CURRICULUM VITAE
Douglas L. Brutlag

Position   Professor Emeritus of Biochemistry & Medicine (by courtesy)
Stanford University School of Medicine

Born   December 19, 1946; Alexandria, Minnesota
Nationalities U.S. and French Citizenships

Address   Department of Biochemistry
Beckman Center, B400, MC 5307
Stanford University School of Medicine
Stanford, California 94305-5307
Phone   (650) 723-6593
Fax: (650) 723-6783
E-mail   brutlag@stanford.edu

Teaching   http://brutlag.stanford.edu/courses.html
Research   http://brutlag.stanford.edu/
CV   http://cmgm.stanford.edu/~brutlag/

Educational History
9/64 – 9/68 B.S. with honors, George W. Green Award for Creative Scholarship in Biology, California Institute of Technology.
9/68 – 6/72 Ph.D. with Great Distinction, Dept. of Biochemistry, Stanford University.

Professional Experience
6/72 – 6/74 Research Scientist at the Commonwealth Scientific and Industrial Research Organization, Canberra, Australia Laboratory of Dr. Jim Peacock.
9/74 – 1980 Assistant Professor of Biochemistry, Dept. of Biochemistry, Stanford University.
9/80 – 1995. Associate Professor of Biochemistry, Dept. of Biochemistry, Stanford University.
9/95 – pres. Professor of Biochemistry and Medicine (by courtesy), Stanford University.
9/81 – 9/82 Sabbatical leave at Pasteur Institute, Paris, France.
9/80   Cofounder of IntelliCorp and IntelliGenetics Inc.
9/80 – 8/85 Board of Directors, IntelliCorp Inc.
5/86 – 9/91 Board of Directors; IntelliGenetics Inc.
9/80 – 5/86 Scientific Advisory Board IntelliCorp
9/93 – 9/98 Editorial Board of *Journal of Computational Biology*
6/96 – 6/00 Cofounder and member of *International Society for Computational Biology*
9/97 – 9/03 Chairman, Scientific Advisory Board Time Logic, Inc.
9/97 – 2/02 Scientific Advisory Board, DoubleTwist, Inc.
9/00 – 2/02 Chief Scientific Officer, DoubleTwist Inc.
3/03 – 6/06. Chairman, Scientific Advisory Board, Pathwork Informatics
6/03 – pres. Presidential Scientific Advisory Board, Max Planck Institute.

Douglas L. Brutlag

Stanford Medical School Service

1975 – 1979	Medical School Committee on Courses and Curriculum
1979 – 1981	Chairman and founder, Medical School Scholars Committee
1983 – 1986	Medical School Senate, Biochemistry Representative
	Ad hoc Senate Committee on Computing and the Curriculum (Chase Committee)
1991	*Ad hoc* Senate Curriculum Review Committee (Chairman of Preclinical Subgroup)
1991 – 2008.	Biomedical Informatics Admissions Committee
1992 – 2005	Director of the Bioinformatics Resource, Stanford University.
1992 – 1995	Medical School Senate, Biochemistry Representative
1995	*Ad hoc* Dean's grievance committee (appointed by Associate Dean Cutler)
1997 – 1999	*Ad hoc* Committee on Medical School Classrooms (appointed by Associate Dean Shortliffe)
1998 – 1999	Medical School Committee on Core Curriculum
2001 – 2004	Medical School Senate, Basic Science Representative
2005 – 2008	Medical School Senate, Biochemistry Representative

Stanford University Service

1992 – 1995	Stanford Senate Committee on Academic Computing and Information Systems (Appointed by Associate Dean Etchemendy)
1996 – 1998	Chairman, Stanford Senate Committee on Academic Computing and Information Systems.
1993 – 1996	Chairman, Stanford Senate Committee on Distributed Information & Computer Environments (Chair DICE Committee, appointed by Vice Provost Street)
1994– 1996	Research Administration Review Subcommittee (appointed by Dean Kruger)
1995	Chairman, Provost's Search Committee for CIO and head of Academic Computing (appointed by Provost Rice)
1993 – 1998	Stanford Senate Subcommittee on Administrative Computing (SAC)
1996 – 1998	Chairman; Infrastructure Advisory Group
1995 – 1997	*Ex officio* member of Stanford's Infrastructure and Architecture Review Board (computer and network architecture!)
1994 – 1998	Member of President's Commission on Technology in Teaching and Learning
1995 – 1996	Chairman, Subcommittee on Infrastructure of the President's Commission on Technology in Teaching and Learning.
1996 – 1998	University Classroom Committee (appointed by Dean Etchemendy)
2002 – 2004	Stanford Committee on Libraries (C-LIB)
2003 – 2004	Chairman, Stanford Committee on Libraries (C-LIB)
2006 – 2008	Chairman, Stanford Committee on Libraries (C-LIB)

