

## CURRICULUM VITAE

**Russ Biagio Altman, MD, PhD**

### LICENSURE AND CERTIFICATION:

1991 California State Medical Board, License G072413

### EDUCATION:

1983 A.B. Biochemistry and Molecular Biology, Harvard College;  
Cambridge, Massachusetts  
1989 Ph.D. Medical Information Sciences, Stanford University; Stanford,  
California  
1990 M.D. Stanford University; Stanford, California

### POSTDOCTORAL TRAINING:

1990 - 91 Internship, Internal Medicine, Stanford University Medical School;  
Stanford, California  
1991 - 92 Residency, Internal Medicine, Stanford University Medical  
School; Stanford, California

### BOARD ELIGIBILITY:

1992 Diplomate, American Board of Internal Medicine, Certificate  
#142388  
2002 Recertified November, 2002

### NON-ACADEMIC APPOINTMENTS:

1982 Undergraduate Research Assistant, Professor William N.  
Lipscomb (Nobel Laureate), Department of Chemistry, Harvard  
University; Cambridge, Massachusetts  
1982 - 83 Undergraduate Research Assistant, Professor Stephen C. Harrison,  
Department of Biochemistry and Molecular Biology, Harvard  
University; Cambridge, Massachusetts  
1984 - 89 Doctoral Research, Preceptors: Professor Bruce G. Buchanan,  
Stanford Departments of Computer Science and Medicine; and  
Professor Oleg Jardetzky, Stanford Magnetic Resonance  
Laboratory; Stanford, California  
1987 - 88 Principal Investigator for Pharmalogics Incorporated, Frederick J.  
Dotzler, Crosspoint Ventures, C.E.O.; Mountain View, California  
1989-92 Research Assistant, Post-Doctoral, Professor Oleg Jardetzky,  
Stanford Magnetic Resonance Laboratory; Stanford, California  
7/1/93 – 6/30/96 Assistant Director, Stanford Medical Scientist Training Program,  
Stanford University; Stanford, California  
7/1/96 – 6/30/00 Associate Director, Stanford Medical Scientist Training Program,  
Stanford University; Stanford, California

4/1/00 – Present      Director, Stanford Biomedical Informatics Training Program  
9/15/00 –Present      Director, Stanford Center for Biomedical Computation

**ACADEMIC APPOINTMENTS:**

9/1/92 - 8/31/95      Assistant Professor of Medicine (General Internal Medicine),  
Stanford University School of Medicine, Stanford, CA  
1/1/93 - 4/30/99      Assistant Professor of Computer Science (by courtesy), Stanford  
University, Stanford, CA.  
9/1/95 - 4/30/99      Assistant Professor of Medicine (General Internal Medicine),  
Stanford University School of Medicine, Stanford, CA  
5/1/99 - 8/31/01      Associate Professor of Medicine (Medical Informatics, General  
Internal Medicine) with tenure  
5/1/99 - 8/31/02      Associate Professor of Computer Science (by courtesy)  
9/1/01 - 11/01/04      Associate Professor of Genetics and Medicine (Medical  
Informatics, General Internal Medicine), Stanford University  
School of Medicine, Stanford, CA  
10/1/02 - 11/1/04      Associate Professor of Computer Science (by courtesy), Stanford  
University, Stanford, CA  
11/1/04-              Professor of Genetics, Medicine & (by courtesy) Computer  
Science, Stanford University, Stanford, CA

**HONORS AND AWARDS:**

1979              Awards for General Excellence, Regis High School; NY, NY.  
1979              Award for Excellence in Classical Greek Translation, Regis High  
School; New York, NY  
1983              Phi Beta Kappa, Harvard College Chapter; Boston, MA  
1983              Summa Cum Laude, Harvard College; Boston, MA  
1983              Medical Scientist Training Program, NIH Predoctoral Fellowship  
1987              Medical Information Sciences, Ph.D. oral exam passed *with  
distinction*  
1991              Howard Hughes Institute Post-Doctoral Fellowship  
1992              Finalist, Stanford Hospital Medical Resident Teaching Award  
1993              Charles E. Culpeper Foundation Medical Scholar  
1994              Nominated, Albert Gores University Teaching Award  
1996              National Science Foundation CAREER Award  
1997              Presidential Early Career Award for Scientists and Engineers  
1998              Stanford School of Medicine Hume Faculty Scholar  
1998              Western Society for Clinical Investigation, Young Investigator  
Award  
1998              Fellow, American College of Physicians  
1998              Fellow, American College of Medical Informatics  
2000              Stanford Graduate Teaching Award (first time awarded)

