very important pharmacogene information for ABCG2** *PHARMACOGENETICS AND GENOMICS*  
Fohner, A. E., Brackman, D. J., Giacomini, K. M., Altman, R. B., Klein, T. E.  
2017; 27 (11): 420–27
- **Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges** *HUMAN MUTATION*  
Daneshjou, R., Wang, Y., Bromberg, Y., Bovo, S., Martelli, P. L., Babbi, G., Di Lena, P., Casadio, R., Edwards, M., Gifford, D., Jones, D. T., Sundaram, L., Bhat, et al  
2017; 38 (9): 1182–92
- **PharmGKB summary: pazopanib pathway, pharmacokinetics** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Sharma, M. R., Altman, R. B., Klein, T. E.  
2017; 27 (8): 307–12
- **Shallow Representation Learning via Kernel PCA Improves QSAR Modelability** *JOURNAL OF CHEMICAL INFORMATION AND MODELING*  
Rensi, S. E., Altman, R. B.  
2017; 57 (8): 1859–67
- **3D deep convolutional neural networks for amino acid environment similarity analysis** *BMC BIOINFORMATICS*  
Torg, W., Altman, R. B.

2017; 18: 302

- **PharmGKB summary: sorafenib pathways** *PHARMACOGENETICS AND GENOMICS*  
Gong, L., Giacomini, M. M., Giacomini, C., Maitland, M. L., Altman, R. B., Klein, T. E.  
2017; 27 (6): 240-246
- **Decaying relevance of clinical data towards future decisions in data-driven inpatient clinical order sets.** *International journal of medical informatics*  
Chen, J. H., Alagappan, M., Goldstein, M. K., Asch, S. M., Altman, R. B.  
2017; 102: 71-79
- **PharmGKB summary: voriconazole pathway, pharmacokinetics** *PHARMACOGENETICS AND GENOMICS*  
Barbarino, J. M., Obeng, A. O., Klein, T. E., Altman, R. B.  
2017; 27 (5): 201-209
- **Artificial intelligence (AI) systems for interpreting complex medical datasets** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Altman, R. B.  
2017; 101 (5): 585-86
- **Opportunities for developing therapies for rare genetic diseases: focus on gain-of-function and allostery.** *Orphanet journal of rare diseases*  
Chen, B., Altman, R. B.  
2017; 12 (1): 61-?
- **Development of an automated assessment tool for MedWatch reports in the FDA adverse event reporting system.** *Journal of the American Medical Informatics Association*  
Han, L., Ball, R., Pamer, C. A., Altman, R. B., Proestel, S.  
2017
- **Imputing gene expression to maximize platform compatibility** *BIOINFORMATICS*  
Zhou, W., Han, L., Altman, R. B.  
2017; 33 (4): 522-528
- **PharmGKB summary: Macrolide antibiotic pathway, pharmacokinetics/pharmacodynamics.** *Pharmacogenetics and genomics*  
Fohner, A. E., Sparreboom, A., Altman, R. B., Klein, T. E.  
2017
- **"The Pharmacogenomics Research Network Translational Pharmacogenetics Program: Outcomes and Metrics of Pharmacogenetic Implementations Across Diverse Healthcare Systems".** *Clinical pharmacology & therapeutics*  
Luzum, J. A., Pakyz, R. E., Elsey, A. R., Haidar, C. E., Peterson, J. F., Whirl-Carrillo, M., Handelman, S. K., Palmer, K., Pulley, J. M., Beller, M., Schildcrout, J. S., Field, J. R., Weitzel, et al  
2017
- **PharmGKB summary: ivacaftor pathway, pharmacokinetics/pharmacodynamics** *PHARMACOGENETICS AND GENOMICS*  
Fohner, A. E., McDonagh, E. M., Clancy, J. P., Carrillo, M. W., Altman, R. B., Klein, T. E.  
2017; 27 (1): 39-42
- **Cohort-specific imputation of gene expression improves prediction of warfarin dose for African Americans.** *Genome medicine*  
Gottlieb, A. n., Daneshjou, R. n., DeGorter, M. n., Bourgeois, S. n., Svensson, P. J., Wadelius, M. n., Deloukas, P. n., Montgomery, S. B., Altman, R. B.  
2017; 9 (1): 98
- **Flexible Analog Search with Kernel PCA Embedded Molecule Vectors.** *Computational and structural biotechnology journal*  
Rensi, S., Altman, R. B.  
2017; 15: 320-327
- **STAMS: STRING-assisted module search for genome wide association studies and application to autism.** *Bioinformatics*  
Hillenmeyer, S., Davis, L. K., Gamazon, E. R., Cook, E. H., Cox, N. J., Altman, R. B.  
2016; 32 (24): 3815-3822
- **PharmGKB summary: very important pharmacogene information for MT-RNR1.** *Pharmacogenetics and genomics*  
Barbarino, J. M., McGregor, T. L., Altman, R. B., Klein, T. E.

2016; 26 (12): 558-567

- **The International SSRI Pharmacogenomics Consortium (ISPC): a genome-wide association study of antidepressant treatment response.** *Translational psychiatry*  
Biernacka, J. M., Sangkuhl, K., Jenkins, G., WHALEY, R. M., Barman, P., Batzler, A., Altman, R. B., Arolt, V., Brockmüller, J., Chen, C. H., Domschke, K., Hall-Flavin, D. K., Hong, et al  
2016; 6 (11)
- **Exploring the Heritability of Pharmacogene Expression**  
Mitchell, S. L., Gamazon, E. R., Hillenmeyer, S. P., Altman, R. B., Cox, N. J., Davis, L. K.  
WILEY-BLACKWELL.2016: 653
- **Imputing Gene Expression to Maximize Platform Compatibility.** *Bioinformatics*  
Zhou, W., Han, L., Altman, R. B.  
2016
- **Estimation of Maximum Recommended Therapeutic Dose Using Predicted Promiscuity and Potency.** *Clinical and translational science*  
Liu, T., Oprea, T., Ursu, O., Hasselgren, C., Altman, R. B.  
2016
- **Response to Open Peer Commentaries on "Human Germline CRISPR-Cas Modification: Toward a Regulatory Framework".** *American journal of bioethics*  
Evitt, N. H., Mascharak, S., Altman, R. B.  
2016; 16 (10): W1-2
- **Computing disease incidence, prevalence and comorbidity from electronic medical records.** *Journal of biomedical informatics*  
Bagley, S. C., Altman, R. B.  
2016; 63: 108-111
- **Predicting inpatient clinical order patterns with probabilistic topic models vs conventional order sets.** *Journal of the American Medical Informatics Association*  
Chen, J. H., Goldstein, M. K., Asch, S. M., Mackey, L., Altman, R. B.  
2016
- **PharmGKB summary: ivacaftor pathway, pharmacokinetics/pharmacodynamics.** *Pharmacogenetics and genomics*  
Fohner, A. E., McDonagh, E. M., Clancy, J. P., Whirl Carrillo, M., Altman, R. B., Klein, T. E.  
2016: -?
- **PharmGKB summary: isoniazid pathway, pharmacokinetics.** *Pharmacogenetics and genomics*  
Klein, D. J., Boukouvala, S., McDonagh, E. M., Shuldiner, S. R., Laurieri, N., Thorn, C. F., Altman, R. B., Klein, T. E.  
2016; 26 (9): 436-444
- **Population-specific single-nucleotide polymorphism confers increased risk of venous thromboembolism in African Americans.** *Molecular genetics & genomic medicine*  
Daneshjou, R., Cavallari, L. H., Weeke, P. E., Karczewski, K. J., Drozda, K., Perera, M. A., Johnson, J. A., Klein, T. E., Bustamante, C. D., Roden, D. M., Shaffer, C., Denny, J. C., Zehnder, et al  
2016; 4 (5): 513-520
- **Human induced pluripotent stem cell-derived cardiomyocytes recapitulate the predilection of breast cancer patients to doxorubicin-induced cardiotoxicity** *NATURE MEDICINE*  
BurrIDGE, P. W., Li, Y. F., Matsa, E., Wu, H., Ong, S., Sharma, A., Holmstrom, A., Chang, A. C., Coronado, M. J., Ebert, A. D., Knowles, J. W., Telli, M. L., Witteles, et al  
2016; 22 (5): 547-556
- **Constraints on Biological Mechanism from Disease Comorbidity Using Electronic Medical Records and Database of Genetic Variants** *PLOS COMPUTATIONAL BIOLOGY*  
Bagley, S. C., Sirota, M., Chen, R., Butte, A. J., Altman, R. B.  
2016; 12 (4)
- **OrderRex: clinical order decision support and outcome predictions by data-mining electronic medical records.** *Journal of the American Medical Informatics Association*  
Chen, J. H., Podchiyska, T., Altman, R. B.

2016; 23 (2): 339-348

- **PharmGKB summary: very important pharmacogene information for RYR1** *PHARMACOGENETICS AND GENOMICS*  
Alvarellos, M. L., Krauss, R. M., Wilke, R. A., Altman, R. B., Klein, T. E.  
2016; 26 (3): 138-144
- **SEPARATING THE CAUSES AND CONSEQUENCES IN DISEASE TRANSCRIPTOME.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Li, Y. F., Xin, F. n., Altman, R. B.  
2016; 21: 381-92
- **Large-scale extraction of gene interactions from full-text literature using DeepDive.** *Bioinformatics (Oxford, England)*  
Mallory, E. K., Zhang, C., Ré, C., Altman, R. B.  
2016; 32 (1): 106-13
- **Current Progress in Bioinformatics 2016** *BRIEFINGS IN BIOINFORMATICS*  
Altman, R.  
2016; 17 (1): 1
- **DYNAMICALLY EVOLVING CLINICAL PRACTICES AND IMPLICATIONS FOR PREDICTING MEDICAL DECISIONS**  
Chen, J. H., Goldstein, M. K., Asch, S. M., Altman, R. B.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2016: 195-206
- **Towards Clinical Bioinformatics: Redux 2015.** *Yearbook of medical informatics*  
Altman, R. B.  
2016: S6-7
- **STAMS: STRING-assisted module search for genome wide association studies and application to autism** *Bioinformatics*  
Hillenmeyer, S. P., Davis, L. K., Gamazon, E. R., Cook, E. H., Cox, N. J., Altman, R. B.  
2016: 3815-22
- **Predicting non-small cell lung cancer prognosis by fully automated microscopic pathology image features.** *Nature communications*  
Yu, K., Zhang, C., Berry, G. J., Altman, R. B., Ré, C., Rubin, D. L., Snyder, M.  
2016; 7: 12474-?
- **DYNAMICALLY EVOLVING CLINICAL PRACTICES AND IMPLICATIONS FOR PREDICTING MEDICAL DECISIONS.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Chen, J. H., Goldstein, M. K., Asch, S. M., Altman, R. B.  
2016; 21: 195-206
- **Large-scale extraction of gene interactions from full-text literature using DeepDive** *BIOINFORMATICS*  
Mallory, E. K., Zhang, C., Re, C., Altman, R. B.  
2016; 32 (1): 106-113
- **Human Germline CRISPR-Cas Modification: Toward a Regulatory Framework.** *American journal of bioethics*  
Evitt, N. H., Mascharak, S., Altman, R. B.  
2015; 15 (12): 25-29
- **PharmGKB summary: succinylcholine pathway, pharmacokinetics/pharmacodynamics** *PHARMACOGENETICS AND GENOMICS*  
Alvarellos, M. L., McDonagh, E. M., Patel, S., McLeod, H. L., Altman, R. B., Klein, T. E.  
2015; 25 (12): 622-630
- **Unmet needs: Research helps regulators do their jobs** *SCIENCE TRANSLATIONAL MEDICINE*  
Altman, R. B., Khuri, N., Salit, M., Giacomini, K. M.  
2015; 7 (315)
- **Informatics: Make sense of health data** *NATURE*  
Elliott, J. H., Grimshaw, J., Altman, R., Bero, L., Goodman, S. N., Henry, D., Macleod, M., Tovey, D., Tugwell, P., White, H., Sim, I.  
2015; 527 (7576): 31-32

- **Personalization in practice** *SCIENCE*  
Iyengar, R., Altman, R. B., Troyanskaya, O., FitzGerald, G. A.  
2015; 350 (6258): 282–83
- **Sequence to Medical Phenotypes: A Framework for Interpretation of Human Whole Genome DNA Sequence Data.** *PLoS genetics*  
Dewey, F. E., Grove, M. E., Priest, J. R., Waggott, D., Batra, P., Miller, C. L., Wheeler, M., Zia, A., Pan, C., Karzcewski, K. J., Miyake, C., Whirl-Carrillo, M., Klein, et al  
2015; 11 (10)
- **Sequence to Medical Phenotypes: A Framework for Interpretation of Human Whole Genome DNA Sequence Data** *PLOS GENETICS*  
Dewey, F. E., Grove, M. E., Priest, J. R., Waggott, D., Batra, P., Miller, C. L., Wheeler, M., Zia, A., Pan, C., Karzcewski, K. J., Miyake, C., Whirl-Carrillo, M., Klein, et al  
2015; 11 (10)
- **PharmGKB summary: peginterferon-alpha pathway** *PHARMACOGENETICS AND GENOMICS*  
Shuldiner, S. R., Gong, L., Muir, A. J., Altman, R. B., Klein, T. E.  
2015; 25 (9): 465-474
- **High Resolution Prediction of Calcium-Binding Sites in 3D Protein Structures Using FEATURE.** *Journal of chemical information and modeling*  
Zhou, W., Tang, G. W., Altman, R. B.  
2015; 55 (8): 1663-1672
- **PharmGKB summary: pathways of acetaminophen metabolism at the therapeutic versus toxic doses** *PHARMACOGENETICS AND GENOMICS*  
Mazaleuskaya, L. L., Sangkuhl, K., Thorn, C. F., FitzGerald, G. A., Altman, R. B., Klein, T. E.  
2015; 25 (8): 416-426
- **PharmGKB summary: pathways of acetaminophen metabolism at the therapeutic versus toxic doses.** *Pharmacogenetics and genomics*  
Mazaleuskaya, L. L., Sangkuhl, K., Thorn, C. F., FitzGerald, G. A., Altman, R. B., Klein, T. E.  
2015; 25 (8): 416-26
- **Assessment of the Radiation Effects of Cardiac CT Angiography Using Protein and Genetic Biomarkers** *JACC-CARDIOVASCULAR IMAGING*  
Nguyen, P. K., Lee, W. H., Li, Y. F., Hong, W. X., Hu, S., Chan, C., Liang, G., Nguyen, I., Ong, S., Churko, J., Wang, J., Altman, R. B., Fleischmann, et al  
2015; 8 (8): 873-884
- **High Resolution Prediction of Calcium-Binding Sites in 3D Protein Structures Using FEATURE** *JOURNAL OF CHEMICAL INFORMATION AND MODELING*  
Zhou, W., Tang, G. W., Altman, R. B.  
2015; 55 (8): 1663-1672
- **An ontology for Autism Spectrum Disorder (ASD) to infer ASD phenotypes from Autism Diagnostic Interview-Revised data** *JOURNAL OF BIOMEDICAL INFORMATICS*  
Mugzach, O., Peleg, M., Bagley, S. C., Guter, S. J., Cook, E. H., Altman, R. B.  
2015; 56: 333-347
- **Potential Adverse Effects of Anesthesia in Children Reply** *JAMA-JOURNAL OF THE AMERICAN MEDICAL ASSOCIATION*  
Psaty, B. M., Platt, R., Altman, R. B.  
2015; 314 (4): 409
- **Relating Essential Proteins to Drug Side-Effects Using Canonical Component Analysis: A Structure-Based Approach.** *Journal of chemical information and modeling*  
Liu, T., Altman, R. B.  
2015; 55 (7): 1483-1494
- **Achieving high-sensitivity for clinical applications using augmented exome sequencing** *GENOME MEDICINE*  
Patwardhan, A., Harris, J., Leng, N., Bartha, G., Church, D. M., Luo, S., Haudenschild, C., Pratt, M., Zook, J., Salit, M., Tirsch, J., Morra, M., Chervitz, et al  
2015; 7