Douglas L. Brutlag

National and International Service

- National Institutes of Health, Genetics Study Section, 1982-1986.
- National Institutes of Health, Small Business Innovation Research Study Section,1984.
- National Library of Medicine, Strategic Long Range Planning Committee, 1985-86.
- Co-Investigator, BIONET Resource for Computational Molecular Biology, 1985-1989
- Consultant to NIH GenBank Database 1987-1992
- National Library of Medicine, Board of Scientific Counselors, 1989 - 1993.
- Organizer, National Institutes of General Medical Science, Symposium *GenBank the first 15 years.* May 1992
- National Science Foundation Brookhaven Protein Structure Database Site Visit Team, June 1992.
- Organizer, Course on Computer Applications in Molecular Biology, UNIDO & International Centre for Genetic Engineering and Biotechnology, Trieste Italy. July 1989, July 1990, July 1991, and July 1992.
- Organized UNIDO Workshop on Computation Biology, Centre Bioengineering, Moscow, Russia, December 1992.
- Organizer, Course on Computer Applications in Molecular Biology, Australian National Genomic Information Centre, Sydney, Australia, July 1993 and July 1995.
- Outside Reviewer, Imperial Cancer Research Fund Research Projects, 1989 & 1994.
- Chairman and Organizer, Second International Conference on Intelligent Systems in Molecular Biology (ISMB) , Stanford University, August 1994.
- Program Committee for the First, Second, Third, Fourth, Fifth and Sixth International Conferences on Intelligent Systems in Molecular Biology (1993-1997)
- Steering Committee of the International Society for Computational Molecular Biology (1994-1999)
- Organizer, CAMIS Symposium on Genomics and Bioinformatics, Stanford University (1995)
- Organizer Seventh International Conference on Intelligent Systems for Molecular Biology (ISMB), Heidelberg Germany, August 1999.
- Organizer, Dagstuhl Seminar on Bioinformatics, November 2000.
- Presidential Scientific Advisory Board for the Max Planck Institute. June 2003.
- Speaker , Structural, Functional and Evolutionary Genomics Gordon Conference, June 2003
- Chairman and Organizer, Structural, Functional and Evolutionary Genomics Gordon Conference February 2004
- Organizer, Structural, Functional and Evolutionary Genomics Gordon Conference, June 2005

Professional Honors and Memberships

1974 – 1976	Andrew W. Mellon Foundation Fellowship
1975	Elected to Federation of American Soc. for Experimental Biol.
1976	Member, American Society of Biological Chemists
1975 – 1978	Basil O'Connor National Foundation Young Investigator Award
1979 – 1984	Henry and Camille Dreyfus Teacher-Scholar
1981	Guggenheim Fellow (declined).
1981 – 1982	NIH Senior Fogarty International Fellow
1985 – 1993	Member, American Association of Artificial Intelligence.

Douglas L. Brutlag

1986	Elected Fellow, American Association for the Advancement of Science
1992	Computerworld-Smithsonian Award in Science
1995	International Society of Computational Biology founding committee.
2000 – 2003	Honorary Professor of Bioinformatics, Keio University
2001	Fellow of the American College of Medical Informatics

Douglas L. Brutlag

Keynotes and Invited Presentations (since 1995)