**MEMBERSHIPS:**

1987- American Association for Artificial Intelligence (AAAI)  
1991- 1993 Biomatrix Society  
1992- 2000 American Federation for Clinical Research (AFCR)  
1992- American Medical Informatics Association (AMIA)  
1992- American Association for the Advancement of Science (AAAS)  
1992- American College of Physicians  
1993- Protein Society  
1993- Physicians for a National Health Program  
1993- California Physician's Alliance  
1994- Association for Computing Machinery  
1995- 1996 American Educational Research Association  
1995- RNA Society  
1996- Institute of Electrical and Electronic Engineers (IEEE)  
1997- International Society for Computational Biology (ISCB)  
1997-2001 Society for General Internal Medicine (SGIM)

**RESEARCH INTERESTS:**

Bioinformatics  
Biomedical Informatics  
Pharmacogenomics  
Structural genomics  
Physics-based simulation  
RNA structure  
Functional genomics  
Malaria genomics  
Probabilistic representations of molecular structure  
Structured representations of the biomedical literature  
Analysis of biological structures  
High performance computing

**COMMITTEES, BOARDS, AND CONSULTANTSHIPS:**

1991 Committee for Residency Training and Clinical Service  
1991-1992 Physicians Advisory Committee to Stanford Hospital Information Systems  
1991- Admissions Committee, Stanford Medical Information Sciences Training Program (now Biomedical Informatics Training Program)  
1992-1998 Consultant, Medicus Venture Partners; Menlo Park, California  
1992-2001 Admissions Committee, Stanford Medical Scientist Training Program  
1993-1997 Stanford University Department of Medicine Credentials Committee  
1993-1997 Steering Committee, San Diego Supercomputer Center  
1993-1994 Organizing Committee, International Symposium on NMR (in honor of Oleg Jardetzky)

1993-1994	Organizing Committee, Second International Conference on Intelligent Systems for Molecular Biology; Stanford CA
1994-1995	Organizing Committee, Third International Conference on Intelligent Systems for Molecular Biology; Cambridge, England
1995-1997	Executive Committee, San Diego Supercomputer Center
1995-1997	University Senate Committee on Computing and Academic Information Systems
1995-1997	Advisory Committee to Chairman of Department of Medicine
1995-1997	Steering Committee, Intelligent Systems for Molecular Biology
1995-1998	Faculty Senate Committee on Academic Information Systems (C-ACIS)
1995-1997	President's Commission on Technology in Teaching and Learning, Stanford University
1996-	Organizing Committee, Pacific Symposium on Biocomputing
1996	LCME Accreditation Project, Library and Computer Resources Subcommittee & Graduate Education Subcommittee
1997	Organizer, RNA Society Workshop on Online Resources for RNA Science
1997	Dean's Task Force on Alumni, Stanford Medical School
1997	Dean's Task Force on the Future of PhD Education, Stanford Medical School
1997-	Board of Directors, International Society for Computational Biology
1997-2000	Chairman, Publications Committee, International Society for Computational Biology
1997-1998	Program Committee, AMIA Fall Symposium, 1998
1998-2001	Editorial Board, Journal of American Medical Informatics Association
1998-	Editorial Board, Bioinformatics
1998-2002	Thrust Leader, Molecular Sciences, NSF NPACI grant to San Diego Supercomputer Center
1999-2000	Member, National Research Council panel on Internet & Health
2000-	Associate Editor, Bioinformatics
2000-2002	President, International Society for Computational Biology
2000-	Steering Committee member, NIH Pharmacogenetics Research Network and Database Initiative.
2000	Review panel, Burroughs Wellcome Functional Genomics Initiative
2000-2001	Advisor, Cambridge HealthTech Inc. Professional Meetings.
2001-	Editor, Pharmacogenetics
2003-	Associate Editor, Briefings in Bioinformatics
2003-	Associate Editor, Genomics

## **CURRENT GRANTS AND AWARDS:**

### **National Institutes of Health (T15 LM007033)**

PI: Russ B. Altman

Term: 7/01/02-6/30/07

Title: Graduate Training in Biomedical Informatics.

This is a pre- and post-doctoral training grant for biomedical informatics.

### **National Institutes of Health (T32 GM063495)**

PI: Russ B. Altman

Term: 7/01/01-6/30/04

Title: Predoctoral Training Bioinformatics/Computational Biology

This is a Predoctoral Training grant for biomedical computation.