- **PharmGKB summary: Efavirenz pathway, pharmacokinetics** *PHARMACOGENETICS AND GENOMICS*  
McDonagh, E. M., Lau, J. L., Alvarellos, M. L., Altman, R. B., Klein, T. E.  
2015; 25 (7): 363-376
- **Learning the Structure of Biomedical Relationships from Unstructured Text** *PLOS COMPUTATIONAL BIOLOGY*  
Percha, B., Altman, R. B.  
2015; 11 (7)
- **Learning the Structure of Biomedical Relationships from Unstructured Text.** *PLoS computational biology*  
Percha, B., Altman, R. B.  
2015; 11 (7)
- **Evidence for Clinical Implementation of Pharmacogenomics in Cardiac Drugs** *MAYO CLINIC PROCEEDINGS*  
Kaufman, A. L., Spitz, J., Jacobs, M., Sorrentino, M., Yuen, S., Danahey, K., Saner, D., Klein, T. E., Altman, R. B., Ratain, M. J., O'Donnell, P. H.  
2015; 90 (6): 716-729
- **Genomics in the clinic: ethical and policy challenges in clinical next-generation sequencing programs at early adopter USA institutions.** *Personalized medicine*  
Milner, L. C., Garrison, N. A., Cho, M. K., Altman, R. B., Hudgins, L., Galli, S. J., Lowe, H. J., Schrijver, I., Magnus, D. C.  
2015; 12 (3): 269-282
- **Distribute AI benefits fairly** *NATURE*  
Altman, R.  
2015; 521 (7553): 417-18
- **The International SSRI Pharmacogenomics Consortium (ISPC): a genome-wide association study of antidepressant treatment response** *TRANSLATIONAL PSYCHIATRY*  
Biernacka, J. M., Sangkuhl, K., Jenkins, G., WHALEY, R. M., Barman, P., Batzler, A., Altman, R. B., Arolt, V., Brockmoeller, J., Chen, C. H., Domschke, K., Hall-Flavin, D. K., Hong, et al  
2015; 5
- **The International SSRI Pharmacogenomics Consortium (ISPC): a genome-wide association study of antidepressant treatment response.** *Translational psychiatry*  
Biernacka, J. M., Sangkuhl, K., Jenkins, G., Whaley, R. M., Barman, P., Batzler, A., Altman, R. B., Arolt, V., Brockmüller, J., Chen, C. H., Domschke, K., Hall-Flavin, D. K., Hong, et al  
2015; 5: e553
- **Neurotoxicity of Generic Anesthesia Agents in Infants and Children An Orphan Research Question in Search of a Sponsor** *JAMA-JOURNAL OF THE AMERICAN MEDICAL ASSOCIATION*  
Psaty, B. M., Platt, R., Altman, R. B.  
2015; 313 (15): 1515-16
- **PharmGKB summary: very important pharmacogene information for human leukocyte antigen B.** *Pharmacogenetics and genomics*  
Barbarino, J. M., Kroetz, D. L., Klein, T. E., Altman, R. B.  
2015; 25 (4): 205-221
- **PharmGKB summary: very important pharmacogene information for CFTR.** *Pharmacogenetics and genomics*  
McDonagh, E. M., Clancy, J. P., Altman, R. B., Klein, T. E.  
2015; 25 (3): 149-156
- **Variations in the Binding Pocket of an Inhibitor of the Bacterial Division Protein FtsZ across Genotypes and Species** *PLOS COMPUTATIONAL BIOLOGY*  
Miguel, A., Hsin, J., Liu, T., Tang, G., Altman, R. B., Huang, K. C.  
2015; 11 (3)
- **Variations in the binding pocket of an inhibitor of the bacterial division protein FtsZ across genotypes and species.** *PLoS computational biology*  
Miguel, A., Hsin, J., Liu, T., Tang, G., Altman, R. B., Huang, K. C.  
2015; 11 (3)
- **Predicting cancer drug response: advancing the DREAM.** *Cancer discovery*

- Altman, R. B.  
2015; 5 (3): 237-238
- **Enabling the curation of your pharmacogenetic study.** *Clinical pharmacology & therapeutics*  
MCDONAGH, E. M., Whirl-Carrillo, M., Altman, R. B., Klein, T. E.  
2015; 97 (2): 116-119
  - **INTERACTIVE GENOTYPE-BASED DOSING GUIDELINES.**  
Whirl-Carrillo, M., Whaley, R. M., Caudle, K. E., Relling, M. V., Altman, R. B., Klein, T. E.  
WILEY-BLACKWELL.2015: S61
  - **PharmGKB summary: ibuprofen pathways** *PHARMACOGENETICS AND GENOMICS*  
Mazaleuskaya, L. L., Theken, K. N., Gong, L., Thorn, C. F., FitzGerald, G. A., Altman, R. B., Klein, T. E.  
2015; 25 (2): 96-106
  - **Using "big data" to dissect clinical heterogeneity.** *Circulation*  
Altman, R. B., Ashley, E. A.  
2015; 131 (3): 232-233
  - **PharmGKB summary: very important pharmacogene information for CYP4F2** *PHARMACOGENETICS AND GENOMICS*  
Alvarellos, M. L., Sangkuhl, K., Daneshjou, R., Whirl-Carrillo, M., Altman, R. B., Klein, T. E.  
2015; 25 (1): 41-47
  - **A TWENTIETH ANNIVERSARY TRIBUTE TO PSB**  
Hewett, D., Whirl-Carrillo, M., Hunter, L. E., Altman, R. B., Klein, T. E.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2015: 1-7
  - **TRAINING THE NEXT GENERATION OF QUANTITATIVE BIOLOGISTS IN THE ERA OF BIG DATA**  
Pattin, K. A., Greene, A. C., Altman, R. B., Cohen, K. B., Wethington, E., Gorg, C., Hunter, L. E., Muse, S. V., Radivojac, P., Moore, J. H.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2015: 488-92
  - **Data-Mining Electronic Medical Records for Clinical Order Recommendations: Wisdom of the Crowd or Tyranny of the Mob?** *AMIA Joint Summits on Translational Science proceedings AMIA Summit on Translational Science*  
Chen, J. H., Altman, R. B.  
2015; 2015: 435-439
  - **Ranking adverse drug reactions with crowdsourcing.** *Journal of medical Internet research*  
Gottlieb, A., Hoehndorf, R., Dumontier, M., Altman, R. B.  
2015; 17 (3): e80
  - **Achieving high-sensitivity for clinical applications using augmented exome sequencing.** *Genome medicine*  
Patwardhan, A., Harris, J., Leng, N., Bartha, G., Church, D. M., Luo, S., Haudenschild, C., Pratt, M., Zook, J., Salit, M., Tirsch, J., Morra, M., Chervitz, et al  
2015; 7 (1): 71-?
  - **Genomics in the clinic: ethical and policy challenges in clinical next-generation sequencing programs at early adopter USA institutions** *PERSONALIZED MEDICINE*  
Milner, L. C., Garrison, N. A., Cho, M. K., Altman, R. B., Hudgins, L., Galli, S. J., Lowe, H. J., Schrijver, I., Magnus, D. C.  
2015; 12 (3): 269-282
  - **Ranking adverse drug reactions with crowdsourcing.** *Journal of medical Internet research*  
Gottlieb, A., Hoehndorf, R., Dumontier, M., Altman, R. B.  
2015; 17 (3)
  - **A twentieth anniversary tribute to psb.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Hewett, D., Whirl-Carrillo, M., Hunter, L. E., Altman, R. B., Klein, T. E.  
2015; 20: 1-7

- **A community computational challenge to predict the activity of pairs of compounds** *NATURE BIOTECHNOLOGY*  
Bansal, M., Yang, J., Karan, C., Menden, M. P., Costello, J. C., Tang, H., Xiao, G., Li, Y., Allen, J., Zhong, R., Chen, B., Kim, M., Wang, et al  
2014; 32 (12): 1213-+
- **A community effort to assess and improve drug sensitivity prediction algorithms** *NATURE BIOTECHNOLOGY*  
Costello, J. C., Heiser, L. M., Georgii, E., Gonen, M., Menden, M. P., Wang, N. J., Bansal, M., Ammad-ud-din, M., Hintsanen, P., Khan, S. A., Mpindi, J., Kallioniemi, O., Honkela, et al  
2014; 32 (12): 1202-U57
- **PharmGKB summary: gemcitabine pathway** *PHARMACOGENETICS AND GENOMICS*  
Alvarellos, M. L., Lamba, J., Sangkuhl, K., Thorn, C. F., Wang, L., Klein, D. J., Altman, R. B., Klein, T. E.  
2014; 24 (11): 564-574
- **PharmGKB summary: gemcitabine pathway.** *Pharmacogenetics and genomics*  
Alvarellos, M. L., Lamba, J., Sangkuhl, K., Thorn, C. F., Wang, L., Klein, D. J., Altman, R. B., Klein, T. E.  
2014; 24 (11): 564-574
- **Genetic variant in folate homeostasis is associated with lower warfarin dose in African Americans** *BLOOD*  
Daneshjou, R., Gamazon, E. R., Burkley, B., Cavallari, L. H., Johnson, J. A., Klein, T. E., Limdi, N., Hillenmeyer, S., Percha, B., Karczewski, K. J., Langae, T., Patel, S. R., Bustamante, et al  
2014; 124 (14): 2298-2305
- **Genetic variant in folate homeostasis is associated with lower warfarin dose in African Americans.** *Blood*  
Daneshjou, R., Gamazon, E. R., Burkley, B., Cavallari, L. H., Johnson, J. A., Klein, T. E., Limdi, N., Hillenmeyer, S., Percha, B., Karczewski, K. J., Langae, T., Patel, S. R., Bustamante, et al  
2014; 124 (14): 2298-2305
- **PharmGKB summary: uric acid-lowering drugs pathway, pharmacodynamics.** *Pharmacogenetics and genomics*  
McDonagh, E. M., Thorn, C. F., Callaghan, J. T., Altman, R. B., Klein, T. E.  
2014; 24 (9): 464-476
- **PharmGKB summary: very important pharmacogene information for N-acetyltransferase 2.** *Pharmacogenetics and genomics*  
McDonagh, E. M., Boukouvala, S., Aklillu, E., Hein, D. W., Altman, R. B., Klein, T. E.  
2014; 24 (8): 409-425
- **Interpreting the CYP2D6 results from the International Tamoxifen Pharmacogenetics Consortium.** *Clinical pharmacology & therapeutics*  
Province, M. A., Altman, R. B., Klein, T. E.  
2014; 96 (2): 144-146
- **PharmGKB summary: tramadol pathway** *PHARMACOGENETICS AND GENOMICS*  
Gong, L., Stamer, U. M., Tzvetkov, M. V., Altman, R. B., Klein, T. E.  
2014; 24 (7): 374-380
- **Integrating systems biology sources illuminates drug action.** *Clinical pharmacology & therapeutics*  
Gottlieb, A., Altman, R. B.  
2014; 95 (6): 663-669
- **PharmGKB summary: very important pharmacogene information for SLC22A1.** *Pharmacogenetics and genomics*  
Goswami, S., Gong, L., Giacomini, K., Altman, R. B., Klein, T. E.  
2014; 24 (6): 324-328
- **Reconstruction of the Mouse Otocyst and Early Neuroblast Lineage at Single-Cell Resolution** *CELL*  
Durruthy-Durruthy, R., Gottlieb, A., Hartman, B. H., Waldhaus, J., Laske, R. D., Altman, R., Heller, S.  
2014; 157 (4): 964-978
- **PharmGKB summary: abacavir pathway.** *Pharmacogenetics and genomics*  
Barbarino, J. M., Kroetz, D. L., Altman, R. B., Klein, T. E.  
2014; 24 (5): 276-282
- **Genotype-Guided Dosing of Vitamin K Antagonists** *NEW ENGLAND JOURNAL OF MEDICINE*

- Daneshjou, R., Klein, T. E., Altman, R. B.  
2014; 370 (18): 1762–63
- **Genotype-guided dosing of vitamin K antagonists.** *New England journal of medicine*  
Daneshjou, R., Klein, T. E., Altman, R. B.  
2014; 370 (18): 1762-1763
  - **Guidelines for investigating causality of sequence variants in human disease** *NATURE*  
MacArthur, D. G., Manolio, T. A., Dimmock, D. P., Rehm, H. L., Shendure, J., Abecasis, G. R., Adams, D. R., Altman, R. B., Antonarakis, S. E., Ashley, E. A., Barrett, J. C., Biesecker, L. G., Conrad, et al  
2014; 508 (7497): 469-476
  - **Knowledge-based fragment binding prediction.** *PLoS computational biology*  
Tang, G. W., Altman, R. B.  
2014; 10 (4)
  - **Knowledge-based fragment binding prediction.** *PLoS computational biology*  
Tang, G. W., Altman, R. B.  
2014; 10 (4): e1003589
  - **High Precision Prediction of Functional Sites in Protein Structures** *PLOS ONE*  
Buturovic, L., Wong, M., Tang, G. W., Altman, R. B., Petkovic, D.  
2014; 9 (3)
  - **Clinical interpretation and implications of whole-genome sequencing.** *JAMA*  
Dewey, F. E., Grove, M. E., Pan, C., Goldstein, B. A., Bernstein, J. A., Chaib, H., Merker, J. D., Goldfeder, R. L., Enns, G. M., David, S. P., Pakdaman, N., Ormond, K. E., Caleshu, et al  
2014; 311 (10): 1035-1045
  - **Clinical interpretation and implications of whole-genome sequencing.** *JAMA : the journal of the American Medical Association*  
Dewey, F. E., Grove, M. E., Pan, C., Goldstein, B. A., Bernstein, J. A., Chaib, H., Merker, J. D., Goldfeder, R. L., Enns, G. M., David, S. P., Pakdaman, N., Ormond, K. E., Caleshu, et al  
2014; 311 (10): 1035-1045
  - **Environmental and State-Level Regulatory Factors Affect the Incidence of Autism and Intellectual Disability** *PLOS COMPUTATIONAL BIOLOGY*  
Rzhetsky, A., Bagley, S. C., Wang, K., Lyttle, C. S., Cook, E. H., Altman, R. B., Gibbons, R. D.  
2014; 10 (3)
  - **PharmGKB summary: very important pharmacogene information for UGT1A1** *PHARMACOGENETICS AND GENOMICS*  
Barbarino, J. M., Haidar, C. E., Klein, T. E., Altman, R. B.  
2014; 24 (3): 177-183
  - **Coherent functional modules improve transcription factor target identification, cooperativity prediction, and disease association.** *PLoS genetics*  
Karczewski, K. J., Snyder, M., Altman, R. B., Tatonetti, N. P.  
2014; 10 (2)
  - **Coherent functional modules improve transcription factor target identification, cooperativity prediction, and disease association.** *PLoS genetics*  
Karczewski, K. J., Snyder, M., Altman, R. B., Tatonetti, N. P.  
2014; 10 (2)
  - **CYP2D6 Genotype and Adjuvant Tamoxifen: Meta-Analysis of Heterogeneous Study Populations** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Province, M. A., Goetz, M. P., Brauch, H., Flockhart, D. A., Hebert, J. M., Whaley, R., Suman, V. J., Schroth, W., Winter, S., Zembutsu, H., Mushiroda, T., Newman, W. G., Lee, et al  
2014; 95 (2): 216-227
  - **PharmGKB summary: ifosfamide pathways, pharmacokinetics and pharmacodynamics.** *Pharmacogenetics and genomics*  
Lowenberg, D., Thorn, C. F., Desta, Z., Flockhart, D. A., Altman, R. B., Klein, T. E.

2014; 24 (2): 133-138

- **Variation in the Binding Pocket of an Inhibitor of the Bacterial Division Protein FtsZ Across Genotypes, Nucleotide States, and Species**  
Miguel, A. V., Hsin, J., Liu, T., Tang, G., Altman, R. B., Huang, K. C.  
CELL PRESS.2014: 474A-475A
- **Investigating Ligand-Modulation of GPCR Activation Pathways**  
Lawrenz, M., Kohlhoff, K., Shukla, D., Bowman, G., Altman, R., Pande, V.  
CELL PRESS.2014: 14A
- **Path-scan: a reporting tool for identifying clinically actionable variants.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Daneshjou, R., Zappala, Z., Kukurba, K., Boyle, S. M., Ormond, K. E., Klein, T. E., Snyder, M., Bustamante, C. D., Altman, R. B., Montgomery, S. B.  
2014; 19: 229-240
- **PATH-SCAN: A REPORTING TOOL FOR IDENTIFYING CLINICALLY ACTIONABLE VARIANTS**  
Daneshjou, R., Zappala, Z., Kukurba, K., Boyle, S. M., Ormond, K. E., Klein, T. E., Snyder, M., Bustamante, C. D., Altman, R. B., Montgomery, S. B.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2014: 229-40
- **BUILDING THE NEXT GENERATION OF QUANTITATIVE BIOLOGISTS**  
Pattin, K. A., Greene, A. C., Altman, R. B., Hunter, L. E., Ross, D. A., Foster, J. A., Moore, J. H.  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2014: 417-21
- **Identifying Druggable Targets by Protein Microenvironments Matching: Application to Transcription Factors** *CPT-PHARMACOMETRICS & SYSTEMS PHARMACOLOGY*  
Liu, T., Altman, R. B.  
2014; 3 (1)
- **Automated physician order recommendations and outcome predictions by data-mining electronic medical records.** *AMIA Joint Summits on Translational Science proceedings AMIA Summit on Translational Science*  
Chen, J. H., Altman, R. B.  
2014; 2014: 206-210
- **High precision prediction of functional sites in protein structures.** *PloS one*  
Buturovic, L., Wong, M., Tang, G. W., Altman, R. B., Petkovic, D.  
2014; 9 (3)
- **Identifying druggable targets by protein microenvironments matching: application to transcription factors.** *CPT: pharmacometrics & systems pharmacology*  
Liu, T., Altman, R. B.  
2014; 3
- **PharmGKB summary: mycophenolic acid pathway** *PHARMACOGENETICS AND GENOMICS*  
Lamba, V., Sangkuhl, K., Sanghavi, K., Fish, A., Altman, R. B., Klein, T. E.  
2014; 24 (1): 73-79
- **PharmGKB summary: venlafaxine pathway** *PHARMACOGENETICS AND GENOMICS*  
Sangkuhl, K., Stingl, J. C., Turpeinen, M., Altman, R. B., Klein, T. E.  
2014; 24 (1): 62-72
- **Cloud-based simulations on Google Exacycle reveal ligand modulation of GPCR activation pathways** *NATURE CHEMISTRY*  
Kohlhoff, K. J., Shukla, D., Lawrenz, M., Bowman, G. R., Konerding, D. E., Belov, D., Altman, R. B., Pande, V. S.  
2014; 6 (1): 15-21
- **PharmGKB summary: very important pharmacogene information for cytochrome P450, family 2, subfamily C, polypeptide 8** *PHARMACOGENETICS AND GENOMICS*  
Aquilante, C. L., Niemi, M., Gong, L., Altman, R. B., Klein, T. E.  
2013; 23 (12): 721-728