- Keynote, Third International Conference on Intelligent Systems in Molecular Biology, 1995.
- Conference Organizer, Genomics and Bioinformatics: Their Impact on Medicine and Molecular Biology. Stanford University, November 1995.
- Keynote Speaker, SmithKline Beecham Scientific Advisory Board, Harlow England June 1996.
- Invited Speaker, Cambridge Healthtech Conference in Baltimore, June 9,10 1996
- Invited Speaker, Biojapan '96, Tokyo Japan (July 1996).
- Symposium Speaker, Stanford-SmithKline Beecham Symposium (Dec 1996)
- Invited Speaker, Stanford Genetics Department 1997
- Invited Speaker, UC Riverside, Biochemistry 1997
- Invited Speaker, Incyte Pharmaceuticals , 1997
- Invited Speaker, Berlex Biosciences, 1997
- Invited Speaker, DoubleTwist Inc., 1997
- Invited Speaker, National Academy of Sciences, Computers and Biology, 1997
- Invited Speaker at American Association of Medical Colleges, November 1997
- Conference Organizer, American Society for Biochemistry and Molecular Biology, Predicting Function from Genomes, May 1998
- Invited Speaker at Microbiology Gordon Conference, June 1998
- Invited Speaker at Nucleic Acids Gordon Conference, June 1998
- Invited Speaker, IBC Conference on Bioinformatics, Sept 1998
- Invited Speaker, Strata Biosciences, October, 98
- Invited Speaker, SRI Conference on Bioinformatics, October, 98
- Keynote Speaker, Computation Genomics (Celera & SmithKline Beecham, Oct, 1998
- Invited Speaker, SmithKline Beecham Research & Development Labs, October, 1998
- Invited Speaker, Stanford Genome Seminar Series January, 1999
- Invited Speaker, Stanford Genome Center, February, 1999
- Invited Speaker, Strategic Research Institute, Bioinformatics, April , 1999
- Keynote Speaker, DoubleTwist Symposium on Gene Discovery, May 1999
- Invited Speaker, Cambridge HealthTech Institute, , San Francisco, February 1999
- Co-organizer, Intelligent Systems for Molecular Biology, August 1999
- Distinguished Visitor, Haverford College December 1999
- Invited Speaker, National Academy of Sciences, Institute of Medicine, October 2001
- Honorary Professor of Bioinformatics, Keio University November 2001
- Invited Speaker, Genomics Gordon Conference, July 2002
- Keynote speaker, European Conference on Computational Biology, October 2002
- Invited Speaker, l'Ecole Normale Supérieure Paris France December 2002
- Invited Speaker, Columbia University Genome Center, April 2003
- Invited Speaker, University of California, Berkeley, May, 2003
- Invited Speaker, University of Buffalo, Center of Excellence. May 2003
- Keynote Speaker, Proteins and Proteome at ICBA, Ft. Lauderdale Florida December 2004
- Keynote Speaker, New Mexico Bioinformatics Symposium , March 2005
- Invited Speaker, University of Iowa, Ames Iowa, November 2005
- Invited Speaker, Biovision 2010, Alexandria, Egypt

Douglas L. Brutlag

Publications

1. Marushige, K., Brutlag, D., & Bonner, J. (1968). Properties of chromosomal bonhistone protein of rat liver. *Biochemistry, 7*(9), 3149-3155.

2. Brutlag, D., Atkinson, M. R., Setlow, P., & Kornberg, A. (1969). An active fragment of DNA polymerase produced by proteolytic cleavage. *Biochem Biophys Res Commun, 37*(6), 982-989.

3. Brutlag, D., Schlehuber, C., & Bonner, J. (1969). Properties of formaldehyde-treated nucleohistone. *Biochemistry, 8*(8), 3214-3218.

4. Brutlag, Douglas, Schekman, Randy, & Kornberg, Arthur (1971). A Possible Role for RNA Polymerase in the Initiation of M13 DNA Synthesis. *PNAS, 68*(11), 2826-2829.

5. Brutlag, Douglas (1972). *Enzymatic mechanisms in DNA replication.* Unpublished Ph.D., Stanford University. Dept. of Biochemistry. Stanford.

6. Brutlag, Douglas, & Kornberg, Arthur (1972). Enzymatic Synthesis of Deoxyribonucleic Acid. XXXVI. A PROOFREADING FUNCTION FOR THE 3' > 5' EXONUCLEASE ACTIVITY IN DEOXYRIBONUCLEIC ACID POLYMERASES. *J. Biol. Chem., 247*(1), 241-248.

7. Brutlag, D., & Kornberg, A. (1972). Enzymatic synthesis of deoxyribonucleic acid. 36. A proofreading function for the 3' > 5' exonuclease activity in deoxyribonucleic acid polymerases. *J Biol Chem, 247*(1), 241-248.