### **National Institutes of Health (5 U01 GM61374)**

PI: Russ B. Altman

Term: 04/01/00-03/31/05

Title: The Stanford Pharmacogenetics Knowledge Base

The major goal of this project is to create a national repository of genotype and phenotype information related to pharmacogenomics, <http://www.pharmgkb.org/>

### **National Institutes of Health (5)**

PI: Dan Herschlag (Altman, Co-PI on 2 component projects)

Term: 06/06/03-5/31/08

Title: Folding of Tetrahymena Group 1 Ribozyme

The major goal of this project is to combine computational and experimental approaches to understand RNA folding, particularly of the tetrahymena group I intron.

### **National Institutes of Health (5 R01 LM05652)**

PI: Russ B. Altman

Title: Annotating functional sites in 3D biological structures.

Term: 09/15/04– 09/15/09

The major goal of this project is to extend the understanding of structure representation and manipulation in the context of biological macromolecules.

### **National Institutes of Health (U54 GM072970)**

PI: Russ B. Altman

Title: Physics-based simulation of biological structure

Term: 09/15/04– 09/15/09

The goal of this project is to build a National Center for Biomedical Computing (NCBC) under the NIH roadmap program focusing on physics-based modeling of structure at all scales, from atoms to organisms. The Simbios project will build a toolkit called SimTK (<http://simbios.Stanford.edu>).

## **PREVIOUS GRANTS AND AWARDS:**

### **Stanford/Edinburgh Link Program**

PI: Russ B. Altman

Term: 10/1/02-9/30/04

Title: Enhancing the ability of the biomedical literature to support biomedical discovery  
The goal of this grant is to collaborate with U. Edinburgh on the application of natural language processing technology in functional genomics.

### **National Institutes of Health (P20 GM064782)**

PI: Russ B. Altman

Term: 09/20/01-08/31/04

Title: Planning the Stanford Center for Biomedical Computation

The major goal of this project is to prepare and organize Stanford for a Biomedical Computation Center of Excellence.

### **National Institutes of Health (1 R01 LM06244)**

PI: Russ B. Altman

Term: 05/15/95 – 04/14/00, 2 year no-cost extension awarded

Title: Representing Biological Data for Molecular Modeling

The goal of this project is to build a system called RiboWeb to focus on the structure of the 30S ribosomal subunit in procaryotes, to make this resource available to our collaborators in the field of ribosomal structural biology on the internet, and to test it by creating new models of the 30S subunit that better integrate the existing body of structural data.

### **National Science Foundation (NSF DBI-9600637)**

PI: Russ B. Altman

Term: 08/15/96 – 07/31/01

Title: Representing Biological Structure Information for Multiple Uses

This project extends the model for how structural databases are constructed providing a model for how information resources should be built to support scientific progress.

### **Burroughs Wellcome Fund**

PI: Russ B. Altman

Term: 7/1/99-6/30/03

Title: Bioinformatics for malaria functional genomics

The major goal of this project is to create online resources to support understanding the metabolic pathways in malaria, and identify novel drug targets.

### **National Science Foundation (UCSD 10152756)**

(Subcontract to Stanford from University of California, San Diego)

PI: Sidney Karin

Subcontract PI: Russ Altman

Term: 10/01/97 – 09/30/02

Title: National Partnership for Advanced Computing Infrastructure: Stanford  
Subcontract to Molecular Science Thrust

A major goal of this collaborative project is to test the ability of the San Diego SuperComputer software framework to accommodate the Stanford representation of computational tools for analyzing protein sites.

**Stanford Presidential Commission on Technology in Teaching and Learning**

PI: Russ B. Altman

Term: 06/01/97 – 05/31/99

Title: Methods for tailoring course content for multiple audiences

This is a two-year pilot project to deliver bioinformatics content for biologists, computer scientists, and mathematicians using multimedia.

**Sun Microsystems, Incorporated**

PI: Russ B. Altman

Term: 03/01/98 – 02/28/00

Title: SUN hardware grant

This is a grant of a multiprocessor server with extended memory and hard disk capacity to support Dr. Altman's work in Bioinformatics computing.

**Culpeper Foundation**

PI: Russ B. Altman

Term: 06/01/93 – 05/31/96

Title: Culpeper Foundation Medical Scholar Award

This three year unrestricted grant from the Culpeper Foundation supported Dr. Altman's research efforts.

**IBM Corporation**

PI: Russ B. Altman

Term: 06/01/96 – 05/31/98

Title: IBM Faculty Scholar Award

This grant of funds and hardware supported work in the area of knowledge base development and deployment in biology.