- **Identifying phenotypic signatures of neuropsychiatric disorders from electronic medical records.** *Journal of the American Medical Informatics Association*  
Lyalina, S., Percha, B., LePendou, P., Iyer, S. V., Altman, R. B., Shah, N. H.  
2013; 20 (e2): e297-305
- **Identifying phenotypic signatures of neuropsychiatric disorders from electronic medical records.** *Journal of the American Medical Informatics Association*  
Lyalina, S., Percha, B., LePendou, P., Iyer, S. V., Altman, R. B., Shah, N. H.  
2013; 20 (e2): e297-305
- **Genome Wide Analysis of Drug-Induced Torsades de Pointes: Lack of Common Variants with Large Effect Sizes** *PLOS ONE*  
Behr, E. R., Ritchie, M. D., Tanaka, T., Kaeaeab, S., Crawford, D. C., Nicoletti, P., Floratos, A., Sinner, M. F., Kannankeril, P. J., Wilde, A. A., Bezzina, C. R., Schulze-Bahr, E., Zumhagen, et al  
2013; 8 (11)
- **PharmGKB summary: very important pharmacogene information for the epidermal growth factor receptor.** *Pharmacogenetics and genomics*  
Hodoglugil, U., Carrillo, M. W., Hebert, J. M., Karachaliou, N., Rosell, R. C., Altman, R. B., Klein, T. E.  
2013; 23 (11): 636-642
- **PharmGKB summary: tamoxifen pathway, pharmacokinetics.** *Pharmacogenetics and genomics*  
Klein, D. J., Thorn, C. F., Desta, Z., Flockhart, D. A., Altman, R. B., Klein, T. E.  
2013; 23 (11): 643-647
- **Using molecular features of xenobiotics to predict hepatic gene expression response.** *Journal of chemical information and modeling*  
Fernald, G. H., Altman, R. B.  
2013; 53 (10): 2765-2773
- **PharmGKB summary: cyclosporine and tacrolimus pathways** *PHARMACOGENETICS AND GENOMICS*  
Barbarino, J. M., Staatz, C. E., Venkataramanan, R., Klein, T. E., Altman, R. B.  
2013; 23 (10): 563-585
- **A method for inferring medical diagnoses from patient similarities** *BMC MEDICINE*  
Gottlieb, A., Stein, G. Y., Ruppin, E., Altman, R. B., Sharan, R.  
2013; 11
- **PharmGKB summary: methylene blue pathway** *PHARMACOGENETICS AND GENOMICS*  
McDonagh, E. M., Bautista, J. M., Youngster, I., Altman, R. B., Klein, T. E.  
2013; 23 (9): 498-508
- **Genetic variants associated with warfarin dose in African-American individuals: a genome-wide association study.** *Lancet*  
Perera, M. A., Cavallari, L. H., Limdi, N. A., Gamazon, E. R., Konkashbaev, A., Daneshjou, R., Pluzhnikov, A., Crawford, D. C., Wang, J., Liu, N., Tatonetti, N., Bourgeois, S., Takahashi, et al  
2013; 382 (9894): 790-796
- **Challenges in the pharmacogenomic annotation of whole genomes.** *Clinical pharmacology & therapeutics*  
Altman, R. B., Whirl-Carrillo, M., Klein, T. E.  
2013; 94 (2): 211-213
- **K-Means for Parallel Architectures Using All-Prefix-Sum Sorting and Updating Steps** *IEEE TRANSACTIONS ON PARALLEL AND DISTRIBUTED SYSTEMS*  
Kohlhoff, K. J., Pande, V. S., Altman, R. B.  
2013; 24 (8): 1602-1612
- **The Pharmacogenomics Research Network Translational Pharmacogenetics Program: Overcoming Challenges of Real-World Implementation** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Shuldiner, A. R., RELLING, M. V., Peterson, J. F., Hicks, J. K., Freimuth, R. R., Sadee, W., Pereira, N. L., Roden, D. M., Johnson, J. A., Klein, T. E.  
2013; 94 (2): 207-210
- **Challenges in the Pharmacogenomic Annotation of Whole Genomes** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Altman, R. B., Whirl-Carrillo, M., Klein, T. E.

2013; 94 (2): 211-213

- **PharmGKB summary: diuretics pathway, pharmacodynamics** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Ellison, D. H., Turner, S. T., Altman, R. B., Klein, T. E.  
2013; 23 (8): 449-453
- **Pathway analysis of genome-wide data improves warfarin dose prediction** *BMC GENOMICS*  
Daneshjou, R., Tatonetti, N. P., Karczewski, K. J., Sagreiya, H., Bourgeois, S., Drozda, K., Burmester, J. K., Tsunoda, T., Nakamura, Y., Kubo, M., Tector, M., Limdi, N. A., Cavallari, et al  
2013; 14
- **WS-SNPs& GO: a web server for predicting the deleterious effect of human protein variants using functional annotation** *BMC GENOMICS*  
Capriotti, E., Calabrese, R., Fariselli, P., Martelli, P. L., Altman, R. B., Casadio, R.  
2013; 14
- **Collective judgment predicts disease-associated single nucleotide variants** *BMC GENOMICS*  
Capriotti, E., Altman, R. B., Bromberg, Y.  
2013; 14
- **Web-scale pharmacovigilance: listening to signals from the crowd** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
White, R. W., Tatonetti, N. P., Shah, N. H., Altman, R. B., Horvitz, E.  
2013; 20 (3): 404-408
- **Valproic acid pathway: pharmacokinetics and pharmacodynamics** *PHARMACOGENETICS AND GENOMICS*  
Ghodke-Puranik, Y., Thorn, C. F., Lamba, J. K., Leeder, J. S., Song, W., Birnbaum, A. K., Altman, R. B., Klein, T. E.  
2013; 23 (4): 236-241
- **Informatics confronts drug-drug interactions** *TRENDS IN PHARMACOLOGICAL SCIENCES*  
Percha, B., Altman, R. B.  
2013; 34 (3): 178-184
- **Personal genomic measurements: the opportunity for information integration.** *Clinical pharmacology & therapeutics*  
Altman, R. B.  
2013; 93 (1): 21-23
- **Mining for clinical expertise in (undocumented) order sets to power an order suggestion system.** *AMIA Joint Summits on Translational Science proceedings. AMIA Joint Summits on Translational Science*  
Chen, J. H., Altman, R. B.  
2013; 2013: 34-38
- **A method for inferring medical diagnoses from patient similarities.** *BMC medicine*  
Gottlieb, A., Stein, G. Y., Ruppin, E., Altman, R. B., Sharan, R.  
2013; 11: 194-?
- **Inferring the semantic relationships of words within an ontology using random indexing: applications to pharmacogenomics.** *AMIA ... Annual Symposium proceedings / AMIA Symposium. AMIA Symposium*  
Percha, B., Altman, R. B.  
2013; 2013: 1123-1132
- **Proceedings of Pacific Symposium on Biocomputing 2011.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2013
- **PharmGKB: the Pharmacogenomics Knowledge Base.** *Methods in molecular biology (Clifton, N.J.)*  
Thorn, C. F., Klein, T. E., Altman, R. B.  
2013; 1015: 311-320
- **Pathway analysis of genome-wide data improves warfarin dose prediction.** *BMC genomics*  
Daneshjou, R., Tatonetti, N. P., Karczewski, K. J., Sagreiya, H., Bourgeois, S., Drozda, K., Burmester, J. K., Tsunoda, T., Nakamura, Y., Kubo, M., Tector, M., Limdi, N. A., Cavallari, et al  
2013; 14: S11-?

- **Improving data and knowledge management to better integrate health care and research.** *Journal of internal medicine*  
Cases, M. n., Furlong, L. I., Albanell, J. n., Altman, R. B., Bellazzi, R. n., Boyer, S. n., Brand, A. n., Brookes, A. J., Brunak, S. n., Clark, T. W., Gea, J. n., Ghazal, P. n., Graf, et al  
2013
- **PharmGKB summary: zidovudine pathway** *PHARMACOGENETICS AND GENOMICS*  
Ghodke, Y., Anderson, P. L., Sangkuhl, K., Lamba, J., Altman, R. B., Klein, T. E.  
2012; 22 (12): 891-894
- **Impact of the CYP4F2 p.V433M Polymorphism on Coumarin Dose Requirement: Systematic Review and Meta-Analysis** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Danese, E., Montagnana, M., Johnson, J. A., Rettie, A. E., Zambon, C. F., Lubitz, S. A., Suarez-Kurtz, G., Cavallari, L. H., Zhao, L., Huang, M., Nakamura, Y., Mushiroda, T., Kringen, et al  
2012; 92 (6): 746-756
- **Chapter 7: Pharmacogenomics** *PLOS COMPUTATIONAL BIOLOGY*  
Karczewski, K. J., Daneshjou, R., Altman, R. B.  
2012; 8 (12)
- **Introduction to Translational Bioinformatics Collection** *PLOS COMPUTATIONAL BIOLOGY*  
Altman, R. B.  
2012; 8 (12)
- **Metformin pathways: pharmacokinetics and pharmacodynamics** *PHARMACOGENETICS AND GENOMICS*  
Gong, L., Goswami, S., Giacomini, K. M., Altman, R. B., Klein, T. E.  
2012; 22 (11): 820-827
- **Very important pharmacogene summary for VDR** *PHARMACOGENETICS AND GENOMICS*  
Poon, A. H., Gong, L., Brasch-Andersen, C., Litonjua, A. A., Raby, B. A., Hamid, Q., Laprise, C., Weiss, S. T., Altman, R. B., Klein, T. E.  
2012; 22 (10): 758-763
- **The state of the art in text mining and natural language processing for pharmacogenomics** *JOURNAL OF BIOMEDICAL INFORMATICS*  
Coulet, A., Cohen, K. B., Altman, R. B.  
2012; 45 (5): 825-826
- **Pharmacogenomics Knowledge for Personalized Medicine** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Whirl-Carrillo, M., MCDONAGH, E. M., Hebert, J. M., Gong, L., Sangkuhl, K., Thorn, C. F., Altman, R. B., Klein, T. E.  
2012; 92 (4): 414-417
- **Implementing Personalized Medicine: Development of a Cost-Effective Customized Pharmacogenetics Genotyping Array** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Johnson, J. A., Burkley, B. M., Langae, T. Y., Clare-Salzler, M. J., Klein, T. E., Altman, R. B.  
2012; 92 (4): 437-439
- **Mice lacking the  $\beta 2$  adrenergic receptor have a unique genetic profile before and after focal brain ischaemia.** *ASN neuro*  
White, R. E., Palm, C., Xu, L., Ling, E., Ginsburg, M., Daigle, B. J., Han, R., Patterson, A., Altman, R. B., Giffard, R. G.  
2012; 4 (5)
- **PharmGKB summary: very important pharmacogene information for cytochrome P-450, family 2, subfamily A, polypeptide 6** *PHARMACOGENETICS AND GENOMICS*  
McDonagh, E. M., Wassenaar, C., David, S. P., Tyndale, R. F., Altman, R. B., Whirl-Carrillo, M., Klein, T. E.  
2012; 22 (9): 695-708
- **PharmGKB summary: very important pharmacogene information for GSTT1** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Ji, Y., Weinshilboum, R. M., Altman, R. B., Klein, T. E.  
2012; 22 (8): 646-651
- **Bioinformatics and variability in drug response: a protein structural perspective** *JOURNAL OF THE ROYAL SOCIETY INTERFACE*  
Lahti, J. L., Tang, G. W., Capriotti, E., Liu, T., Altman, R. B.  
2012; 9 (72): 1409-1437

- **PharmGKB summary: very important pharmacogene information for CYP3A5** *PHARMACOGENETICS AND GENOMICS*  
Lamba, J., Hebert, J. M., Schuetz, E. G., Klein, T. E., Altman, R. B.  
2012; 22 (7): 555-558
- **Editorial: Current progress in Bioinformatics 2012** *BRIEFINGS IN BIOINFORMATICS*  
Altman, R. B.  
2012; 13 (4): 393-394
- **Translational Bioinformatics: Linking the Molecular World to the Clinical World** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Altman, R. B.  
2012; 91 (6): 994-1000
- **PharmGKB summary: phenytoin pathway.** *Pharmacogenetics and genomics*  
Thorn, C. F., Whirl-Carrillo, M., Leeder, J. S., Klein, T. E., Altman, R. B.  
2012; 22 (6): 466-70
- **PharmGKB summary: phenytoin pathway** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Whirl-Carrillo, M., Leeder, J. S., Klein, T. E., Altman, R. B.  
2012; 22 (6): 466-470
- **PharmGKB summary: caffeine pathway** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Aklillu, E., McDonagh, E. M., Klein, T. E., Altman, R. B.  
2012; 22 (5): 389-395
- **Using ODIN for a PharmGKB revalidation experiment** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*  
Rinaldi, F., Clematide, S., Garten, Y., Whirl-Carrillo, M., Gong, L., Hebert, J. M., Sangkuhl, K., Thorn, C. F., Klein, T. E., Altman, R. B.  
2012
- **Celecoxib pathways: pharmacokinetics and pharmacodynamics** *PHARMACOGENETICS AND GENOMICS*  
Gong, L., Thorn, C. F., Bertagnolli, M. M., Grosser, T., Altman, R. B., Klein, T. E.  
2012; 22 (4): 310-318
- **Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes** *CELL*  
Chen, R., Mias, G. I., Li-Pook-Than, J., Jiang, L., Lam, H. Y., Chen, R., Miriami, E., Karczewski, K. J., Hariharan, M., Dewey, F. E., Cheng, Y., Clark, M. J., Im, et al  
2012; 148 (6): 1293-1307
- **Simbios: an NIH national center for physics-based simulation of biological structures** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Delp, S. L., Ku, J. P., Pande, V. S., Sherman, M. A., Altman, R. B.  
2012; 19 (2): 186-189
- **PharmGKB summary: very important pharmacogene information for G6PD** *PHARMACOGENETICS AND GENOMICS*  
McDonagh, E. M., Thorn, C. F., Bautista, J. M., Youngster, I., Altman, R. B., Klein, T. E.  
2012; 22 (3): 219-228
- **PharmGKB summary: very important pharmacogene information for cytochrome P450, family 2, subfamily C, polypeptide 19** *PHARMACOGENETICS AND GENOMICS*  
Scott, S. A., Sangkuhl, K., Shuldiner, A. R., Hulot, J., Thorn, C. F., Altman, R. B., Klein, T. E.  
2012; 22 (2): 159-165
- **A novel signal detection algorithm for identifying hidden drug-drug interactions in adverse event reports** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Tatonetti, N. P., Fernald, G. H., Altman, R. B.  
2012; 19 (1): 79-85
- **SYSTEMS PHARMACOGENOMICS-BRIDGING THE GAP**  
Ritchie, M., Cox, N., Cheng, C., Weiss, S., Klein, T., Altman, R., P-STAR, PGRN Syst Biol Grp, PharmGKB  
edited by Altman, R. B., Dunker, A. K., Hunter, L., Murray, T., Klein, T. E.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2012: 442

- **Discovery and explanation of drug-drug interactions via text mining.**  
Percha, B., Garten, Y., Altman, R. B.  
2012
- **Interpretome: a freely available, modular, and secure personal genome interpretation engine.**  
Karczewski, K. J., Tirrell, R. P., Cordero, P., Tatonetti, N. P., Dudley, J. T., Salari, K., Altman, R. B.  
2012
- **Chapter 7: Pharmacogenomics.** *PLoS Comput Biol.*, *PMCID: PMC3531317.*  
Karczewski, K. J., Daneshjou, R., Altman, R. B.  
2012; 8 (12): e1002817
- **Mice lacking the beta 2 adrenergic receptor have a unique genetic profile before and after focal brain ischaemia** *ASN NEURO*  
White, R. E., Palm, C., Xu, L., Ling, E., Ginsburg, M., Daigle, B. J., Han, R., Patterson, A., Altman, R. B., Giffard, R. G.  
2012; 4 (5): 343-356
- **Discovery and explanation of drug-drug interactions via text mining.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Percha, B., Garten, Y., Altman, R. B.  
2012: 410-421
- **Interpretome: a freely available, modular, and secure personal genome interpretation engine.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Karczewski, K. J., Tirrell, R. P., Cordero, P., Tatonetti, N. P., Dudley, J. T., Salari, K., Snyder, M., Altman, R. B., Kim, S. K.  
2012: 339-350
- **PharmGKB summary: very important pharmacogene information for CYP1A2** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Akillu, E., Klein, T. E., Altman, R. B.  
2012; 22 (1): 73-77
- **PharmGKB summary: carbamazepine pathway** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Leckband, S. G., Kelseo, J., Leeder, J. S., Mueller, D. J., Klein, T. E., Altman, R. B.  
2011; 21 (12): 906-910
- **Using Multiple Microenvironments to Find Similar Ligand-Binding Sites: Application to Kinase Inhibitor Binding** *PLOS COMPUTATIONAL BIOLOGY*  
Liu, T., Altman, R. B.  
2011; 7 (12)
- **From pharmacogenomic knowledge acquisition to clinical applications: the PharmGKB as a clinical pharmacogenomic biomarker resource** *BIOMARKERS IN MEDICINE*  
McDonagh, E. M., Whirl-Carrillo, M., Garten, Y., Altman, R. B., Klein, T. E.  
2011; 5 (6): 795-806
- **PharmGKB summary: citalopram pharmacokinetics pathway** *PHARMACOGENETICS AND GENOMICS*  
Sangkuhl, K., Klein, T. E., Altman, R. B.  
2011; 21 (11): 769-772
- **PharmGKB summary: methotrexate pathway** *PHARMACOGENETICS AND GENOMICS*  
Mikkelsen, T. S., Thorn, C. F., Yang, J. J., Ulrich, C. M., French, D., Zaza, G., Dunnenberger, H. M., Marsh, S., McLeod, H. L., Giacomini, K., Becker, M. L., Gaedigk, R., Leeder, et al  
2011; 21 (10): 679-686
- **Clinical Pharmacogenetics Implementation Consortium Guidelines for CYP2C9 and VKORC1 Genotypes and Warfarin Dosing** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Johnson, J. A., Gong, L., Whirl-Carrillo, M., Gage, B. F., Scott, S. A., Stein, C. M., Anderson, J. L., Kimmel, S. E., Lee, M. T., Pirmohamed, M., Wadelius, M., Klein, T. E., Altman, et al  
2011; 90 (4): 625-629
- **A new disease-specific machine learning approach for the prediction of cancer-causing missense variants** *GENOMICS*  
Capriotti, E., Altman, R. B.