8. Schekman, Randy, Wickner, William, Westergaard, Ole, Brutlag, Douglas, Geider, Klaus, Bertsch, Leroy L., et al. (1972). Initiation of DNA Synthesis: Synthesis of phi X174 Replicative Form Requires RNA Synthesis Resistant to Rifampicin. *PNAS, 69*(9), 2691-2695.

9. Setlow, Peter, Brutlag, Douglas, & Kornberg, Arthur (1972). Deoxyribonucleic Acid Polymerase: Two Distinct Enzymes in One Polypeptide. I. A PROTEOLYTIC FRAGMENT CONTAINING THE POLYMERASE AND 3' > 5' EXONUCLEASE FUNCTIONS. *J. Biol. Chem., 247*(1), 224-231.

10. Setlow, P., Brutlag, D., & Kornberg, A. (1972). Deoxyribonucleic acid polymerase: two distinct enzymes in one polypeptide. I. A proteolytic fragment containing the polymerase and 3' leads to 5' exonuclease functions. *J Biol Chem, 247*(1), 224-231.

11. Wickner, William, Brutlag, Douglas, Schekman, Randy, & Kornberg, Arthur (1972). RNA Synthesis initiates *in vitro* Conversion of M13 DNA to Its Replicative Form. *PNAS, 69*(4), 965-969.

12. Westergaard, Ole, Brutlag, Douglas, & Kornberg, Arthur (1973). Initiation of Deoxyribonucleic Acid Synthesis. IV. INCORPORATION OF THE RIBONUCLEIC ACID PRIMER INTO THE PHAGE REPLICATIVE FORM. *J. Biol. Chem., 248*(4), 1361-1364.

13. Brutlag, D. L., & Peacock, W. J. (1975). Sequences of highly repeated DNA in Drosophila melanogaster. *In: Peacock WJ, Brock RD, ed. The eukaryote chromosome. Canberra, Australian National Univ Press*, 35-45.

14. Goldring, E. S., Brutlag, D. L., & Peacock, W. J. (1975). Arrangement of the highly repeated

DNA of Drosophila melanogaster. *In: Peacock WJ, Brock RD, ed. The eukaryote chromosome. Canberra, Australian National Univ Press*, 47-59.

15. Carlson, M., & Brutlag, D. (1977). Cloning and characterization of a complex satellite DNA from Drosophila melanogaster. *Cell, 11*(2), 371-381.

16. Rubenstein, J. L., Brutlag, D., & Clayton, D. A. (1977). The mitochondrial DNA of Drosophila melanogaster exists in two distinct and stable superhelical forms. *Cell, 12*(2), 471-482.

17. Brutlag, D., Carlson, M., Fry, K., & Hsieh, T. S. (1978). DNA sequence organization in Drosophila heterochromatin. *Cold Spring Harb Symp Quant Biol, 42 Pt 2*, 1137-1146.

18. Carlson, M., & Brutlag, D. (1978). A gene adjacent to satellite DNA in Drosophila melanogaster. *Proc Natl Acad Sci U S A, 75*(12), 5898-5902.

19. Carlson, M., & Brutlag, D. (1978). One of the copia genes is adjacent to satellite DNA in Drosophila melanogaster. *Cell, 15*(3), 733-742.

20. Brutlag, D., & Peacock, W. J. (1979). Sequences of the 1.672 g/cm3 satellite DNA of Drosophila melanogaster. *J Mol Biol, 135*(3), 565-580.

21. Carlson, M., & Brutlag, D. (1979). Different regions of a complex statellite DNA vary in size and sequence of the repeating unit. *J Mol Biol, 135*(2), 483-500.

22. Fry, K., & Brutlag, D. (1979). Detection and resolution of closely related satellite DNA sequences by molecular cloning. *J Mol Biol, 135*(3), 581-593.

23. Germond, J. E., Rouviere-Yaniv, J., Yaniv, M., & Brutlag, D. (1979). Nicking-closing enzyme assembles nucleosome-like structures *in vitro* . *Proc Natl Acad Sci U S A, 76*(8), 3779-3783.

24. Hsieh, T., & Brutlag, D. (1979). Sequence and sequence variation within the 1.688 g/cm3 satellite DNA of Drosophila melanogaster. *J Mol Biol, 135*(2), 465-481.