## BIBLIOGRAPHY

### PEER REVIEWED JOURNAL PUBLICATIONS (83 TOTAL):

1. **Altman, R.**, Ladner, J., Lipscomb, W. (1982). Quaternary Structural Changes in Aspartat Carbamoyltransferase of E. Coli at pH 8.3 and pH 5.8. *Biochemical and Biophysical Research Communications*, 108(2), 592–596.
2. **Altman, R.** and Jardetzky, O. (1986). New Strategies for the Determination of Macromolecular Structure in Solution. *Journal of Biochemistry*, 100, 1403–1423.
3. Duncan, B., Buchanan, B., Hayes-Roth, B., Lichtarge, O., **Altman, R.**, Brinkley, J., Hewett, M., Cornelius, C., Jardetzky, O. (1986). PROTEAN: A New Method of Deriving Solution Structures of Proteins. *Bulletin of Magnetic Resonance*, 8, 111–119.
4. Brinkley, J., **Altman, R.**, Duncan, B., Buchanan, B., Jardetzky, O. (1988). The Heuristic Refinement Method for the Derivation of Protein Solution Structures: Validation on Cytochrome-b562. *Journal of Chemical Info. & Computer Sciences*, 28(4), 194–210.
5. Jardetzky, O., **Altman, R.**, Madrid, M. (1989). NMR and Protein Structure. *Biofizika*, 34(5), 763–771.
6. Carrara, E., Brinkley, J., Cornelius, C., **Altman, R.**, Brugge, J., Pachter, R., Buchanan, B., Jardetzky, O. (1990). PROTEAN - Part I: Generating Ensembles of Stylized Molecular Fragments using Uncertain Constraints. *Quantative Computer Program Exchange Bulletin*, 10(4), Program 596.
7. **Altman, R.**, Pachter, R., Carrara, E., Jardetzky, O. (1990). PROTEAN - Part II: Molecular Structure Determination from Uncertain Data. *Quantitative Computer Program Exchange Bulletin*, 10(4), Program 596.
8. Arrowsmith, C., Pachter, R., **Altman, R.**, Iyer, S., Jardetzky, O. (1990). Sequence Specific 1H-NMR Assignments and Secondary Structure of E. Coli trp Repressor. *Biochemistry*, 29, 6332–6341.
9. Pachter, R., **Altman, R.**, Jardetzky, O. (1990). The Dependence of a Protein Solution Structure on the Quality of the Input NMR data. Application of the Double-Iterated Kalman Filter Technique to Oxytocin. *Journal of Magnetic Resonance*, 89, 578–584.
10. Pachter, R., **Altman, R.**, Czaplicki, J., Jardetzky, O. (1991). Comparison of the NMR Solution Structure of Cyclosporin A Determined by Different Techniques. *Journal of Magnetic Resonance*, 92, 468–479.
11. Arrowsmith, C., Pachter, R., **Altman, R.**, Jardetzky, O. (1991). The Solution Structures of E. Coli trp Repressor and trp Aporepressor at an Intermediate Resolution. *European Journal of Biochemistry*, 202(2), 53–66.
12. Liu, Y., Zhao, D., **Altman, R.**, Jardetzky, O. (1992). A Systematic Comparison of Three Structure Determination Methods from NMR Data: Dependence upon Quality and Quantity of Data. *Journal of Biomolecular NMR*, 2, 373–388.
13. **Altman, R.**, Pachter, R., Jardetzky, O. (1993). Structural Uncertainty of Proteins in Solution by NMR. A Re-evaluation of the Structure of the Lac Repressor Headpiece, *Journal of Applied Magnetic Resonance*, 4, 441–460.