2011; 98 (4): 310-317

- **PharmGKB summary: very important pharmacogene information for PTGS2** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Grosser, T., Klein, T. E., Altman, R. B.  
2011; 21 (9): 607-613
- **Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence** *PLOS GENETICS*  
Dewey, F. E., Chen, R., Cordero, S. P., Ormond, K. E., Caleshu, C., Karczewski, K. J., Whirl-Carrillo, M., Wheeler, M. T., Dudley, J. T., Byrnes, J. K., Cornejo, O. E., Knowles, J. W., Woon, et al  
2011; 7 (9)
- **Fast Flexible Modeling of RNA Structure Using Internal Coordinates** *IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS*  
Flores, S. C., Sherman, M. A., Bruns, C. M., Eastman, P., Altman, R. B.  
2011; 8 (5): 1247-1257
- **CAMPAIGN: an open-source library of GPU-accelerated data clustering algorithms** *BIOINFORMATICS*  
Kohlhoff, K. J., Sosnick, M. H., Hsu, W. T., Pande, V. S., Altman, R. B.  
2011; 27 (16): 2322-2323
- **Cooperative transcription factor associations discovered using regulatory variation** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Karczewski, K. J., Tatonetti, N. P., Landt, S. G., Yang, X., Slifer, T., Altman, R. B., Snyder, M.  
2011; 108 (32): 13353-13358
- **Platelet aggregation pathway** *PHARMACOGENETICS AND GENOMICS*  
Sanguhl, K., Shuldiner, A. R., Klein, T. E., Altman, R. B.  
2011; 21 (8): 516-521
- **RNA molecules with conserved catalytic cores but variable peripheries fold along unique energetically optimized pathways** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Mitra, S., Laederach, A., Golden, B. L., Altman, R. B., Brenowitz, M.  
2011; 17 (8): 1589-1603
- **Improving the prediction of disease-related variants using protein three-dimensional structure** *European Conference on Computational Biology (ECCB)/Workshop on Annotation, Interpretation and Management of Mutations (AIMM)*  
Capriotti, E., Altman, R. B.  
BIOMED CENTRAL LTD.2011
- **Doxorubicin pathways: pharmacodynamics and adverse effects** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Oshiro, C., Marsh, S., Hernandez-Boussard, T., McLeod, H., Klein, T. E., Altman, R. B.  
2011; 21 (7): 440-446
- **2010 Translational bioinformatics year in review** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Altman, R. B., Miller, K. S.  
2011; 18 (4): 358-366
- **Detecting Drug Interactions From Adverse-Event Reports: Interaction Between Paroxetine and Pravastatin Increases Blood Glucose Levels** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Tatonetti, N. P., Denny, J. C., Murphy, S. N., Fernald, G. H., Krishnan, G., Castro, V., Yue, P., Tsau, P. S., Kohane, I., Roden, D. M., Altman, R. B.  
2011; 90 (1): 133-142
- **Bioinformatics challenges for personalized medicine** *BIOINFORMATICS*  
Fernald, G. H., Capriotti, E., Daneshjou, R., Karczewski, K. J., Altman, R. B.  
2011; 27 (13): 1741-1748
- **PharmGKB summary: dopamine receptor D2** *PHARMACOGENETICS AND GENOMICS*  
Mi, H., Thomas, P. D., Ring, H. Z., Jiang, R., Sanguhl, K., Klein, T. E., Altman, R. B.  
2011; 21 (6): 350-356
- **PharmGKB summary: cytochrome P450, family 2, subfamily J, polypeptide 2: CYP2J2** *PHARMACOGENETICS AND GENOMICS*

- 
- Berlin, D. S., Sangkuhl, K., Klein, T. E., Altman, R. B.  
2011; 21 (5): 308-311
- **Databases in the Area of Pharmacogenetics** *HUMAN MUTATION*  
Sim, S. C., Altman, R. B., Ingelman-Sundberg, M.  
2011; 32 (5): 526-531
  - **Remote Thioredoxin Recognition Using Evolutionary Conservation and Structural Dynamics** *STRUCTURE*  
Tang, G. W., Altman, R. B.  
2011; 19 (4): 461-470
  - **PharmGKB summary: fluoropyrimidine pathways** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Marsh, S., Carrillo, M. W., McLeod, H. L., Klein, T. E., Altman, R. B.  
2011; 21 (4): 237-242
  - **Very important pharmacogene summary: ABCB1 (MDR1, P-glycoprotein)** *PHARMACOGENETICS AND GENOMICS*  
Hodges, L. M., Markova, S. M., Chinn, L. W., Gow, J. M., Kroetz, D. L., Klein, T. E., Altman, R. B.  
2011; 21 (3): 152-161
  - **Pharmacogenomics: "Noninferiority" Is Sufficient for Initial Implementation** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Altman, R. B.  
2011; 89 (3): 348-350
  - **PharmGKB: very important pharmacogene - HMGCR** *PHARMACOGENETICS AND GENOMICS*  
Medina, M. W., Sangkuhl, K., Klein, T. E., Altman, R. B.  
2011; 21 (2): 98-101
  - **Bisphosphonates pathway** *PHARMACOGENETICS AND GENOMICS*  
Gong, L., Altman, R. B., Klein, T. E.  
2011; 21 (1): 50-53
  - **Structural insights into pre-translocation ribosome motions.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Flores, S. C., Altman, R.  
2011: 205-211
  - **Cooperative transcription factor associations discovered using regulatory variation.**  
Karczewski, K. J., Tatonetti, N. P., Landt, S. G., Yang, X., Slifer, T., Altman, R. B.  
2011
  - **Structural insights into pre-translocation ribosome motions.**  
Flores, S. C., Altman, R. B.  
2011
  - **Improving the prediction of disease-related variants using protein three-dimensional structure.** *BMC Bioinformatics.*;12 Suppl4:S3. Epub 2011 Jul 5. *PMCID PMC3194195.*  
Capriotti, E., Altman, R. B.  
2011
  - **Perspective: 2010 Translational bioinformatics year in review.** *JAMIA.*, *PMCID: PMC3128418.*  
Altman, R. B., Miller, K. S.  
2011; 4 (18): 358-366
  - **Integration and publication of heterogeneous text-mined relationships on the Semantic Web.** *Journal of biomedical semantics*  
Coulet, A., Garten, Y., Dumontier, M., Altman, R. B., Musen, M. A., Shah, N. H.  
2011; 2: S10-?
  - **Pharmacogenomics: will the promise be fulfilled?** *NATURE REVIEWS GENETICS*  
Altman, R. B., Kroemer, H. K., McCarty, C. A., Ratain, M. J., Roden, D.  
2011; 12 (1): 69-73

- **Content-based microarray search using differential expression profiles** *BMC BIOINFORMATICS*  
Engreitz, J. M., Morgan, A. A., Dudley, J. T., Chen, R., Thathoo, R., Altman, R. B., Butte, A. J.  
2010; 11
- **KCNH2 pharmacogenomics summary** *PHARMACOGENETICS AND GENOMICS*  
Oshiro, C., Thorn, C. F., Roden, D. M., Klein, T. E., Altman, R. B.  
2010; 20 (12): 775-777
- **Using text to build semantic networks for pharmacogenomics** *JOURNAL OF BIOMEDICAL INFORMATICS*  
Coulet, A., Shah, N. H., Garten, Y., Musen, M., Altman, R. B.  
2010; 43 (6): 1009-1019
- **Independent component analysis: Mining microarray data for fundamental human gene expression modules** *JOURNAL OF BIOMEDICAL INFORMATICS*  
Engreitz, J. M., Daigle, B. J., Marshall, J. J., Altman, R. B.  
2010; 43 (6): 932-944
- **SLC19A1 pharmacogenomics summary** *PHARMACOGENETICS AND GENOMICS*  
Yee, S. W., Gong, L., Badagnani, I., Giacomini, K. M., Klein, T. E., Altman, R. B.  
2010; 20 (11): 708-715
- **An integrative method for scoring candidate genes from association studies: application to warfarin dosing** *AMIA Summit on Translational Bioinformatics*  
Tatonetti, N. P., Dudley, J. T., Sagreiya, H., Butte, A. J., Altman, R. B.  
BIOMED CENTRAL LTD.2010
- **VKORC1 Pharmacogenomics Summary** *PHARMACOGENETICS AND GENOMICS*  
Owen, R. P., Gong, L., Sagreiya, H., Klein, T. E., Altman, R. B.  
2010; 20 (10): 642-644
- **Recent progress in automatically extracting information from the pharmacogenomic literature** *PHARMACOGENOMICS*  
Garten, Y., Coulet, A., Altman, R. B.  
2010; 11 (10): 1467-1489
- **The utility of general purpose versus specialty clinical databases for research: Warfarin dose estimation from extracted clinical variables** *JOURNAL OF BIOMEDICAL INFORMATICS*  
Sagreiya, H., Altman, R. B.  
2010; 43 (5): 747-751
- **Maternal-fetal and neonatal pharmacogenomics: a review of current literature** *JOURNAL OF PERINATOLOGY*  
Blumenfeld, Y. J., Reynolds-May, M. F., Altman, R. B., El-Sayed, Y. Y.  
2010; 30 (9): 571-579
- **Turning limited experimental information into 3D models of RNA** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Flores, S. C., Altman, R. B.  
2010; 16 (9): 1769-1778
- **Thiopurine pathway** *PHARMACOGENETICS AND GENOMICS*  
Zaza, G., Cheok, M., Krynetskaia, N., Thorn, C., Stocco, G., Hebert, J. M., McLeod, H., Weinshilboum, R. M., Relling, M. V., Evans, W. E., Klein, T. E., Altman, R. B.  
2010; 20 (9): 573-574
- **PharmGKB summary: very important pharmacogene information for CYP2B6** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Lamba, J. K., Lamba, V., Klein, T. E., Altman, R. B.  
2010; 20 (8): 520-523
- **Clopidogrel pathway** *PHARMACOGENETICS AND GENOMICS*  
Sanguhl, K., Klein, T. E., Altman, R. B.  
2010; 20 (7): 463-465

- **Extending and evaluating a warfarin dosing algorithm that includes CYP4F2 and pooled rare variants of CYP2C9** *PHARMACOGENETICS AND GENOMICS*  
Sagrieya, H., Berube, C., Wen, A., Ramakrishnan, R., Mir, A., Hamilton, A., Altman, R. B.  
2010; 20 (7): 407-413
- **Very important pharmacogene summary: thiopurine S-methyltransferase** *PHARMACOGENETICS AND GENOMICS*  
Wang, L., Pelleycounter, L., Weinshilboum, R., Johnson, J. A., Hebert, J. M., Altman, R. B., Klein, T. E.  
2010; 20 (6): 401-405
- **Clinical implementation of pharmacogenomics: overcoming genetic exceptionalism** *LANCET ONCOLOGY*  
Relling, M. V., Altman, R. B., Goetz, M. P., Evans, W. E.  
2010; 11 (6): 507-509
- **Challenges in the clinical application of whole-genome sequencing** *LANCET*  
Ormond, K. E., Wheeler, M. T., Hudgins, L., Klein, T. E., Butte, A. J., Altman, R. B., Ashley, E. A., Greely, H. T.  
2010; 375 (9727): 1749-1751
- **Warfarin pharmacogenetics: a single VKORC1 polymorphism is predictive of dose across 3 racial groups** *BLOOD*  
Limdi, N. A., Wadelius, M., Cavallari, L., Eriksson, N., Crawford, D. C., Lee, M. M., Chen, C., Motsinger-Reif, A., Sagrieya, H., Liu, N., Wu, A. H., Gage, B. F., Jorgensen, et al  
2010; 115 (18): 3827-3834
- **Vascular endothelial growth factor pathway** *PHARMACOGENETICS AND GENOMICS*  
Maitland, M. L., Lou, X. J., Ramirez, J., Desai, A. A., Berlin, D. S., McLeod, H. L., Weichselbaum, R. R., Ratain, M. J., Altman, R. B., Klein, T. E.  
2010; 20 (5): 346-349
- **Cytochrome P450 2C9-CYP2C9** *PHARMACOGENETICS AND GENOMICS*  
Van Booven, D., Marsh, S., McLeod, H., Carrillo, M. W., Sangkuhl, K., Klein, T. E., Altman, R. B.  
2010; 20 (4): 277-281
- **Teaching computers to read the pharmacogenomics literature ... so you don't have to** *PHARMACOGENOMICS*  
Garten, Y., Altman, R. B.  
2010; 11 (4): 515-518
- **Pharmacogenomics and bioinformatics: PharmGKB** *PHARMACOGENOMICS*  
Thorn, C. F., Klein, T. E., Altman, R. B.  
2010; 11 (4): 501-505
- **DNATwist: A Web-Based Tool for Teaching Middle and High School Students About Pharmacogenomics** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Berlin, D. S., Person, M. G., Mittal, A., Oppezco, M. A., Chin, D. B., Starr, B., Klein, T. E., Schwartz, D. L., Altman, R. B.  
2010; 87 (4): 393-395
- **PharmGKB very important pharmacogene: SLCO1B1** *PHARMACOGENETICS AND GENOMICS*  
Oshiro, C., Mangravite, L., Klein, T., Altman, R.  
2010; 20 (3): 211-216
- **Using Pre-existing Microarray Datasets to Increase Experimental Power: Application to Insulin Resistance** *PLOS COMPUTATIONAL BIOLOGY*  
Daigle, B. J., Deng, A., McLaughlin, T., Cushman, S. W., Cam, M. C., Reaven, G., Tsao, P. S., Altman, R. B.  
2010; 6 (3)
- **Identification of recurring protein structure microenvironments and discovery of novel functional sites around CYS residues** *BMC STRUCTURAL BIOLOGY*  
Wu, S., Liu, T., Altman, R. B.  
2010; 10
- **PharmGKB summary: very important pharmacogene information for angiotensin-converting enzyme** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Klein, T. E., Altman, R. B.