25. Hsieh, T., & Brutlag, D. L. (1979). A protein that preferentially binds Drosophila satellite DNA. *Proc Natl Acad Sci U S A, 76*(2), 726-730.

26. Nelson, T., & Brutlag, D. (1979). Addition of homopolymers to the 3'-ends of duplex DNA with terminal transferase. *Methods Enzymol, 68*, 41-50.

27. Nelson, T., Hsieh, T. S., & Brutlag, D. (1979). Extracts of Drosophila embryos mediate chromatin assembly *in vitro* . *Proc Natl Acad Sci U S A, 76*(11), 5510-5514.

28. Brutlag, D. L. (1980). Molecular arrangement and evolution of heterochromatic DNA. *Annu Rev Genet, 14*, 121-144.

29. Hsieh, T., & Brutlag, D. (1980). ATP-dependent DNA topoisonmerase from D. melanogaster reversibly catenates duplex DNA rings. *Cell, 21*(1), 115-125.

30. Nelson, T., Wiegand, R., & Brutlag, D. (1981). Ribonucleic acid and other polyanions facilitate chromatin assembly *in vitro* . *Biochemistry, 20*(9), 2594-2601.

31. Wiegand, R. C., & Brutlag, D. L. (1981). Histone acetylase from Drosophila melanogaster specific for H4. *J Biol Chem, 256*(9), 4578-4583.

32. Bach, R., Friedland, P., Brutlag, D. L., & Kedes, L. (1982). MAXAMIZE. A DNA sequencing strategy advisor. *Nucleic Acids Res, 10*(1), 295-304.

33. Brutlag, D. L., Clayton, J., Friedland, P., & Kedes, L. H. (1982). SEQ: a nucleotide sequence analysis and recombination system. *Nucleic Acids Res, 10*(1), 279-294.

34. Friedland, P., Kedes, L., Brutlag, D., Iwasaki, Y., & Bach, R. (1982). GENESIS, a knowledge-based genetic engineering simulation system for representation of genetic data and experiment planning. *Nucleic Acids Res, 10*(1), 323-340.

35. Glover, C. V., Shelton, E. R., & Brutlag, D. L. (1983). Purification and characterization of a type II casein kinase from Drosophila melanogaster. *J Biol Chem, 258*(5), 3258-3265.

36. Osheroff, N., & Brutlag, D. L. (1983). Recognition of supercoiled DNA by *Drosophila* DNA topoisomerase II. *Mechanisms in DNA Replication and Recombination, UCLA Symposia on Molecular and Cellular Biology* (Vol. 10, pp. 55-64.). New York: Alan R. Liss.

37. Osheroff, N., Shelton, E. R., & Brutlag, D. L. (1983). DNA topoisomerase II from Drosophila melanogaster. Relaxation of supercoiled DNA. *J Biol Chem, 258*(15), 9536-9543.

38. Shelton, E. R., Osheroff, N., & Brutlag, D. L. (1983). DNA topoisomerase II from Drosophila melanogaster. Purification and physical characterization. *J Biol Chem, 258*(15), 9530-9535.

39. Abarbanel, R. M., Wieneke, P. R., Mansfield, E., Jaffe, D. A., & Brutlag, D. L. (1984). Rapid searches for complex patterns in biological molecules. *Nucleic Acids Res, 12*(1 Pt 1), 263-280.

40. Dahmus, G. K., Glover, C. V., Brutlag, D. L., & Dahmus, M. E. (1984). Similarities in structure and function of calf thymus and Drosophila casein kinase II. *J Biol Chem, 259*(14), 9001-9006.

41. Gilson, E., Clement, J. M., Brutlag, D., & Hofnung, M. (1984). A family of dispersed repetitive extragenic palindromic DNA sequences in E. coli. *Embo J, 3*(6), 1417-1421.

42. Altenberg, L., & Brutlag, D. (1986). Selection for modularity in the genome: Reading Frame Evidence for Exon Shuffling.

43. Heller, R. A., Shelton, E. R., Dietrich, V., Elgin, S. C., & Brutlag, D. L. (1986). Multiple forms and cellular localization of Drosophila DNA topoisomerase II. *J Biol Chem, 261*(17), 8063-8069.

44. Kornher, J. S., & Brutlag, D. (1986). Proximity-dependent enhancement of Sgs-4 gene expression in D. melanogaster. *Cell, 44*(6), 879-883.