14. **Altman, R.**, Hughes, C., Jardetzky, O. (1994). Compositional Characteristics of Disordered Regions in Proteins. *Protein and Peptide Letters*, 1(2), 120–127.
15. **Altman, R.**, Hughes, C., and Gerstein, M. (1995). Methods for Displaying Macromolecular Structural Uncertainty: Application to the Globins. *Journal of Molecular Graphics*, 13, 142–152.
16. **Altman, R.** (1995). A Probabilistic Approach to Determining Biological Structure: Integrating Uncertain Data Sources. *International Journal of Human Computer Studies*, 42, 593–616.
17. Bagley, S. and **Altman, R.** (1995). Characterizing the Microenvironment Surrounding Protein Sites. *Protein Science*, 4, 622–635.
18. Gerstein, M. and **Altman, R.** (1995). Average Core Structures and Variability Measures for Protein Families: Application Immunoglobulins. *Journal of Molecular Biology*, 251, 161–175.
19. Gerstein, M. and **Altman, R.** (1995). Using a Measure of Structural Variation to Define a Core for the Globins. *CABIOS Computer Applications in the Biosciences*, 11, 633–644.
20. **Altman, R.** and Merino, J. (1996). Umbilical Cord Knot. *New England Journal of Medicine*, 334(9), 573.
21. Chen, C., Chen, R., **Altman, R.** (1996). Constraining Volume by Matching Moments of a Distance Distribution. *Computer Applications in the Biosciences*, 12(4), 319–326.
22. Fink, D., Chen, R., Noller, H., **Altman, R.** (1996). Computational Methods for Defining the Allowed Conformational Space of 16S rRNA Based on Chemical Footprinting Data. *RNA* 2(9), 851–866.
23. Bagley, S. and **Altman, R.** (1996). Conserved Features in the Active Site of Nonhomologous Serine Proteases. *Folding & Design*, 1(5), 371–379.
24. Schmidt, R., Gerstein, M., **Altman, R.** (1997). LPFC: An Internet Library of Protein Family Core Structures. *Protein Science*, 6, 246–248.
25. **Altman, R.** (1997). Informatics in the Care of Patients: Ten Notable Challenges. *Western Journal of Medicine* 166(2), 118–122.
26. Felciano, R., Chen, R., **Altman, R.** (1997). RNA Secondary Structure as a Reusable Interface to Biological Information Resources, *Gene* 190, 59–70.
27. Chen, C., Singh, J., **Altman, R.** (1998). The Hierarchical Organization of Molecular Structure Computations. *Journal of Computational Biology*, 5(3), 409–422.
28. Gennari, J., Cheng, H., **Altman, R.**, Musen M. (1998). Reuse, CORBA, and Knowledge-Based Systems, *International Journal of Human-Computer Studies*, 49(4), 523–546.
29. Chen, C., Singh, J., **Altman, R.** (1999). Using Imperfect Secondary Structure Predictions to Improve Molecular Structure Computations, *Bioinformatics*, 15(1), 53-65.
30. **Altman, R.**, Chen, R., Abernethy, N., Bada, M. (1999). RiboWeb: An Ontology-Based System for Collaborative Molecular Biology. *IEEE Intelligent Systems and Their Application*, 14(5), 68-76.

31. Abernethy, N. and **Altman, R.** (1999). SOPHIA: A Flexible, Web-Based Knowledge Server. *IEEE Intelligent Systems and Their Applications*, 14(4), 79-85.
32. Chen, R. and **Altman, R.** (1999). A Knowledge-based Method for Diagnosing Data-Model Conflicts in Computational Biology. *J Am Med Inform Assoc*, 6(5), 374-392.
33. Wei, L., Huang, E., **Altman, R.** (1999). Are Predicted Structures Good Enough to Preserve Functional sites? *Structure (with Folding & Design)*, 7(6), 643-650.
34. Bada, M. and **Altman, R.** (2000). Computational Modeling of Structured Experimental Data. *Methods in Enzymology*, 317, 470-491.
35. Joseph, S., Carrillo, M., Kondo, H., Noller, H., **Altman, R.** (2000). Calculation of the relative geometry of tRNAs in the ribosome from directed hydroxyl-radical probing data. *RNA* 6, 220-232.
36. **Altman, R.** (2000). The interactions between clinical informatics and bioinformatics: a case study. *J Am Med Inform Assoc.*, 7(5), 439-443.
37. Raychaudhuri, S., Sutphin, P., Chang, J., **Altman, R.** (2001). Basic microarray analysis: grouping and feature reduction. *Trends in Biotechnology*, 19(5), 189-193.
38. Troyanskaya, O., Cantor, M., Sherlock G., Brown P., Hastie, T., Tibshirani, R., Botstein, D., **Altman, R.** (2001). Missing value estimation methods for DNA microarrays. *Bioinformatics*, 17(0), 1-6.
39. **Altman, R.**, Raychaudhuri, S. (2001). Whole-genome expression analysis: challenges beyond clustering. *Curr Opin Struct Biol.*, 11(3), 340-347.
40. Williams, G., Dugan, J., **Altman, R.** (2001). Constrained global optimization for estimating molecular structure from atomic distances. *J Comput Biol.*, 8(5), 523-547.
41. Garber, M., Troyanskaya, O., Schluens, K., Petersen, S., Thaesler, Z., Pacyna-Gengelbach, M., van de Rijn, M., Rosen, G., Perou, C., Whyte, R., **Altman, R.**, Brown, P., Botstein, D., Petersen, I. (2001). Diversity of gene expression in adenocarcinoma of the lung. *Proc Natl Acad Sci USA*, 98(24), 13784-13789.
42. Klein, T., Chang, J., Cho, M., Easton, K., Fergerson, R., Hewett, M., Lin, Z., Liu, Y., Liu, S., Oliver, D., Rubin, D., Shafa, F., Stuart, J., **Altman, R.** (2001). Integrating genotype and phenotype information: an overview of the PharmGKB project. *Pharmacogenomics J.*, 1(3), 167-170.
43. Hewett, M., Oliver, D., Rubin, D., Easton, K., Stuart, J., **Altman, R.**, Klein, T. PharmGKB: the Pharmacogenetics Knowledge Base. *Nucleic Acids Res.*, 30(1), 163-165.
44. Raychaudhuri, S., Chang, J., Sutphin, P., **Altman, R.** (2002). Associating genes with gene ontology codes using a maximum entropy analysis of biomedical literature. *Genome Res.*, 12(1), 203-214.
45. **Altman, R.**, Klein, T. (2002). Challenges for biomedical informatics and pharmacogenomics. *Annu Rev Pharmacol Toxicol.*, 42, 113-133.
46. Rubin, D., Shafa, F., Oliver, D., Hewett, M., **Altman, R.** (2002). Representing genetic sequence data for pharmacogenomics: an evolutionary approach using ontological and relational models. *Bioinformatics*, 18 Suppl 1, S207-S215.