2010; 20 (2): 143-146

- **Extraction of genotype-phenotype-drug relationships from text: from entity recognition to bioinformatics application.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Coulet, A., Shah, N., Hunter, L., Barral, C., Altman, R. B.  
2010: 485-487
- **Improving the prediction of pharmacogenes using text-derived drug-gene relationships.**  
Garten, Y., Tatonetti, N. P., Altman, R. B.  
edited by Altman, R., Dunker, K., Hunter, L.  
2010
- **Predicting RNA structure by multiple template homology modeling.**  
Flores, S. C., Wan, Y., Russell, R., Altman, R. B.  
edited by Altman, R., Dunker, K., Hunter, L.  
2010
- **Proceedings of Pacific Symposium on Biocomputing 2010.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2010
- **Extraction of genotype-phenotype-drug relationships from text: from entity recognition to bioinformatics application.**  
Coulet, A., Shah, N., Hunter, L., Barral, C., Altman, R. B.  
edited by Altman, R., Dunker, K., Hunter, L.  
2010
- **An integrative method for scoring candidate genes from association studies: application to warfarin dosing.** *BMC Bioinformatics.*, 11 Suppl 9:S9. *PMCID: PMC2967750.*  
Tatonetti, N. P., Dudley, J. T., Sagreiya, H., Butte, A. J., Altman, R. B.  
2010
- **Editorial: Current progress in Bioinformatics 2010** *BRIEFINGS IN BIOINFORMATICS*  
Altman, R. B.  
2010; 11 (1): 1-2
- **Very important pharmacogene summary ADRB2** *PHARMACOGENETICS AND GENOMICS*  
Litonjua, A. A., Gong, L., Duan, Q. L., Shin, J., Moore, M. J., Weiss, S. T., Johnson, J. A., Klein, T. E., Altman, R. B.  
2010; 20 (1): 64-69
- **Improving the prediction of pharmacogenes using text-derived drug-gene relationships.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Garten, Y., Tatonetti, N. P., Altman, R. B.  
2010: 305-314
- **Predicting RNA structure by multiple template homology modeling.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Flores, S. C., Wan, Y., Russell, R., Altman, R. B.  
2010: 216-227
- **Knowledge-based instantiation of full atomic detail into coarse-grain RNA 3D structural models** *BIOINFORMATICS*  
Jonikas, M. A., Radmer, R. J., Altman, R. B.  
2009; 25 (24): 3259-3266
- **Prediction of calcium-binding sites by combining loop-modeling with machine learning** *BMC STRUCTURAL BIOLOGY*  
Liu, T., Altman, R. B.  
2009; 9
- **Taxane pathway** *PHARMACOGENETICS AND GENOMICS*  
Oshiro, C., Marsh, S., McLeod, H., Carrillo, M. W., Klein, T., Altman, R.  
2009; 19 (12): 979-983

- **Selective serotonin reuptake inhibitors pathway** *PHARMACOGENETICS AND GENOMICS*  
Sangkuhl, K., Klein, T. E., Altman, R. B.  
2009; 19 (11): 907-909
- **Generating Genome-Scale Candidate Gene Lists for Pharmacogenomics** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Hansen, N. T., Brunak, S., Altman, R. B.  
2009; 86 (2): 183-189
- **A Double-Blind, Randomized, Saline-Controlled Study of the Efficacy and Safety of EUFLEXXA (R) for Treatment of Painful Osteoarthritis of the Knee, With an Open-Label Safety Extension (The FLEXX Trial)** *SEMINARS IN ARTHRITIS AND RHEUMATISM*  
Altman, R. D., Rosen, J. E., Bloch, D. A., Hatoum, H. T., Korner, P.  
2009; 39 (1): 1-9
- **Improving Structure-Based Function Prediction Using Molecular Dynamics** *STRUCTURE*  
Glazer, D. S., Radmer, R. J., Altman, R. B.  
2009; 17 (7): 919-929
- **Codeine and morphine pathway** *PHARMACOGENETICS AND GENOMICS*  
Thorn, C. F., Klein, T. E., Altman, R. B.  
2009; 19 (7): 556-558
- **Direct-to-Consumer Genetic Testing: Failure Is Not an Option** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Altman, R. B.  
2009; 86 (1): 15-17
- **Platinum pathway** *PHARMACOGENETICS AND GENOMICS*  
Marsh, S., McLeod, H., Dolan, E., Shukla, S. J., Rabik, C. A., Gong, L., Hernandez-Boussard, T., Lou, X. J., Klein, T. E., Altman, R. B.  
2009; 19 (7): 563-564
- **Antiestrogen pathway (aromatase inhibitor)** *PHARMACOGENETICS AND GENOMICS*  
Desta, Z., Nguyen, A., Flockhart, D., Skaar, T., Fletcher, R., Weinshilboum, R., Berlin, D. S., Klein, T. E., Altman, R. B.  
2009; 19 (7): 554-555
- **Cytochrome P450 2D6** *PHARMACOGENETICS AND GENOMICS*  
Owen, R. P., Sangkuhl, K., Klein, T. E., Altman, R. B.  
2009; 19 (7): 559-562
- **Etoposide pathway** *PHARMACOGENETICS AND GENOMICS*  
Yang, J., Bogni, A., Schuetz, E. G., Ratain, M., Dolan, M. E., McLeod, H., Gong, L., Thorn, C., Relling, M. V., Klein, T. E., Altman, R. B.  
2009; 19 (7): 552-553
- **Very important pharmacogene summary: sulfotransferase 1A1** *PHARMACOGENETICS AND GENOMICS*  
Hildebrandt, M., Adjei, A., Weinshilboum, R., Johnson, J. A., Berlin, D. S., Klein, T. E., Altman, R. B.  
2009; 19 (6): 404-406
- **New feature: pathways and important genes from PharmGKB** *PHARMACOGENETICS AND GENOMICS*  
Elchelbaum, M., Altman, R. B., Ratain, M., Klein, T. E.  
2009; 19 (6): 403-403
- **Pharmspresso: a text mining tool for extraction of pharmacogenomic concepts and relationships from full text** *1st Summit on Translational Bioinformatics*  
Garten, Y., Altman, R. B.  
BIOMED CENTRAL LTD.2009
- **Coarse-grained modeling of large RNA molecules with knowledge-based potentials and structural filters** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Jonikas, M. A., Radmer, R. J., Laederach, A., Das, R., Pearlman, S., Herschlag, D., Altman, R. B.  
2009; 15 (2): 189-199
- **TOWARDS A CYTOKINE-CELL INTERACTION KNOWLEDGEBASE OF THE ADAPTIVE IMMUNE SYSTEM** *Pacific Symposium on Biocomputing*

Shen-Orr, S. S., Goldberger, O., Garten, Y., Rosenberg-Hasson, Y., Lovelace, P. A., Hirschberg, D. L., Altman, R. B., Davis, M. M., Butte, A. J.  
WORLD SCIENTIFIC PUBL CO PTE LTD.2009: 439–450

- **Proceedings of Pacific Symposium on Biocomputing 2009.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2009
- **The International Warfarin Pharmacogenetics Consortium. Warfarin Dosing Using Clinical and Pharmacogenetic Data.** *New England Journal of Medicine.*  
Altman, R. B.  
2009; 8 (360): 753-64
- **Pharmspresso: a text mining tool for extraction of pharmacogenomic concepts and relationships from full text.** *BMC Bioinformatics.*, 10 Suppl 2:S6. *PMCID: PMC2646239.*  
Garten, Y., Altman, R. B.  
2009
- **A general framework for dose optimization.** *AMIA ... Annual Symposium proceedings / AMIA Symposium. AMIA Symposium*  
Turcott, R. G., Sagreiya, H., Ashley, E. A., Altman, R. B., Das, A. K.  
2009; 2009: 656-660
- **New feature: pathways and important genes from PharmGKB.** *Pharmacogenetics and genomics*  
Eichelbaum, M. n., Altman, R. B., Ratain, M. n., Klein, T. E.  
2009; 19 (6): 403
- **Predicting drug side-effects by chemical systems biology** *GENOME BIOLOGY*  
Tatonetti, N. P., Liu, T., Altman, R. B.  
2009; 10 (9)
- **Efficient Algorithms to Explore Conformation Spaces of Flexible Protein Loops** *7th International Workshop on Algorithms in Bioinformatics (WABI 2007)*  
Yao, P., Dhanik, A., Marz, N., Propper, R., Kou, C., Liu, G., van den Bedem, H., Latombe, J., Halperin-Landsberg, I., Altman, R. B.  
IEEE COMPUTER SOC.2008: 534–45
- **PharmGKB: an integrated resource of pharmacogenomic data and knowledge.** *Current protocols in bioinformatics / editorial board, Andreas D. Baxevanis ... [et al.]*  
Gong, L., Owen, R. P., Gor, W., Altman, R. B., Klein, T. E.  
2008; Chapter 14: Unit14 7-?
- **The Simbios National Center: Systems Biology in Motion.** *Proceedings of the IEEE. Institute of Electrical and Electronics Engineers*  
Schmidt, J. P., Delp, S. L., Sherman, M. A., Taylor, C. A., Pande, V. S., Altman, R. B.  
2008; 96 (8): 1266
- **The Simbios National Center: Systems biology in motion** *PROCEEDINGS OF THE IEEE*  
Schmidt, J. P., Delp, S. L., Sherman, M. A., Taylor, C. A., Pande, V. S., Altman, R. B.  
2008; 96 (8): 1266-1280
- **High-throughput single-nucleotide structural mapping by capillary automated footprinting analysis** *NUCLEIC ACIDS RESEARCH*  
Mitra, S., Shcherbakova, I. V., Altman, R. B., Brenowitz, M., Laederach, A.  
2008; 36 (11)
- **Interview: Russ Altman speaks to Shreeya Nanda, Commissioning Editor.** *Pharmacogenomics*  
Altman, R. B.  
2008; 9 (6): 663-665
- **iTools: A Framework for Classification, Categorization and Integration of Computational Biology Resources** *PLOS ONE*  
Dinov, I. D., Rubin, D., Lorensen, W., Dugan, J., Ma, J., Murphy, S., Kirschner, B., Bug, W., Sherman, M., Floratos, A., Kennedy, D., Jagadish, H. V., Schmidt, et al  
2008; 3 (5)
- **M-BISON: Microarray-based integration of data sources using networks** *BMC BIOINFORMATICS*

- Daigle, B. J., Altman, R. B.  
2008; 9
- **The chemical genomic portrait of yeast: Uncovering a phenotype for all genes** *SCIENCE*  
Hillenmeyer, M. E., Fung, E., Wildenhain, J., Pierce, S. E., Hoon, S., Lee, W., Proctor, M., St Onge, R. P., Tyers, M., Koller, D., Altman, R. B., Davis, R. W., Nislow, et al  
2008; 320 (5874): 362-365
  - **PharmGKB and the international warfarin pharmacogenetics consortium: The changing role for pharmacogenomic databases and single-drug pharmacogenetics** *HUMAN MUTATION*  
Owen, R. P., Altman, R. B., Klein, T. E.  
2008; 29 (4): 456-460
  - **Structural inference of native and partially folded RNA by high-throughput contact mapping** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Dast, R., Kudaravalli, M., Jonikas, M., Laederach, A., Fong, R., Schwans, J. P., Baker, D., Piccirilli, J. A., Altman, R. B., Herschlag, D.  
2008; 105 (11): 4144-4149
  - **MScanner: a classifier for retrieving medline citations** *BMC BIOINFORMATICS*  
Poulter, G. L., Rubin, D. L., Altman, R. B., Seoighe, C.  
2008; 9
  - **An XML-based interchange format for genotype-phenotype data** *HUMAN MUTATION*  
Whirl-Carrillo, M., Woon, M., Thorn, C. E., Klein, T. E., Altman, R. B.  
2008; 29 (2): 212-219
  - **The pharmacogenetics and pharmacogenomics knowledge base: accentuating the knowledge** *NUCLEIC ACIDS RESEARCH*  
Hernandez-Boussard, T., Whirl-Carrillo, M., Hebert, J. M., Gong, L., Owen, R., Gong, M., Gor, W., Liu, F., Truong, C., Whaley, R., Woon, M., Zhou, T., Altman, et al  
2008; 36: D913-D918
  - **Proceedings of Pacific Symposium on Biocomputing 2008.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2008
  - **Combining molecular dynamics and machine learning to improve protein function recognition**  
Glazer, D., Radmer, R., Altman, R.  
edited by Altman, R., Dunker, K., Hunter, L.  
2008
  - **Structural inference of native and partially folded RNA by high-throughput contact mapping.**  
Das, R., Kudaravalli, M., Jonikas, M., Laederach, A., Fong, R., Schwans, J., Altman, R. B.  
2008
  - **The chemical genomic portrait of yeast: uncovering a phenotype for all genes.** *Science.*, *PMCID: PMC2794835*  
Hillenmeyer, M., Fung, E., Wildenhain, J., Pierce, S., Hoon, S., Lee, W., Altman, R. B.  
2008; 5874 (320): 362-5
  - **PharmGKB and the International Warfarin Pharmacogenetics Consortium: the changing role for pharmacogenomic databases and single-drug pharmacogenetics.** *Hum Mutat.*  
Owen, R., Altman, R., Klein, T.  
2008; 29 (4): 456-60
  - **The FEATURE framework for protein function annotation: modeling new functions, improving performance, and extending to novel applications.** *BMC Genomics.*, 9 *Suppl 2:S2. PMCID: PMC2559884.*  
Halperin, I., Glazer, D., Wu, S., Altman, R.  
2008
  - **PharmGKB: UNDERSTANDING THE EFFECTS OF INDIVIDUAL GENETIC VARIANTS** *DRUG METABOLISM REVIEWS*  
Sanguhl, K., Berlin, D. S., Altman, R. B., Klein, T. E.

2008; 40 (4): 539-551

- **The FEATURE framework for protein function annotation: modeling new functions, improving performance, and extending to novel applications.** *BMC genomics*  
Halperin, I., Glazer, D. S., Wu, S., Altman, R. B.  
2008; 9: S2-?
- **Text mining for biology - the way forward: opinions from leading scientists** *GENOME BIOLOGY*  
Altman, R. B., Bergman, C. M., Blake, J., Blaschke, C., Cohen, A., Gannon, F., Grivell, L., Hahn, U., Hersh, W., Hirschman, L., Jensen, L. J., Krallinger, M., Mons, et al  
2008; 9
- **Semiautomated and rapid quantification of nucleic acid footprinting and structure mapping experiments** *NATURE PROTOCOLS*  
Laederach, A., Das, R., Vicens, Q., Pearlman, S. M., Brenowitz, M., Herschlag, D., Altman, R. B.  
2008; 3 (9): 1395-1401
- **Commentaries on "Informatics and Medicine: From Molecules to Populations"** *METHODS OF INFORMATION IN MEDICINE*  
Altman, R. B., Balling, R., Brinkley, J. F., Coiera, E., Consorti, F., Dhansay, M. A., Geissbuhler, A., Hersh, W., Kwankam, S. Y., Lorenzi, N. M., Martin-Sanchez, E., Mihalas, G. I., Shahar, et al  
2008; 47 (4): 296-317
- **The ethics of characterizing difference: guiding principles on using racial categories in human genetics** *GENOME BIOLOGY*  
Lee, S. S., Mountain, J., Koenig, B., Altman, R., Brown, M., Camarillo, A., Cavalli-Sforza, L., Cho, M., Eberhardt, J., Feldman, M., Ford, R., Greely, H., King, et al  
2008; 9 (7)
- **Combining molecular dynamics and machine learning to improve protein function recognition.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Glazer, D. S., Radmer, R. J., Altman, R. B.  
2008: 332-343
- **The SeqFEATURE library of 3D functional site models: comparison to existing methods and applications to protein function annotation** *GENOME BIOLOGY*  
Wu, S., Liang, M. P., Altman, R. B.  
2008; 9 (1)
- **Robust recognition of zinc binding sites in proteins** *PROTEIN SCIENCE*  
Ebert, J. C., Altman, R. B.  
2008; 17 (1): 54-65
- **Predicting allosteric communication in myosin via a pathway of conserved residues** *JOURNAL OF MOLECULAR BIOLOGY*  
Tang, S., Liao, J., Dunn, A. R., Altman, R. B., Spudich, J. A., Schmidt, J. P.  
2007; 373 (5): 1361-1373
- **The education potential of the pharmacogenetics and pharmacogenomics knowledge base (PharmGKB)** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Owen, R. P., Klein, T. E., Altman, R. B.  
2007; 82 (4): 472-475
- **Ontological issues in pharmacogenomics** *MONIST*  
Altman, R. B.  
2007; 90 (4): 523-533
- **Current progress in bioinformatics 2007** *BRIEFINGS IN BIOINFORMATICS*  
Altman, R. B.  
2007; 8 (5): 277-278
- **Using surface envelopes to constrain molecular modeling** *PROTEIN SCIENCE*  
Dugan, J. M., Altman, R. B.  
2007; 16 (7): 1266-1273

- **Coplanar and coaxial orientations of RNA bases and helices** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Laederach, A., Chan, J. M., Schwartzman, A., Willgohe, E., Altman, R. B.  
2007; 13 (5): 643-650
- **Genetic nondiscrimination legislation: a critical prerequisite for pharmacogenomics data sharing** *PHARMACOGENOMICS*  
Altman, R. B., Benowitz, N., Gurwitz, D., Lunshof, J., Relling, M., Lamba, J., Wieben, E., Mooney, S., Giacomini, K., Weiss, S., Johnson, J. A., McLeod, H., Flockhart, et al  
2007; 8 (5): 519-519
- **Distinct contribution of electrostatics, initial conformational ensemble, and macromolecular stability in RNA folding** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Laederach, A., Shcherbakova, I., Jonikas, M. A., Altman, R. B., Brenowitz, M.  
2007; 104 (17): 7045-7050
- **PharmGKB: a logical home for knowledge relating genotype to drug response phenotype** *NATURE GENETICS*  
Altman, R. B.  
2007; 39 (4): 426-426
- **The Pharmacogenetics Research Network: From SNP discovery to clinical drug response** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Giacomini, K. M., Brett, C. M., Altman, R. B., Benowitz, N. L., Dolan, M. E., Flockhart, D. A., Johnson, J. A., Hayes, D. F., Klein, T., Krauss, R. M., Kroetz, D. L., McLeod, H. L., Nguyen, et al  
2007; 81 (3): 328-345
- **Biomedical informatics training at Stanford in the 21st century** *JOURNAL OF BIOMEDICAL INFORMATICS*  
Altman, R. B., Klein, T. E.  
2007; 40 (1): 55-58
- **The PharmGKB: integration, aggregation, and annotation of pharmacogenomic data and knowledge** *CLINICAL PHARMACOLOGY & THERAPEUTICS*  
Hodge, A. E., Altman, R. B., Klein, T. E.  
2007; 81 (1): 21-24
- **Proceedings of Pacific Symposium on Biocomputing 2007.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2007
- **Distinct contribution of electrostatics, initial conformational ensemble, and macromolecular stability in RNA folding.**  
Laederach, A., Shcherbakova, I., Jonikas, M., Altman, R., Brenowitz, M.  
2007
- **In Current Pharmacogenomics**  
Thorn, C., Whirl-Carrillo, M., Klein, T., Altman, R.  
Bentham Science Publishers..2007
- **The education potential of the pharmacogenetics and pharmacogenomics knowledge base (PharmGKB).** *Clin Pharmacol Ther.*  
Owen, R., Klein, T., Altman, R.  
2007; 82 (4): 472-5
- **Clustering protein environments for function prediction: finding PROSITE motifs in 3D.** *BMC Bioinformatics.*, 8 Suppl 4:S10. *PMCID: PMC1892080.*  
Yoon, S., Ebert, J., Chung, E., De Micheli, G., Altman, R.  
2007
- **PharmGKB: integration, aggregation, and annotation of pharmacogenomic data and knowledge.** *Clin Pharmacol Ther.*  
Hodge, A., Altman, R., Klein, T.  
2007; 1 (81): 21-4
- **ST Weissandl Zineh for the Pharmacogenetics Research Network. The Pharmacogenetics Research Network: From SNP Discovery to Clinical Drug Response.** *Clinical Pharmacology & Therapeutics.*  
Giacomini, K. M., Brett, C. M., Altman, R. B., Benowitz, N. L., Dolan, M. E., Flockhart, D. A.