45. Lohe, A. R., & Brutlag, D. L. (1986). Multiplicity of satellite DNA sequences in Drosophila melanogaster. *Proc Natl Acad Sci U S A, 83*(3), 696-700.

46. Smith, D. H., Brutlag, D., Friedland, P., & Kedes, L. H. (1986). BIONET: national computer resource for molecular biology. *Nucleic Acids Res, 14*(1), 17-20.

47. Heller, R., Philip, M., & Brutlag, D. (1987). Structure of the Embryonic Transcript encoding the

Drosophila DNA topoisomerase II.

48. Lohe, A. R., & Brutlag, D. L. (1987). Adjacent satellite DNA segments in Drosophila structure of junctions. *J Mol Biol, 194*(2), 171-179.

49. Lohe, A. R., & Brutlag, D. L. (1987). Identical satellite DNA sequences in sibling species of Drosophila. *J Mol Biol, 194*(2), 161-170.

50. Philip, M., Heller, R., & Brutlag, D. (1987). Cloning and Characterization of the Gene for *Drosophila* DNA topoisomerase II.

51. Brutlag, D. L. (1988). Expert System Simulations as Active Learning Environments. In R. R. Colwell (Ed.), *Biomolecular Data: A Resource in Transition* (pp. 185-188.). Oxford: Oxford university Press.

52. Brutlag, D. L., & Kristofferson, D. (1988). BIONET: An NIH Computer Resource for Molecular Biology. In R. R. Colwell (Ed.), *Biomolecular Data: A Resource in Transition* (Vol. . pp. 287-294.). Oxford: Oxford University Press.

53. Fairman, R., & Brutlag, D. L. (1988). Expression of the Drosophila type II topoisomerase is developmentally regulated. *Biochemistry, 27*(2), 560-565.

54. Goldstein, A., & Brutlag, D. L. (1989). Is there a relationship between DNA sequences encoding peptide ligands and their receptors? *Proc Natl Acad Sci U S A, 86*(1), 42-45.

55. Hipeau-Jacquotte, R., Brutlag, D. L., & Bregegere, F. (1989). Conversion and reciprocal exchange between tandem repeats in Drosophila melanogaster. *Mol Gen Genet, 220*(1), 140-146.

56. Brutlag, D. L., Dautricourt, J. P., Maulik, S., & Relph, J. (1990). Improved sensitivity of biological sequence database searches. *Comput Appl Biosci, 6*(3), 237-245.

57. Brutlag, D. L., Galper, A. R., & Millis, D. H. (1990). *Rule-Based Simulation of DNA Metabolism: I. Prediction of Enzyme Action* (KSL Report No. 90-71): Stanford University.

58. Galper, A. R., & Brutlag, D. L. (1990). *Parallel Similarity Search and Alignment with the Dynamic Programming Method* (No. KSL Report 90-74): Stanford University.

59. Galper, A. R., Millis, D. H., & Brutlag, D. L. (1990). *Simulating DNA Metabolism: A knowledge-Based Approach.* Paper presented at the AAAI Special Symposium., Stanford University.

60. Barsalou, T., & Brutlag, D. L. (1991). Searching gene and protein sequence databases. *MD Comput, 8*(3), 144-149.

61. Brutlag, D. L., Galper, A. R., & Millis, D. H. (1991). Knowledge-based simulation of DNA metabolism: prediction of enzyme action. *Comput Appl Biosci, 7*(1), 9-19.

62. Brutlag, D. L., Dautricourt, J. P., Diaz, R., Fier, J., Moxon, B., & Stamm, R. (1993). BLAZE: An implementation of the Smith-Waterman Comparison Algorithm on a Massively Parallel Computer. *Computers and Chemistry, 17*, 203-207.

63. Brutlag, D. L., & Klingler, T. M. (1993). *Automatic Discovery of Protein Motifs.* Paper presented at

the Ninth International Biotechnology Symposium, Crystal City, Virginia.

64. Galper, A. R., Millis, D. H., & Brutlag, D. L. (1993). Knowledge-Based Simulation of DNA metabolism: Prediction of Action and Envisionment of Pathways. In L. Hunter (Ed.), *Artificial Intelligence in Molecular Biology* (pp. 365-395). Menlo Park: AAAI Press.