47. Waugh, A., Gendron, P., **Altman, R.**, Brown, J., Case, D., Gautheret, D., Harvey, S., Leontis, N., Westbrook, J., Westhof, E., Zuker, M., Major, F. (2002). RNAML: a standard syntax for exchanging RNA information. *RNA*, 8(6), 707-717.
48. Peleg, M., Yeh, I., **Altman, R.** (2002). Modeling biological processes using workflow and Petri Net models. *Bioinformatics*, 18(6), 825-837.
49. Kivi, M., Liu, X., Raychaudhuri, S., **Altman, R.**, Small, P. (2002). Determining the genomic locations of repetitive DNA sequences with a whole-genome microarray: IS6110 in Mycobacterium tuberculosis. *J Clin Microbiol.*, 40(6), 2192-2198.
50. Whirl-Carrillo, M., Gabashvili, I., Bada, M., Banatao, D., **Altman, R.** (2002). Mining biochemical information: lessons taught by the ribosome. *RNA*, 8(3), 279-289.
51. Han, J., **Altman, R.**, Kumar, V., Mannila, H., Pregibon, D. (2002). Emerging Scientific Applications in Data Mining. *Communications of the ACM*, 45(8), 54-58.
52. Chang, J., Schuetze, H., **Altman, R.** (2002). Creating an Online Dictionary of Abbreviations from MEDLINE. *J Am Med Inform Assoc.*, 9(6), 612-620.
53. Troyanskaya, O., Garber, M., Brown, P., Botstein, D., **Altman, R.** (2002). Nonparametric Methods for Identifying Differentially Expressed Genes in Microarray Data. *Bioinformatics*, 18(11), 1454-1461.
54. Yeh, I., Karp, P., Noy, N., **Altman, R.** (2002). Knowledge Acquisition, Consistency Checking and Concurrency Control for Gene Ontology. *Bioinformatics*, 19(2), 241-248.
55. Chang, J., **Altman, R.** (2002). Promises of text processing: natural language processing meets AI. *Drug Discov Today*, 7(19), 992-993.
56. Raychaudhuri, S., Schuetze, H., **Altman, R.** (2002). Using text analysis to identify functionally coherent gene groups. *Genome Research*, 12(10), 1582-1590.
57. Mooney, S., Klein, T., **Altman, R.**, Trifiro, M., Gottlieb, B. (2003). A functional analysis of disease-associated mutations in the androgen receptor gene. *Nucleic Acids Res.*, 31(8), e42.
58. **Altman, R.**, Dugan, J. (2003). Defining bioinformatics and structural bioinformatics. *Methods Biochem Anal.* 44, 3-14.
59. Raychaudhuri, S., **Altman, R.** (2003). A literature-based method for assessing the functional coherence of a gene group. *Bioinformatics*, 19(3), 396-401.
60. **Altman, R.**, Flockhart, D., Sherry, S., Oliver, D., Rubin, D., Klein, T. (2003). Indexing pharmacogenetic knowledge on the World Wide Web. *Pharmacogenetics*, 13(1), 3-5.
61. Wei, L., **Altman, R.** (2003). Recognizing Complex, Asymmetric Functional Sites in Protein Structures Using a Bayesian Scoring Function. *Journal of Bioinformatics and Computational Biology*, 1(1) 119-138.
62. Liang, M., Banatao, D., Klein, T., Brutlag, D., **Altman, R.** (2003). WebFEATURE: An interactive Web tool for identifying and visualizing functional sites on macromolecular structures. *Nucleic Acids Research*, 31(13), 3324-3327.
63. Raychaudhuri, S., Schuetze, H., **Altman, R.** (2003). Inclusion of Textual Documentation in the Analysis of Multidimensional Data Sets: Application to Gene Expression Data. *Machine Learning*, 52, 119-145.