2007; 81: 328-345

- **The FEATURE framework for protein function annotation: modelling new functions, improving performance, and extending to novel applications** *BMC GENOMICS*  
Halperin, I., Glazer, D. S., Wu, S., Altman, R. B.  
2007; 9
- **Extracting Subject Demographic Information From Abstracts of Randomized Clinical Trial Reports** *12th World Congress on Health (Medical) Informatics*  
xu, r., Garten, Y., Supekar, K. S., Das, A. K., Altman, R. B., Garber, A. M.  
I O S PRESS.2007: 550-554
- **Clustering protein environments for function prediction: finding PROSITE motifs in 3D** *2nd Automated Function Prediction Meeting*  
Yoon, S., Ebert, J. C., Chung, E., De Micheli, G., Altman, R. B.  
BIOMED CENTRAL LTD.2007
- **Integrating large-scale genotype and phenotype data** *OMICS-A JOURNAL OF INTEGRATIVE BIOLOGY*  
Hernandez-Boussard, T., Woon, M., Klein, T. E., Altman, R. B.  
2006; 10 (4): 545-554
- **Pharmacogenomics: Challenges and opportunities** *ANNALS OF INTERNAL MEDICINE*  
Roden, D. M., Altman, R. B., Benowitz, N. L., Flockhart, D. A., Giacomini, K. M., Johnson, J. A., Krauss, R. M., McLeod, H. L., Ratain, M. J., Relling, M. V., Ring, H. Z., Shuldiner, A. R., Weinshilboum, et al  
2006; 145 (10): 749-757
- **Annual progress in bioinformatics 2006** *BRIEFINGS IN BIOINFORMATICS*  
Altman, R. B.  
2006; 7 (3): 209-210
- **The incidentalome - A threat to genomic medicine** *JAMA-JOURNAL OF THE AMERICAN MEDICAL ASSOCIATION*  
Kohane, I. S., Masys, D. R., Altman, R. B.  
2006; 296 (2): 212-215
- **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*  
Laederach, A., Shcherbakova, I., Liang, M. P., Brenowitz, M., Altman, R. B.  
2006; 358 (4): 1179-1190
- **Delivering diverse data to multiple audiences: the PharmGKB model** *SCIENTIST*  
Altman, R. B.  
2006; 20 (4): 49-50
- **Choosing SNPs using feature selection.** *Journal of bioinformatics and computational biology*  
Phuong, T. M., Lin, Z., Altman, R. B.  
2006; 4 (2): 241-257
- **The RNA Ontology Consortium: An open invitation to the RNA community** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Leontis, N. B., Altman, R. B., Berman, H. M., Brenner, S. E., Brown, J. W., Engelke, D. R., Harvey, S. C., Holbrook, S. R., Jossinet, F., Lewis, S. E., Major, F., Mathews, D. H., Richardson, et al  
2006; 12 (4): 533-541
- **Pharmacogenomics: The relevance of emerging genotyping technologies.** *MLO: medical laboratory observer*  
Hernandez-Boussard, T., Klein, T. E., Altman, R. B.  
2006; 38 (3): 24-?
- **Drug targets for Plasmodium falciparum: A post-genomic review/survey** *MINI-REVIEWS IN MEDICINAL CHEMISTRY*  
Yeh, I., Altman, R. B.  
2006; 6 (2): 177-202
- **A call for the creation of personalized medicine databases** *NATURE REVIEWS DRUG DISCOVERY*  
Gurwitz, D., Lunshof, J. E., Altman, R. B.

---

2006; 5 (1): 23-26

- **Proceedings of Pacific Symposium on Biocomputing 2006.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2006
- **Physics-based simulation of biological structures** *3rd IEEE International Symposium on Biomedical Imaging*  
Delp, S. L., Anderson, F. C., Altman, R. B.  
IEEE.2006: 802–803
- **Structural characterization of proteins using residue environments** *PROTEINS-STRUCTURE FUNCTION AND BIOINFORMATICS*  
Mooney, S. D., Liang, M. H., DeConde, R., Altman, R. B.  
2005; 61 (4): 741-747
- **Time to organize the bioinformatics resourceome** *PLOS COMPUTATIONAL BIOLOGY*  
Cannata, N., Merelli, E., Altman, R. B.  
2005; 1 (7): 531-533
- **Health-information altruists - A potentially critical resource** *NEW ENGLAND JOURNAL OF MEDICINE*  
Kohane, I. S., Altman, R. B.  
2005; 353 (19): 2074-2077
- **A statistical approach to scanning the biomedical literature for pharmacogenetics knowledge** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Rubin, D. L., Thorn, C. F., Klein, T. E., Altman, R. B.  
2005; 12 (2): 121-129
- **Using Petri net tools to study properties and dynamics of biological systems** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Peleg, M., Rubin, D., Altman, R. B.  
2005; 12 (2): 181-199
- **SAFA: Semi-automated footprinting analysis software for high-throughput quantification of nucleic acid footprinting experiments** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Das, R., Laederach, A., Pearlman, S. M., Herschlag, D., Altman, R. B.  
2005; 11 (3): 344-354
- **PharmGKB: the pharmacogenetics and pharmacogenomics knowledge base.** *Methods in molecular biology (Clifton, N.J.)*  
Thorn, C. F., Klein, T. E., Altman, R. B.  
2005; 311: 179-191
- **Proceedings of Pacific Symposium on Biocomputing 2005.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2005
- **PharmGKB: The Pharmacogenetics and Pharmacogenomics Knowledge Base.**  
Thorn, C., Klein, T., Altman, R.  
edited by Innocenti, F.  
2005
- **Choosing SNPs Using Feature Selection.**  
Phuong, T., Lin, Z., Altman, R.  
2005
- **Introduction to ontologies in biomedicine: from powertools to assistants.** *In Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics.*  
Altman, R.  
Wiley Online Library..2005: 1
- **PharmGKB: The Pharmacogenetics and Pharmacogenomics Knowledge Base.** *Pharmacogenomics: Methods and Applications*  
Thorn, C., Klein, T., Altman, R.

edited by Innocenti, F.  
Totowa: Humana Press..2005: 177-192

- **Challenges in creating an infrastructure for physics-based simulation of biological structures** *IEEE Computational Systems Bioinformatics Conference*  
Altman, R. B.  
IEEE COMPUTER SOC.2005: 3-3
- **Biomedical term mapping databases** *NUCLEIC ACIDS RESEARCH*  
Wren, J. D., Chang, J. T., Pustejovsky, J., Adar, E., Garner, H. R., Altman, R. B.  
2005; 33: D289-D293
- **Choosing SNPs using feature selection** *IEEE Computational Systems Bioinformatics Conference*  
Phuong, T. M., Lin, Z., Altman, R. B.  
IEEE COMPUTER SOC.2005: 301-309
- **Finding haplotype tagging SNPs by use of principal components analysis** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Lin, Z., Altman, R. B.  
2004; 75 (5): 850-861
- **Computational functional genomics** *IEEE SIGNAL PROCESSING MAGAZINE*  
Liang, M. P., Troyanskaya, O. G., Laederach, A., Brutlag, D. L., Altman, R. B.  
2004; 21 (6): 62-69
- **Tools for loading MEDLINE into a local relational database** *BMC BIOINFORMATICS*  
Oliver, D. E., Bhalotia, G., Schwartz, A. S., Altman, R. B., Hearst, M. A.  
2004; 5
- **Approaches for protecting privacy in the genomic era** *GENETIC ENGINEERING NEWS*  
Lin, Z., Owen, A. B., Altman, R. B.  
2004; 24 (17): 6-?
- **Extracting and characterizing gene-drug relationships from the literature** *PHARMACOGENETICS*  
Chang, J. T., Altman, R. B.  
2004; 14 (9): 577-586
- **Genomic research and human subject privacy** *SCIENCE*  
Lin, Z., Owen, A. B., Altman, R. B.  
2004; 305 (5681): 183-183
- **An "omics" view of drug development** *DRUG DEVELOPMENT RESEARCH*  
Altman, R. B., Rubin, D. L., Klein, T. E.  
2004; 62 (2): 81-85
- **Computational analysis of Plasmodium falciparum metabolism: Organizing genomic information to facilitate drug discovery** *GENOME RESEARCH*  
Yeh, W., Hanekamp, T., Tsoka, S., Karp, P. D., Altman, R. B.  
2004; 14 (5): 917-924
- **Training the next generation of informaticians: The impact of "BISTI" and bioinformatics - A report from the American College of Medical Informatics** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Friedman, C. P., Altman, R. B., Kohane, I. S., McCormick, K. A., Miller, P. L., Ozbolt, J. G., Shortliffe, E. H., Stormo, G. D., Szczepaniak, M. C., Tuck, D., Williamson, J.  
2004; 11 (3): 167-172
- **Eukaryotic regulatory element conservation analysis and identification using comparative genomics** *GENOME RESEARCH*  
Liu, Y. Y., Liu, X. S., Wei, L. P., Altman, R. B., Batzoglou, S.  
2004; 14 (3): 451-458
- **Editorial: Building successful biological databases** *BRIEFINGS IN BIOINFORMATICS*  
Altman, R. B.

2004; 5 (1): 4-5

- **GAPSCORE: finding gene and protein names one word at a time** *BIOINFORMATICS*  
Chang, J. T., Schutze, H., Altman, R. B.  
2004; 20 (2): 216-225
- **Using surface envelopes for discrimination of molecular models** *PROTEIN SCIENCE*  
Dugan, J. M., Altman, R. B.  
2004; 13 (1): 15-24
- **Modeling and analyzing biomedical processes using workflow/Petri Net models and tools** *11th World Congress on Medical Informatics*  
Peleg, M., Tu, S., Manindroo, A., Altman, R. B.  
I O S PRESS.2004: 74-78
- **Proceedings of Pacific Symposium on Biocomputing 2004.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2004
- **Building successful biological databases.** *Brief Bioinform.*  
Altman, R.  
2004; 1 (5): 4-5
- **A resource to acquire and summarize pharmacogenetics knowledge in the literature** *11th World Congress on Medical Informatics*  
Rubin, D. L., Carrillo, M., Woon, M., Conroy, J., Klein, T. E., Altman, R. B.  
I O S PRESS.2004: 793-797
- **PharmGKB: the pharmacogenetics and pharmacogenomics knowledge base** *PHARMACOGENOMICS JOURNAL*  
Klein, T. E., Altman, R. B.  
2004; 4 (1): 1-1
- **Ribosomal dynamics inferred from variations in experimental measurements** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Gabashvili, I. S., Whirl-Carrillo, M., Bada, M., Banatao, D. R., Altman, R. B.  
2003; 9 (11): 1301-1307
- **MutDB: annotating human variation with functionally relevant data** *BIOINFORMATICS*  
Mooney, S. D., Altman, R. B.  
2003; 19 (14): 1858-1860
- **Investigating hypoxic tumor physiology through gene expression patterns** *ONCOGENE*  
Denko, N. C., Fontana, L. A., Hudson, K. M., Sutphin, P. D., Raychaudhuri, S., Altman, R., Giaccia, A. J.  
2003; 22 (37): 5907-5914
- **Pharmacokinetics of oral gallium maltolate administered in a single or multiple dose schedule in patients with Paget's disease of bone or primary hyperparathyroidism: A pilot study.**  
Lum, B. L., Gottlieb, A., Altman, R., Sayre, P. H., Valone, F.  
AMER SOC BONE & MINERAL RES.2003: S391
- **Large scale study of protein domain distribution in the context of alternative splicing** *NUCLEIC ACIDS RESEARCH*  
Liu, S., Altman, R. B.  
2003; 31 (16): 4828-4835
- **Microenvironment analysis and identification of magnesium binding sites in RNA** *NUCLEIC ACIDS RESEARCH*  
Banatao, D. R., Altman, R. B., Klein, T. E.  
2003; 31 (15): 4450-4460
- **The computational analysis of scientific literature to define and recognize gene expression clusters** *NUCLEIC ACIDS RESEARCH*  
Raychaudhuri, S., Chang, J. T., Imam, F., Altman, R. B.  
2003; 31 (15): 4553-4560
- **A Bayesian framework for combining heterogeneous data sources for gene function prediction (in *Saccharomyces cerevisiae*)** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

- Troyanskaya, O. G., Dolinski, K., Owen, A. B., Altman, R. B., Botstein, D.  
2003; 100 (14): 8348-8353
- **Identification of promoter regions in the human genome by using a retroviral plasmid library-based functional reporter gene assay** *GENOME RESEARCH*  
Khambata-Ford, S., Liu, Y. Y., Gleason, C., Dickson, M., Altman, R. B., Batzoglu, S., Myers, R. M.  
2003; 13 (7): 1765-1774
  - **Inclusion of textual documentation in the analysis of multidimensional data sets: Application to gene expression data** *MACHINE LEARNING*  
Raychaudhuri, S., Schutze, H., Altman, R. B.  
2003; 52 (1-2): 119-145
  - **WebFEATURE: an interactive web tool for identifying and visualizing functional sites on macromolecular structures** *NUCLEIC ACIDS RESEARCH*  
Liang, M. P., Banatao, D. R., Klein, T. E., Brutlag, D. L., Altman, R. B.  
2003; 31 (13): 3324-3327
  - **Genetic sequence data for pharmacogenomics** *CURRENT OPINION IN DRUG DISCOVERY & DEVELOPMENT*  
Altman, R. B.  
2003; 6 (3): 297-303
  - **A functional analysis of disease-associated mutations in the androgen receptor gene** *NUCLEIC ACIDS RESEARCH*  
Mooney, S. D., Klein, T. E., Altman, R. B., Trifiro, M. A., GOTTLIEB, B.  
2003; 31 (8)
  - **Recognizing complex, asymmetric functional sites in protein structures using a Bayesian scoring function.** *Journal of bioinformatics and computational biology*  
Wei, L., Altman, R. B.  
2003; 1 (1): 119-138
  - **Complexities of managing biomedical information.** *Omics : a journal of integrative biology*  
Altman, R. B.  
2003; 7 (1): 127-129
  - **A literature-based method for assessing the functional coherence of a gene group** *BIOINFORMATICS*  
Raychaudhuri, S., Altman, R. B.  
2003; 19 (3): 396-401
  - **Mining heterogeneous ribosomal structure data** *47th Annual Meeting of the Biophysical-Society*  
Gabashvili, I. S., Whirl-Carrillo, M., Bada, M., Banatao, D. R., Altman, R. B.  
CELL PRESS.2003: 463A-463A
  - **Knowledge acquisition, consistency checking and concurrency control for Gene Ontology (GO)** *BIOINFORMATICS*  
Yeh, I., Karp, P. D., Noy, N. F., Altman, R. B.  
2003; 19 (2): 241-248
  - **Indexing pharmacogenetic knowledge on the World Wide Web** *PHARMACOGENETICS*  
Altman, R. B., Flockhart, D. A., Sherry, S. T., Oliver, D. E., Rubin, D. L., Klein, T. E.  
2003; 13 (1): 3-5
  - **Proceedings of Pacific Symposium on Biocomputing 2003.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2003
  - **A Personalized and Automated dbSNP Surveillance System.**  
Liu, S., Lin, S., Woon, M., Klein, T., Altman, R.  
2003
  - **Bayesian framework for combining heterogeneous data sources for gene function prediction (in *Saccharomyces cerevisiae*).**  
Troyanskaya, O., Dolinski, K., Owen, A., Altman, R., Botstein, D.