65. Klingler, T. M., & Brutlag, D. L. (1993). Detection of correlations in tRNA sequences with structural implications. *Proc Int Conf Intell Syst Mol Biol, 1*, 225-233.

66. Naor, D., & Brutlag, D. L. (Eds.). (1993). *On Suboptimal Alignments of Biological Sequences* (Vol. 684). Padova, Italy: Springer-Verlag.

67. Altman, R., Brutlag, D., Karp, P., & Searls, D. (Eds.). (1994). *Proc Int Conf Intell Syst Mol Biol* (1st ed. Vol. 2). Menl Park, CA: AAAI Press.

68. Brutlag, D. L. (1994). Understanding the Human Genome. In P. Leder, D. A. Clayton & E. Rubenstein (Eds.), *Scientific American: Introduction to Molecular Medicine* (pp. 153-168). New York NY: Scientific American Inc.

69. Galper, A. R., & Brutlag, D. L. (1994). Computational Simulations of Biological Systems. In D. W. Smith (Ed.), *Biocomputing: Informatics and Genome Projects* (pp. 269-306.). New York NY: Academic Press.

70. Klingler, T. M., & Brutlag, D. L. (1994). Discovering structural correlations in alpha-helices. *Protein Sci, 3*(10), 1847-1857.

71. Klingler, T. M., & Brutlag, D. L. (1994). Discovering side-chain correlation in alpha-helices. *Proc Int Conf Intell Syst Mol Biol, 2*, 236-243.

72. Naor, D., & Brutlag, D. L. (1994). On near-optimal alignments of biological sequences. *J Comput Biol, 1*(4), 349-366.

73. Wu, T. D., & Brutlag, D. L. (1995). Identification of protein motifs using conserved amino acid properties and partitioning techniques. *Proc Int Conf Intell Syst Mol Biol, 3*, 402-410.

74. Brutlag, D. L., & Sternberg, M. J. (1996). Sequences and topology challenges for algorithms and experts. *Curr Opin Struct Biol, 6*(3), 343-345.

75. Tomita, M., Shimizu, N., & Brutlag, D. L. (1996). Introns and reading frames: correlation between splicing sites and their codon positions. *Mol Biol Evol, 13*(9), 1219-1223.

76. Wu, T. D., & Brutlag, D. L. (1996). Discovering empirically conserved amino acid substitution groups in databases of protein families. *Proc Int Conf Intell Syst Mol Biol, 4*, 230-240.

77. Nevill-Manning, C. G., Sethi, K. S., Wu, T. D., & Brutlag, D. L. (1997). Enumerating and ranking discrete motifs. *Proc Int Conf Intell Syst Mol Biol, 5*, 202-209.

78. Singh, A. P., & Brutlag, D. L. (1997). Hierarchical protein structure superposition using both secondary structure and atomic representations. *Proc Int Conf Intell Syst Mol Biol, 5*, 284-293.

79. Brutlag, D. L. (1998). Genomics and computational molecular biology. *Curr Opin Microbiol, 1*(3),

340-345.

80. Nevill-Manning, C. G., Wu, T. D., & Brutlag, D. L. (1998). Highly specific protein sequence motifs for genome analysis. *Proc Natl Acad Sci U S A, 95*(11), 5865-5871.

81. Rindfleisch, T. C., & Brutlag, D. L. (1998). Directions for clinical research and genomic research into the next decade: implications for informatics. *J Am Med Inform Assoc, 5*(5), 404-411.

82. Wu, T. D., Schmidler, S. C., Hastie, T., & Brutlag, D. L. (1998). Regression analysis of multiple protein structures. *J Comput Biol, 5*(3), 585-595.

83. Wu, T. D., Schmidler, S. C., Hastie, T., & Brutlag, D. L. (1998). Modeling and superposition of multiple protein structures using affine transformations: analysis of the globins. *Pac Symp Biocomput*, 509-520.

84. Lengauer, T., Schneider, R., Bork, P., Brutlag, D., Glasgow, J., Mewes, Hans-Werner, et al. (1999). *Proc Int Conf Intell Syst Mol Biol*, Heidelberg, Germany.

85. Singh, A. P., Latombe, J. C., & Brutlag, D. L. (1999). A motion planning approach to flexible ligand binding. *Proc Int Conf Intell Syst Mol Biol*, 252-261.