64. Banatao, D., **Altman, R.**, Klein, T. (2003). Microenvironment analysis and identification of magnesium binding sites in RNA. *Nucleic Acids Research*, 31(15), 4450-4460.
65. Liu, S., **Altman, R.** (2003). Large scale study of protein domain distribution in the context of alternative splicing. *Nucleic Acids Research*, 31(16), 4828-4835.
66. Chang, J., Schütze, H, **Altman, R.** (2003). GAPSCORE: Finding Gene and Protein Names One Word at a Time. *Bioinformatics*, in press.
67. Raychaudhuri, S., Chang, J., Imam, F., **Altman, R.** (2003). The computational analysis of scientific literature to define and recognize gene expression clusters. *Nucleic Acids Reseach*, 31(15), 4450-60.
68. Gabashvili, I., Whirl-Carrillo, M., Bada, , Banatao, D., **Altman, R.** (2003). Ribosomal dynamics inferred from variations in experimental measurements. *RNA*. Nov 2003, 9(11), 1301-7.
69. Mooney, S., **Altman, R.** (2003). MutDB: annotating human variation with functionally relevant data. *Bioinformatics*. Sep 22, 2003, 19(14), 1858-60.
70. Denko, N., Fontana, L., Hudson, K., Sutphin, P., Raychaudhuri, S., **Altman, R.**, Giaccia A. (2003) Investigating hypoxic tumor physiology through gene expression patterns. *Oncogene*. Sep 1, 2003, 22(37), 5907-14.
71. Troyanskaya, O., Dolinski, K., Owen, A., **Altman, R.**, Botstein, D. (2003) A Bayesian framework for combining heterogeneous data sources for gene function prediction (in *Saccharomyces cerevisiae*). *Proc Natl Acad Sci U S A*. Jul 8, 2003, 100(14), 8348-53. Epub, Jun 25, 2003.
72. Khambata-Ford, S., Liu, Y., Gleason, C., Dickson, M., **Altman, R.**, Batzoglou, S., Myers, R. (2003). Identification of promoter regions in the human genome by using a retroviral plasmid library-based functional reporter gene assay. *Genome Res*. Jul 2003, 13(7), 1765-74.
73. Dugan, J., **Altman, R.** (2004). Using surface envelopes for discrimination of molecular models. *Protein Sci.*, Jan 2004, 13(1), 15-24.
74. Chang, J., Schutze, H., **Altman, R.** (2004). GAPSCORE: finding gene and protein names one word at a time. *Bioinformatics* 2004 Jan 22;20(2):216-25.
75. Liu, Y., Liu, X., Wei, L., **Altman, R.**, Batzoglou S. (2004). Eukaryotic regulatory element conservation analysis and identification using comparative genomics. *Genome Res*. 2004 Mar;14(3):451-8.
76. Yeh, I., Hanekamp, T., Tsoka, S, Karp, P., **Altman, R.** (2004). Computational Analysis of Plasmodium falciparum Metabolism: Organizing Genomic Information to Facilitate Drug Discovery. *Genome Res*. 2004 Apr 12
77. Friedman, C., **Altman, R.**, Kohane, I., McCormick, K., Miller, P., Ozbolt, J., Shortliffe, E., Stormo, G., Szczepaniak, M., Tuck, D., Williamson, J. (2004). Training the Next Generation of Informaticians: The Impact of "BISTI" and Bioinformatics--A Report from the American College of Medical Informatics. *J Am Med Inform Assoc*. 2004 May-Jun;11(3):167-72. Epub 2004 Feb 05.
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83. **Altman RB**. (2004) Building successful biological databases. *Brief Bioinform*. Mar;5(1):4-5.