2003

- **The expanding scope of bioinformatics: sequence analysis and beyond.** *Heredity*  
Altman, R.  
2003; 5 (90): 345
- **Preface.** *Bioinformatics and Functional Genomics.*  
Altman, R., In Pevsner, J.  
2003
- **Recognizing Complex, Asymmetric Functional Sites in Protein Structures Using a Bayesian Scoring Function.** *Journal of Bioinformatics and Computational Biology*  
Wei, L., Altman, R.  
2003; 1 (1): 119-138
- **Automatic construction of 3D structural motifs for protein function prediction** *2nd International Computational Systems Bioinformatics Conference*  
Liang, M. P., Brutlag, D. L., Altman, R. B.  
IEEE COMPUTER SOC.2003: 613-614
- **A personalized and automated dbSNP surveillance system** *2nd International Computational Systems Bioinformatics Conference*  
Liu, S., Lin, S., Woon, M., Klein, T. E., Altman, R. B.  
IEEE COMPUTER SOC.2003: 132-136
- **Defining bioinformatics and structural bioinformatics.** *Methods of biochemical analysis*  
Altman, R. B., Dugan, J. M.  
2003; 44: 3-14
- **Automated construction of structural motifs for predicting functional sites on protein structures.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Liang, M. P., Brutlag, D. L., Altman, R. B.  
2003: 204-215
- **Qualitative models of molecular function: Linking genetic polymorphisms of tRNA to their functional sequelae** *PROCEEDINGS OF THE IEEE*  
Peleg, M., Gabashvili, I. S., Altman, R. B.  
2002; 90 (12): 1875-1886
- **Creating an online dictionary of abbreviations from MEDLINE** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Chang, J. T., Schutze, H., Altman, R. B.  
2002; 9 (6): 612-620
- **Nonparametric methods for identifying differentially expressed genes in microarray data** *BIOINFORMATICS*  
Troyanskaya, O. G., Garber, M. E., Brown, P. O., Botstein, D., Altman, R. B.  
2002; 18 (11): 1454-1461
- **Using text analysis to identify functionally coherent gene groups** *GENOME RESEARCH*  
Raychaudhuri, S., Schutze, H., Altman, R. B.  
2002; 12 (10): 1582-1590
- **Promises of text processing: natural language processing meets AI** *DRUG DISCOVERY TODAY*  
Chang, J. T., Altman, R. B.  
2002; 7 (19): 992-993
- **Emerging scientific applications in data mining** *COMMUNICATIONS OF THE ACM*  
Han, J. W., Altman, R. B., Kumar, V., Mannila, H., Pregibon, D.  
2002; 45 (8): 54-58
- **Determining the genomic locations of repetitive DNA sequences with a whole-genome microarray: IS6110 in Mycobacterium tuberculosis** *JOURNAL OF CLINICAL MICROBIOLOGY*  
Kivi, M., Liu, X. M., Raychaudhuri, S., Altman, R. B., Small, P. M.

2002; 40 (6): 2192-2198

- **RNAML: A standard syntax for exchanging RNA information** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Waugh, A., Gendron, P., Altman, R., Brown, J. W., Case, D., GAUTHERET, D., Harvey, S. C., Leontis, N., Westbrook, J., Westhof, E., Zuker, M., Major, F.  
2002; 8 (6): 707-717
- **Modelling biological processes using workflow and Petri Net models** *BIOINFORMATICS*  
Peleg, M., Yeh, I., Altman, R. B.  
2002; 18 (6): 825-837
- **Mining biochemical information: Lessons taught by the ribosome** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Whirl-Carrillo, M., Gabashvili, I. S., Bada, M., Banatao, D. R., Altman, R. B.  
2002; 8 (3): 279-289
- **PharmGKB: The Pharmacogenetics Knowledge Base** *NUCLEIC ACIDS RESEARCH*  
Hewett, M., Oliver, D. E., Rubin, D. L., Easton, K. L., Stuart, J. M., Altman, R. B., Klein, T. E.  
2002; 30 (1): 163-165
- **Qualitative models of molecular function: linking genetic polymorphisms of tRNA to their functional sequelae.**  
Peleg, M., Gabashvili, I., S., Altman, R.  
edited by Akay, M.  
2002
- **Using Binning to Maintain Confidentiality of Medical Data.**  
Lin, Z., Hewett, M., Altman  
2002
- **Proceedings of Pacific Symposium on Biocomputing 2002.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2002
- **Scoring Functions Sensitive to Alignment Error Have a More Difficult Search: A Paradox for Threading.** *In Structures and Mechanisms*  
Chang, J., Carrillo, M., Waugh, A., Wei, L., Altman, R.  
ACS Publications..2002: 309-320
- **Representing genetic sequence data for pharmacogenomics: an evolutionary approach using ontological and relational models.** *Bioinformatics, 18 Suppl 1*  
Rubin, D., Shafa, F., Oliver, D., Hewett, M., Altman, R.  
2002: S207-S215
- **Preface. Microarrays For An Integrative Genomics.**  
Altman, R., In Kohane, I., Kho, A., Butte, A.  
2002: xii-xv
- **Emerging Scientific Applications in Data Mining.** *Communications of the ACM*  
Han, J., Altman, R., Kumar, V., Mannila, H., Pregibon, D.  
2002; 8 (45): 54-58
- **Scoring functions sensitive to alignment error have a more difficult search: A paradox for threading** *Symposium held in Honor of William N Lipscomb on Structures and Mechanisms*  
Chang, J., Carrillo, M. W., Waugh, A., Wei, L. P., Altman, R. B.  
AMER CHEMICAL SOC.2002: 309-320
- **Modeling molecular function and failure: Misreading of genetic code by the ribosome**  
Gabashvili, I. S., Peleg, M., Altman, R. B.  
CELL PRESS.2002: 167A-168A
- **Using binning to maintain confidentiality of medical data** *Annual Symposium of the American-Medical-Informatics-Association*  
Lin, Z., Hewett, M., Altman, R. B.

---

HANLEY & BELFUS INC MED PUBLISHERS.2002: 454-458

- **Representing genetic sequence data for pharmacogenomics: an evolutionary approach using ontological and relational models.** *Bioinformatics*  
Rubin, D. L., Shafa, F., Oliver, D. E., Hewett, M., Altman, R. B.  
2002; 18: S207-15
- **Automating data acquisition into ontologies from pharmacogenetics relational data sources using declarative object definitions and XML.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Rubin, D. L., Hewett, M., Oliver, D. E., Klein, T. E., Altman, R. B.  
2002: 88-99
- **Ontology development for a pharmacogenetics knowledge base.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Oliver, D. E., Rubin, D. L., Stuart, J. M., Hewett, M., Klein, T. E., Altman, R. B.  
2002: 65-76
- **Challenges for biomedical informatics and pharmacogenomics** *ANNUAL REVIEW OF PHARMACOLOGY AND TOXICOLOGY*  
Altman, R. B., Klein, T. E.  
2002; 42: 113-133
- **Associating genes with gene ontology codes using a maximum entropy analysis of biomedical literature** *GENOME RESEARCH*  
Raychaudhuri, S., Chang, J. T., Sutphin, P. D., Altman, R. B.  
2002; 12 (1): 203-214
- **Diversity of gene expression in adenocarcinoma of the lung** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Garber, M. E., Troyanskaya, O. G., Schluens, K., Petersen, S., Thaesler, Z., Pacyna-Gengelbach, M., van de Rijn, M., Rosen, G. D., Perou, C. M., Whyte, R. I., Altman, R. B., Brown, P. O., Botstein, et al  
2001; 98 (24): 13784-13789
- **Challenges for intelligent systems in biology** *IEEE INTELLIGENT SYSTEMS*  
Altman, R. B.  
2001; 16 (6): 14-18
- **Missing value estimation methods for DNA microarrays** *BIOINFORMATICS*  
Troyanskaya, O., Cantor, M., Sherlock, G., BROWN, P., Hastie, T., Tibshirani, R., Botstein, D., Altman, R. B.  
2001; 17 (6): 520-525
- **Whole-genome expression analysis: challenges beyond clustering** *CURRENT OPINION IN STRUCTURAL BIOLOGY*  
Altman, R. B., Raychaudhuri, S.  
2001; 11 (3): 340-347
- **Basic microarray analysis: grouping and feature reduction** *TRENDS IN BIOTECHNOLOGY*  
Raychaudhuri, S., Sutphin, P. D., Chang, J. T., Altman, R. B.  
2001; 19 (5): 189-193
- **ViewFeature: integrated feature analysis and visualization.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Banatao, D. R., Huang, C. C., Babbitt, P. C., Altman, R. B., Klein, T. E.  
2001: 240-250
- **Proceedings of Pacific Symposium on Biocomputing 2001.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2001
- **Using metacomputing tools to facilitate large scale analyses of biological databases.**  
Waugh, A., Williams, G., Wei, L., Altman, R.  
edited by Altman, R., Dunker, K., Hunter, L.  
2001
- **Challenges for intelligent systems in biology.** *IEEE Intelligent Systems*  
Altman, R.

2001; 6 (16): 14-18

- **Integrating genotype and phenotype information: an overview of the PharmGKB project.** *Pharmacogenetics Research Network and Knowledge Base. pharmacogenomics journal*  
Klein, T. E., Chang, J. T., Cho, M. K., Easton, K. L., FERGERSON, R., Hewett, M., Lin, Z., Liu, Y., Liu, S., Oliver, D. E., Rubin, D. L., SHAFA, F., Stuart, et al  
2001; 1 (3): 167-170
- **Constrained global optimization for estimating molecular structure from atomic distances** *JOURNAL OF COMPUTATIONAL BIOLOGY*  
Williams, G. A., Dugan, J. M., Altman, R. B.  
2001; 8 (5): 523-547
- **Including biological literature improves homology search.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Chang, J. T., Raychaudhuri, S., Altman, R. B.  
2001: 374-383
- **Using meta computing tools to facilitate large-scale analyses of biological databases.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Waugh, A., WILLIAMS, G. A., Wei, L., Altman, R. B.  
2001: 360-371
- **Biomedical computation at Stanford University: a larger umbrella for the future** *M D COMPUTING*  
Altman, R. B.  
2000; 17 (6): 35-37
- **The interactions between clinical informatics and bioinformatics: A case study** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Altman, R. B.  
2000; 7 (5): 439-443
- **Calculation of the relative geometry of tRNAs in the ribosome from directed hydroxyl-radical probing data** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Joseph, S., Whirl, M. L., Kondo, D., Noller, H. F., Altman, R. B.  
2000; 6 (2): 220-232
- **Computational modeling of structural experimental data** *RNA-LIGAND INTERACTIONS PT A*  
Bada, M. A., Altman, R. B.  
2000; 317: 470-491
- **The new peer review** *Annual Symposium of the American-Medical-Informatics-Association*  
Kohane, I. S., Altman, R. B.  
HANLEY & BELFUS INC.2000: 433-437
- **Proceedings of Pacific Symposium on Biocomputing 2000.**  
edited by Altman, R., Dunker, K., Hunter, L.  
2000
- **National Research Council Panel. Networking Health: Prescriptions for the Internet.**  
Altman, R. B.  
Washington, DC: National Academy Press..2000: 1
- **Bioinformatics. Medical Informatics: Computer Applications in Health Care**  
Altman, R.  
edited by Shortliffe, T., Wiederhold, G., Fagan, L.  
Heidelberg: Springer-Verlag..2000: 638-660
- **Calculation of the relative geometry of tRNAs in the ribosome from directed hydroxyl-radical probing data.** *RNA, PMID: PMC1369908.*  
Joseph, S., Carrillo, M., Kondo, H., Noller, H., Altman, R.  
2000; 6: 220-232

- **Pattern recognition of genomic features with microarrays: site typing of Mycobacterium tuberculosis strains.** *Proceedings. International Conference on Intelligent Systems for Molecular Biology*  
Raychaudhuri, S., Stuart, J. M., Liu, X., Small, P. M., Altman, R. B.  
2000; 8: 286-295
- **Principal components analysis to summarize microarray experiments: application to sporulation time series.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Raychaudhuri, S., Stuart, J. M., Altman, R. B.  
2000: 455-466
- **Generating interactive molecular documentaries using a library of graphical actions.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Pulavarthi, P., Chiang, R., Altman, R. B.  
2000: 266-277
- **AI in medicine - The spectrum of challenges from managed care to molecular medicine** *AI MAGAZINE*  
Altman, R. B.  
1999; 20 (3): 67-77
- **Automated diagnosis of data-model conflicts using metadata** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Chen, R. O., Altman, R. B.  
1999; 6 (5): 374-392
- **RiboWeb: An ontology-based system for collaborative molecular biology** *IEEE INTELLIGENT SYSTEMS & THEIR APPLICATIONS*  
Altman, R. B., Bada, M., Chai, X. Q., Carillo, M. W., Chen, R. O., Abernethy, N. F.  
1999; 14 (5): 68-76
- **Sophia: A flexible, Web-based knowledge server** *IEEE INTELLIGENT SYSTEMS & THEIR APPLICATIONS*  
Abernethy, N. F., Wu, J. J., Hewett, M., Altman, R. B.  
1999; 14 (4): 79-85
- **Are predicted structures good enough to preserve functional sites?** *STRUCTURE*  
Wei, L. P., Huang, E. S., Altman, R. B.  
1999; 7 (6): 643-650
- **Using imperfect secondary structure predictions to improve molecular structure computations** *BIOINFORMATICS*  
Chen, C. C., Singh, J. P., Altman, R. B.  
1999; 15 (1): 53-65
- **Proceedings of Pacific Symposium on Biocomputing 1999.**  
edited by Altman, R., Dunker, K., Hunter, L.  
1999
- **RiboWeb: An Ontology-Based System for Collaborative Molecular Biology.** *IEEE Intelligent Systems and Their Application*  
Altman, R., Chen, R., Abernethy, N., Bada, M.  
1999; 5 (14): 68-76
- **AI in medicine: The spectrum of challenges from managed care to molecular medicine.** *AI Magazine*  
Altman, R.  
1999; 3 (20): 67-77
- **Hierarchical organization of molecular structure computations** *JOURNAL OF COMPUTATIONAL BIOLOGY*  
Chen, C. C., Singh, J. P., Altman, R. B.  
1998; 5 (3): 409-422
- **Reuse, CORBA, and knowledge-based systems** *INTERNATIONAL JOURNAL OF HUMAN-COMPUTER STUDIES*  
Gennari, J. H., Cheng, H. N., Altman, R. B., Musen, M. A.  
1998; 49 (4): 523-546

- **Recognizing protein binding sites using statistical descriptions of their 3D environments.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Wei, L., Altman, R. B.  
1998: 497-508
- **Determination of the Spatial Distribution of Protein Structure Using Solution Data.**  
Altman, R., Duncan, B., Brinkley, J., Buchanan, B., Jardetzky, O.  
edited by Jaroszewski, J., Schaumburg, K., Kofod, H.  
1998
- **Bioinformatics in Support of Molecular Medicine.**  
Altman, R.  
1998
- **SOPHIA: Providing Basic Knowledge Services with a Common DBMS.**  
Abernethy, N., Altman, R.  
edited by Borgida, A., Chaudhri, V., Staudt, M.  
1998
- **MHCWeb: Converting a WWW Database into a Knowledge-based Collaborative Environment.**  
Hon, L., Abernethy, N., Brusica, V., Chai, J., Altman, R.  
1998
- **Updated Bibliography Using the RELATED ARTICLES Function within PubMed.**  
Liu, X., Altman, R.  
1998
- **Graphical Style Sheets: Towards Reusable Representations of Biomedical Graphics.**  
Felciano, R., Altman, R.  
1998
- **Proceedings of Pacific Symposium on Biocomputing 1998.**  
edited by Altman, R., Dunker, K., Hunter, L.  
1998
- **PROTEAN: Deriving Protein Structure from Constraints.** *Blackboard Systems*  
Hayes-Roth, B., Buchanan, B., Lichtarge, O., Hewett, M., Altman, R., Brinkley, J.  
edited by Engelmores, R., Morgan, A.  
Workingham: Addison-Wesley..1998: 417-431
- **Probabilistic and Statistical Descriptions of Protein Structure.** *Computational Biology: Pattern Analysis and Machine Learning Methods*  
Wei, L., Chang, J., Altman, R.  
edited by Salzberg, S., Searls, D., Kasif, S.  
London, UK: Elsevier Science..1998: 207-225
- **The Hierarchical Organization of Molecular Structure Computation.** *In: RECOMB-98*  
Chen, C., Singh, J., Altman, R.  
New York: ACM Press..1998: 51-59
- **A Curriculum for Bioinformatics: The Time is Ripe.** *Bioinformatics*  
Altman, R.  
1998; 7 (14): 549-550
- **The Hierarchical Organization of Molecular Structure Computations.** *Journal of Computational Biology*  
Chen, C., Singh, J., Altman, R.  
1998; 3 (5): 409-422
- **Updating a bibliography using the RELATED ARTICLES function within PubMed** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Liu, X. L., Altman, R. B.