#### **INVITED REVIEWS/LETTERS/EDITORIALS (7 TOTAL):**

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6. **Altman, R.** (2003). Genetic sequence data for pharmacogenomics. *Curr Opin Drug Discov Devel*. May 2003, 6(3), 297-303.
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#### **PEER-REVIEWED CONFERENCE PROCEEDINGS (42 TOTAL):**

**(NOTE: In computer science and bioinformatics, there is a tradition of critically reviewed manuscripts presented at conferences. More than 3/4 of the publications on this list are fully indexed in PubMed, and are peer reviewed at a level comparable to other biological journal publications.)**

1. Hayes-Roth, B., Buchanan, B., Lichtarge, O., Hewett, M., **Altman, R.**, Brinkley, J., Cornelius, C., Duncan, B., Jardetzky, O. (1986). Protean: Deriving Protein Structure from Constraints. In: Proceedings of AAAI-86, Fifth National Congress on Artificial Intelligence 2 (pp. 904-909). Menlo Park, CA: AAAI Press.
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  12. Oliver, D. and **Altman, R.** (1994). Extraction of SNOMED Concepts from Medical Record Texts. In: Proceedings of Eighteenth Annual Symposium on Computer Applications in Medical Care (pp. 179–183). New York: McGraw-Hill.
  13. Fridsma, D. and **Altman, R.** (1994). A Survey of Patient Access to Electronic Mail: Attitudes, Barriers and Opportunities. In: Proceedings of Eighteenth Annual Symposium on Computer Applications in Medical Care (pp. 15-19). New York: McGraw-Hill.
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1. **Altman, R.**, Brutlag, D., Karp, P., Lathrop, R., Searls, D. (eds.). (1994). Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology (Stanford, CA). Menlo Park, CA: AAAI Press.
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#### **CHAPTERS OF BOOKS (12 TOTAL):**

1. **Altman, R.**, Duncan, B., Brinkley, J., Buchanan, B., Jardetzky, O. (1988). Determination of the Spatial Distribution of Protein Structure Using Solution Data. In: J. Jaroszewski, K. Schaumburg & H. Kofod (eds), NMR Spectroscopy in Drug Research Alfred Benzon Symposium 26 (pp. 209–232). Monksgaard, Copenhagen.

2. Hayes-Roth, B., Buchanan, B., Lichtarge, O., Hewett, M., **Altman, R.**, Brinkley, J., Cornelius, C., Duncan, B., Jardetzky, O. (1988). PROTEAN: Deriving Protein Structure from Constraints. In: R. Englemore & A. Morgan (eds.), Blackboard Systems (pp. 417–431). Workingham: Addison-Wesley.
3. **Altman, R.** and Jardetzky, O. (1989). The Heuristic Refinement Method for the Determination of the Solution Structure of Proteins from NMR Data. In: N. Oppenheimer & T. James (eds.), Nuclear Magnetic Resonance, Part B: Structure and Mechanisms (Methods in Enzymology, Vol. 177) (pp.218-247). New York: Academic Press.
4. Duncan, B., Brinkley, J., **Altman, R.**, Buchanan, B., Jardetzky, O. (1989). Artificial Intelligence Techniques and NMR Spectroscopy: Application to the Structure of Proteins in Solution. In: J. Pettegrew (ed.), Nuclear Magnetic Resonance: The Principles and Applications of NMR Spectroscopy and Imaging to Biomedical Research (pp. 99–123). New York: Springer-Verlag.
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9. **Altman, R.** (2000). Bioinformatics. In: T. Shortliffe, G. Wiederhold, and L. Fagan (eds.), Medical Informatics: Computer Applications in Health Care (pp. 638-660), Heidelberg: Springer-Verlag.
10. **Altman, R.**, Preface. In Kohane, I., Kho, A., Butte, A. (2002). *Microarrays For An Integrative Genomics*. Mar 2002, xii-xv.
11. **Altman, R.**, Dugan, J. (2003). Defining Bioinformatics and Structural Bioinformatics. In: H. Weissig & P. Bourne (eds.). Structural Bioinformatics (pp. 3-14). Hoboken: Wiley-Liss, Inc.
12. **Altman, R.**, Preface. In Pevsner, J. (2003). *Bioinformatics and Functional Genomics*. Oct 2003

**ABSTRACTS:** None

## **INVITED LECTURES AND PRESENTATIONS (6 from over 100):**

“AI in Medicine: Challenges from managed care to molecular medicine.” Annual Conference of American Association for Artificial Intelligence, Invited Talk, Madison, WI, July 29, 1998.

“Bioinformatics in support of molecular medicine.” Annual Conference of the American Medical Informatics Association, Invited Talk, Orlando, FL, November 9, 1998.

“Challenges for Discovery in Molecular Biology” Knowledge Discovery and Data Mining Conference, 2001, San Francisco, CA, August 28, 2001.

“Challenges for Knowledge Management in Bioinformatics” IEEE Computer Society Bioinformatics Conference, August 16, 2002.

"Finding pharmacogenetics knowledge in odd places" Vanderbilt University, Department of Medicine Grand Rounds, Sep 12, 2002.

"Building a genotype-phenotype database" University of Pennsylvania, Program in Bioinformatics, Dec. 9, 2003.