1998: 750-754

- **MHCWeb: Converting a WWW database into a knowledge-based collaborative environment** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Hon, L., Abernethy, N. F., Brusica, V., Chai, J., Altman, R. B.  
1998: 947-951
- **Bioinformatics in support of molecular medicine** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*  
Altman, R. B.  
1998: 53-61
- **A surface measure for probabilistic structural computations.** *Proceedings / ... International Conference on Intelligent Systems for Molecular Biology ; ISMB. International Conference on Intelligent Systems for Molecular Biology*  
Schmidt, J. P., Chen, C. C., Cooper, J. L., Altman, R. B.  
1998; 6: 148-156
- **RNA secondary structure as a reusable interface to biological information resources (Reprinted from Gene-Combis, vol 190, pg GC59-GC70, 1997)** *GENE*  
Felciano, R. M., Chen, R. O., Altman, R. B.  
1997; 190 (2): GC59–GC70
- **Informatics in the care of patients: Ten notable challenges** *WESTERN JOURNAL OF MEDICINE*  
Altman, R. B.  
1997; 166 (2): 118-122
- **LPFC: An Internet library of protein family core structures** *PROTEIN SCIENCE*  
Schmidt, R., Gerstein, M., Altman, R. B.  
1997; 6 (1): 246-248
- **Proceedings of Pacific Symposium on Biocomputing 1997.**  
edited by Altman, R., Dunker, K., Hunter, L.  
1997
- **RiboWeb: Linking Structural Computations to a Knowledge Base of Published Experimental Data.**  
Chen, R., Felciano, R., Altman, R.  
1997
- **Standardized Representations of the Literature: Combining Diverse Sources of Ribosomal Data.**  
Altman, R., Abernethy, N., Chen, R.  
1997
- **Using the Radial Distribution of Physical Features to Compare Amino Acid Environments.**  
Wei, L., Altman, R., Chang, J.  
edited by Altman, R., Dunker, K., Hunter, L.  
1997
- **Using the radial distributions of physical features to compare amino acid environments and align amino acid sequences.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Wei, L., Altman, R. B., Chang, J. T.  
1997: 465-476
- **Standardized representations of the literature: Combining diverse sources of ribosomal data** *5th International Conference on Intelligent Systems for Molecular Biology (ISMB-97)*  
Altman, R. B., Abernethy, N. F., Chen, R. O.  
AMER ASSOC ARTIFICIAL INTELLIGENCE.1997: 15–24
- **RIBOWEB: Linking structural computations to a knowledge base of published experimental data** *5th International Conference on Intelligent Systems for Molecular Biology (ISMB-97)*  
Chen, R. O., Felciano, R., Altman, R. B.  
AMER ASSOC ARTIFICIAL INTELLIGENCE.1997: 84–87

- **RNA secondary structure as a reusable interface to biological information resources** *GENE-COMBIS*  
Felciano, R. M., Chen, R. O., Altman, R. B.  
1997; 190: GC59-GC70
- **Computational methods for defining the allowed conformational space of 16S rRNA based on chemical footprinting data** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Fink, D. L., Chen, R. O., Noller, H. F., Altman, R. B.  
1996; 2 (9): 851-866
- **Constraining volume by matching the moments of a distance distribution** *COMPUTER APPLICATIONS IN THE BIOSCIENCES*  
Chen, C. C., Chen, R. O., Altman, R. B.  
1996; 12 (4): 319-326
- **Images in clinical medicine. Knotted umbilical cord.** *New England journal of medicine*  
Altman, R. B., Merino, J. E.  
1996; 334 (9): 573-?
- **Knotted umbilical cord** *NEW ENGLAND JOURNAL OF MEDICINE*  
Altman, R. B., Merino, J. E.  
1996; 334 (9): 573-573
- **An evaluation of the TransFER model for sharing clinical decision-support applications.** *Proceedings : a conference of the American Medical Informatics Association / ... AMIA Annual Fall Symposium. AMIA Fall Symposium*  
Sujansky, W., Altman, R.  
1996: 468-472
- **Using tee radial distributions of physical features to compare amino acid environments and align amino acid sequences** *2nd Pacific Symposium on Biocomputing (PSB)*  
Wei, L. P., Altman, R. B., Chang, J. T.  
WORLD SCIENTIFIC PUBL CO PTE LTD.1996: 465-476
- **Conserved Features in the Active Site of Nonhomologous Serine Proteases.** *Folding & Design*  
Bagley, S., Altman, R.  
1996; 5 (1): 371-379
- **A programming course in bioinformatics for computer and information science students.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Altman, R. B., Koza, J.  
1996: 73-84
- **Conserved features in the active site of nonhomologous serine proteases** *FOLDING & DESIGN*  
Bagley, S. C., Altman, R. B.  
1996; 1 (5): 371-379
- **Lamprey: tracking users on the World Wide Web.** *Proceedings : a conference of the American Medical Informatics Association / ... AMIA Annual Fall Symposium. AMIA Fall Symposium*  
Felciano, R. M., Altman, R. B.  
1996: 757-761
- **Using a measure of structural variation to define a core for the globins** *COMPUTER APPLICATIONS IN THE BIOSCIENCES*  
Gerstein, M., Altman, R. B.  
1995; 11 (6): 633-644
- **AVERAGE CORE STRUCTURES AND VARIABILITY MEASURES FOR PROTEIN FAMILIES - APPLICATION TO THE IMMUNOGLOBULINS** *JOURNAL OF MOLECULAR BIOLOGY*  
Gerstein, M., Altman, R. B.  
1995; 251 (1): 161-175
- **METHODS FOR DISPLAYING MACROMOLECULAR STRUCTURAL UNCERTAINTY - APPLICATION TO THE GLOBINS** *JOURNAL OF MOLECULAR GRAPHICS & MODELLING*  
Altman, R. B., Hughes, C., Gerstein, M. B.

1995; 13 (3): 142-152

- **A PROBABILISTIC APPROACH TO DETERMINING BIOLOGICAL STRUCTURE - INTEGRATING UNCERTAIN DATA SOURCES** *INTERNATIONAL JOURNAL OF HUMAN-COMPUTER STUDIES*  
ALTMAN, R. B.  
1995; 42 (6): 593-616
- **CHARACTERIZING THE MICROENVIRONMENT SURROUNDING PROTEIN SITES** *PROTEIN SCIENCE*  
Bagley, S. C., Altman, R. B.  
1995; 4 (4): 622-635
- **Characterizing oriented protein structural sites using biochemical properties.** *Proceedings / ... International Conference on Intelligent Systems for Molecular Biology ; ISMB. International Conference on Intelligent Systems for Molecular Biology*  
Bagley, S. C., Wei, L., Cheng, C., Altman, R. B.  
1995; 3: 12-20
- **SHAPE-BASED MODELS FOR INTERACTIVE SEGMENTATION OF MEDICAL IMAGES** *Conference on Image Processing - Medical Imaging 1995*  
Hinshaw, K. P., Altman, R. B., Brinkley, J. F.  
SPIE - INT SOC OPTICAL ENGINEERING.1995: 771-780
- **Proceedings of the Third International Conference on Intelligent Systems for Molecular Biology (Cambridge, England).**  
edited by Rawlings, C., Clark, D., Altman, R.  
1995
- **Computing the Structure of Large Complexes: Applying Constraint Satisfaction Techniques to Modeling the 16S Ribosomal RNA.** *Biomolecular NMR Spectroscopy*  
Chen, R., Fink, D., Altman, R.  
edited by Markley, J., Opella, S.  
London: Oxford University Press..1995: 279-299
- **A Probabilistic Approach to Determining Biological Structure: Integrating Uncertain Data Sources.** *International Journal of Human Computer Studies*  
Altman, R.  
1995; 42: 593-616
- **Constraint satisfaction techniques for modeling large complexes: application to the central domain of 16S ribosomal RNA.** *Proceedings / ... International Conference on Intelligent Systems for Molecular Biology ; ISMB. International Conference on Intelligent Systems for Molecular Biology*  
Altman, R. B., Weiser, B., Noller, H. F.  
1994; 2: 10-18
- **Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology (Stanford, CA).**  
edited by Altman, R., Brutlag, D., Karp, P.  
1994
- **Compositional Characteristics of Disordered Regions in Proteins.** *Protein and Peptide Letters*  
Altman, R., Hughes, C., Jardetzky, O.  
1994; 2 (1): 120-127
- **PARALLEL PROTEIN STRUCTURE DETERMINATION FROM UNCERTAIN DATA** *Supercomputing 94*  
Chen, C. C., Singh, J. P., Poland, W. B., Altman, R. B.  
I E E E, COMPUTER SOC PRESS.1994: 570-579
- **PROBABILISTIC CONSTRAINT SATISFACTION - APPLICATION TO RADIOSURGERY** *18th Annual Symposium on Computer Applications in Medical Care - Transforming Information, Changing Health Care*  
Altman, R. B., Tombropoulos, R.  
BMJ PUBLISHING GROUP.1994: 780-784
- **EXTRACTION OF SNOMED CONCEPTS FROM MEDICAL RECORD TEXTS** *18th Annual Symposium on Computer Applications in Medical Care - Transforming Information, Changing Health Care*  
Oliver, D. E., Altman, R. B.

BMJ PUBLISHING GROUP.1994: 179-183

- **A SURVEY OF PATIENT ACCESS TO ELECTRONIC MAIL - ATTITUDES, BARRIERS, AND OPPORTUNITIES** *18th Annual Symposium on Computer Applications in Medical Care - Transforming Information, Changing Health Care*  
Fridsma, D. B., Ford, P., Altman, R.  
BMJ PUBLISHING GROUP.1994: 15-19
- **TOWARDS A STANDARD QUERY MODEL FOR SHARING DECISION-SUPPORT APPLICATIONS** *18th Annual Symposium on Computer Applications in Medical Care - Transforming Information, Changing Health Care*  
Sujansky, W., Altman, R.  
BMJ PUBLISHING GROUP.1994: 325-331
- **Finding an average core structure: application to the globins.** *Proceedings / ... International Conference on Intelligent Systems for Molecular Biology ; ISMB. International Conference on Intelligent Systems for Molecular Biology*  
Altman, R. B., Gerstein, M.  
1994; 2: 19-27
- **Probabilistic structure calculations: a three-dimensional tRNA structure from sequence correlation data.** *Proceedings / ... International Conference on Intelligent Systems for Molecular Biology ; ISMB. International Conference on Intelligent Systems for Molecular Biology*  
Altman, R. B.  
1993; 1: 12-20
- **STRUCTURAL UNCERTAINTY OF PROTEINS IN SOLUTION BY NMR - A REEVALUATION OF THE STRUCTURE OF THE LAC REPRESSOR HEADPIECE** *APPLIED MAGNETIC RESONANCE*  
Altman, R. B., Pachter, R., Jardetzky, O.  
1993; 4 (4): 441-460
- **Probabilistic constraint satisfaction with structural models: application to organ modeling by radial contours.** *Proceedings / the ... Annual Symposium on Computer Application [sic] in Medical Care. Symposium on Computer Applications in Medical Care*  
Altman, R. B., Brinkley, J. F.  
1993: 492-496
- **A SYSTEMATIC COMPARISON OF 3 STRUCTURE DETERMINATION METHODS FROM NMR DATA - DEPENDENCE UPON QUALITY AND QUANTITY OF DATA** *JOURNAL OF BIOMOLECULAR NMR*  
Liu, Y. J., Zhao, D. Q., Altman, R., Jardetzky, O.  
1992; 2 (4): 373-388
- **THE SOLUTION STRUCTURES OF ESCHERICHIA-COLI-TRP REPRESSOR AND TRP APOREPRESSOR AT AN INTERMEDIATE RESOLUTION** *EUROPEAN JOURNAL OF BIOCHEMISTRY*  
Arrowsmith, C., Pachter, R., Altman, R., Jardetzky, O.  
1991; 202 (1): 53-66
- **COMPARISON OF THE NMR SOLUTION STRUCTURES OF CYCLOSPORINE-A DETERMINED BY DIFFERENT TECHNIQUES** *JOURNAL OF MAGNETIC RESONANCE*  
Pachter, R., Altman, R. B., Czaplicki, J., Jardetzky, O.  
1991; 92 (3): 468-479
- **Determination of Large Protein Structures from NMR Data: Definition of the Solution Structure of the TRP Repressor.** *Computational Aspects of the Study of Biological Macromolecules by NMR Spectroscopy*  
Altman, R., Arrowsmith, C., Pachter, R., Jardetzky, O.  
edited by Hoch, J., Poulsen, F., Redfield, C.  
New York: Plenum Publishing Corp..1991: 363-374
- **DETERMINATION OF LARGE PROTEIN STRUCTURES FROM NMR DATA - DEFINITION OF THE SOLUTION STRUCTURE OF THE TRP REPRESSOR** *NATO ADVANCED RESEARCH WORKSHOP ON COMPUTATIONAL ASPECTS OF THE STUDY OF BIOLOGICAL MACROMOLECULES BY NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY*  
Altman, R. B., Arrowsmith, C. H., Pachter, R., Jardetzky, O.  
PLENUM PRESS DIV PLENUM PUBLISHING CORP.1991: 363-374
- **SEQUENCE-SPECIFIC H-1-NMR ASSIGNMENTS AND SECONDARY STRUCTURE IN SOLUTION OF ESCHERICHIA-COLI TRP REPRESSOR** *BIOCHEMISTRY*  
Arrowsmith, C. H., Pachter, R., Altman, R. B., Iyer, S. B., Jardetzky, O.

1990; 29 (27): 6332-6341

- **PROTEAN - Part II: Molecular Structure Determination from Uncertain Data.** *Quantitative Computer Program Exchange Bulletin*  
Altman, R., Pachter, R., Carrara, E., Jardetzky, O.  
1990; 4 (10): 596
- **PROTEAN - Part I: Generating Ensembles of Stylized Molecular Fragments using Uncertain Constraints.** *Quantative Computer Program Exchange Bulletin*  
Carrara, E., Brinkley, J., Cornelius, C., Altman, R., Brugge, J., Pachter, R.  
1990; 4 (10): 596
- **NMR AND PROTEIN-STRUCTURE** *BIOFIZIKA*  
Jardetzky, O., Altman, R., Madrid, M.  
1989; 34 (5): 763-771
- **HEURISTIC REFINEMENT METHOD FOR DETERMINATION OF SOLUTION STRUCTURE OF PROTEINS FROM NUCLEAR-MAGNETIC-RESONANCE DATA** *METHODS IN ENZYMOLOGY*  
Altman, R. B., Jardetzky, O.  
1989; 177: 218-?
- **NMR AND PROTEIN-STRUCTURE** *24TH CONGRESS AMPERE : MAGNETIC RESONANCE AND RELATED PHENOMENA*  
Jardetzky, O., Altman, R., Madrid, M.  
ELSEVIER SCIENCE PUBL B V.1989: 401-412
- **DETERMINATION OF STRUCTURAL UNCERTAINTY FROM NMR AND OTHER DATA - THE LAC REPRESSOR HEADPIECE** *NATO ADVANCED STUDY INST AND 10TH COURSE OF THE INTERNATIONAL SCHOOL OF PURE AND APPLIED BIOSTRUCTURE : PROTEIN STRUCTURE AND ENGINEERING*  
Altman, R. B., Pachter, R., Jardetzky, O.  
PLENUM PRESS DIV PLENUM PUBLISHING CORP.1989: 79-95
- **Artificial Intelligence Techniques and NMR Spectroscopy: Application to the Structure of Proteins in Solution.** *Nuclear Magnetic Resonance: The Principles and Applications of NMR Spectroscopy and Imaging to Biomedical Research*  
Duncan, B., Brinkley, J., Altman, R., Buchanan, B., Jardetzky, O.  
edited by Pettegrew, J.  
New York: Springer-Verlag..1989: 99-123
- **The Determination of Structural Uncertainty from NMR and Other Data: The Lac Repressor Headpiece.** *Protein Structure and Engineering.*  
Altman, R., Pachter, R., Jardetzky, O.  
edited by Jardetzky, O.  
New York: Plenum Publishing Corp..1989: 1
- **The Heuristic Refinement Method for the Determination of the Solution Structure of Proteins from NMR Data.** *Nuclear Magnetic Resonance, Part B: Structure and Mechanisms (Methods in Enzymology)*  
Altman, R., Jardetzky, O.  
edited by Oppenheimer, N., James, T.  
New York: Academic Press..1989: 218-247
- **NMR and Protein Structure.** *Biofizika*  
Jardetzky, O., Altman, R., Madrid, M.  
1989; 5 (34): 763-771
- **HEURISTIC REFINEMENT METHOD FOR THE DERIVATION OF PROTEIN SOLUTION STRUCTURES - VALIDATION ON CYTOCHROME B-562** *JOURNAL OF CHEMICAL INFORMATION AND COMPUTER SCIENCES*  
Brinkley, J. F., Altman, R. B., Duncan, B. S., Buchanan, B. G., Jardetzky, O.  
1988; 28 (4): 194-210
- **The Heuristic Refinement Method for the Derivation of Protein Solution Structures: Validation on Cytochrome-b562.** *Journal of Chemical Info. & Computer Sciences*  
Brinkley, J., Altman, R., Duncan, B., Buchanan, B., Jardetzky, O.  
1988; 4 (28): 194-210

- **Positive Strand RNA Viruses**

Harrison, S., C., Sorger, P., K., Stockley, P., G., Hogle, J., Altman, R., Strong, R., K.  
1987

- **NEW STRATEGIES FOR THE DETERMINATION OF MACROMOLECULAR STRUCTURE IN SOLUTION** *JOURNAL OF BIOCHEMISTRY*

Altman, R. B., Jardetzky, O.  
1986; 100 (6): 1403-1423

- **PROTEAN: A New Method of Deriving Solution Structures of Proteins.** *Bulletin of Magnetic Resonance*

Duncan, B., Buchanan, B., Hayes-Roth, B., Lichtarge, O., Altman, R., Brinkley, J.  
1986; 8: 111-119

- **QUATERNARY STRUCTURAL-CHANGES IN ASPARTATE CARBAMOYLTRANSFERASE OF ESCHERICHIA-COLI AT PH 8.3 AND PH 5.8** *BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS*

Altman, R. B., Ladner, J. E., Lipscomb, W. N.  
1982; 108 (2): 592-595

## PRESENTATIONS

- TedMed 2015 Talk: What really happens when you mix medications? - TedMED 2015 (11/2015 - 11/1/2015)
- TedxStanford Talk: Personalized prescriptions - Stanford (6/2013 - 6/2013)