86. Wu, T. D., Nevill-Manning, C. G., & Brutlag, D. L. (1999). Minimal-risk scoring matrices for sequence analysis. *J Comput Biol, 6*(2), 219-235.

87. Schmidler, S. C., Liu, J. S., & Brutlag, D. L. (2000). Bayesian segmentation of protein secondary structure. *J Comput Biol, 7*(1-2), 233-248.

88. Wu, T. D., Nevill-Manning, C. G., & Brutlag, D. L. (2000). Fast probabilistic analysis of sequence function using scoring matrices. *Bioinformatics, 16*(3), 233-244.

89. Apaydin, M. S., Singh, A. P., Brutlag, D. L., & Latombe, J. C. (2001). Capturing Molecular Energy Landscapes with Probabilistic Conformational Roadmaps. *International Conference on Robotics and Automatons 2001*, 932-939.

90. Huang, J. Y., & Brutlag, D. L. (2001). The EMOTIF database. *Nucleic Acids Res, 29*(1), 202-204.

91. Liu, X., Brutlag, D. L., & Liu, J. S. (2001). BioProspector: discovering conserved DNA motifs in upstream regulatory regions of co-expressed genes. *Pac Symp Biocomput*, 127-138.

92. Apaydin, M. S., Brutlag, D. L., Guestrin, C., Hsu, D., & Latombe, J- C. (2002). Stochastic Roadmap Simulation: An Efficient Representation and Algorithm for Analyzing Molecular Motion. *Recomb 2002, 9*, 12-21.

93. Apaydin, M. S., Brutlag, D. L., Guestrin, C., Hsu, D., & Latombe, J- C. (2002). *Stochastic Conformational Roadmaps for Computing Ensemble Properties of Molecular Motion.* Paper presented at the Fifth International Workshop on Algorithmic Foundations of Robotics (WAFR), Nice, France.

94. Apaydin, M. S., Guestrin, C., Varma, C., Brutlag, D. L., & Latombe, J- C. (2002). Stochastic Roadmap Simulation for the Study of Ligand-Protein Interactions. *Bioinformatics, 18*, S18-S26.

95. Apaydin, M. S., Guestrin, C. E., Varma, C., Brutlag, D. L., & Latombe, J. C. (2002). Stochastic roadmap simulation for the study of ligand-protein interactions. *Bioinformatics, 18 Suppl 2*, S18-26.

96. Brutlag, D., Apaydin, S., Guestrin, C., Hsu, D., Varma, C., Singh, A., et al. (2002). Using robotics to fold proteins and dock ligands. *Bioinformatics, 18 Suppl 2*, S74.

97. Liu, X. S., Brutlag, D. L., & Liu, J. S. (2002). An algorithm for finding protein-DNA binding sites with applications to chromatin-immunoprecipitation microarray experiments. *Nat Biotechnol, 20*(8), 835-839.

98. Apaydin, M. S., Brutlag, D. L., Guestrin, C., Hsu, D., Latombe, J. C., & Varma, C. (2003). Stochastic roadmap simulation: an efficient representation and algorithm for analyzing molecular motion. *J Comput Biol, 10*(3-4), 257-281.

99. Ben-Hur, A., & Brutlag, D. (2003). Remote homology detection: a motif based approach. *Bioinformatics, 19 Suppl 1*, i26-33.

100. Bennett, S. P., Lu, L., & Brutlag, D. L. (2003). 3MATRIX and 3MOTIF: a protein structure visualization system for conserved sequence motifs. *Nucleic Acids Res, 31*(13), 3328-3332.

101. Bennett, S. P., Nevill-Manning, C. G., & Brutlag, D. L. (2003). 3MOTIF: visualizing conserved protein sequence motifs in the protein structure database. *Bioinformatics, 19*(4), 541-542.

102. Liang, M. P., Banatao, D. R., Klein, T. E., Brutlag, D. L., & Altman, R. B. (2003). WebFEATURE: An interactive web tool for identifying and visualizing functional sites on macromolecular structures. *Nucleic Acids Res, 31*(13), 3324-3327.

103. Liang, M. P., Brutlag, D. L., & Altman, R. B. (2003). Automated construction of structural motifs for predicting functional sites on protein structures. *Pac Symp Biocomput*, 204-215.

104. Saxonov, S., Tan, P., & Brutlag, D. L. (2003). eProteome: A Resource of Proteome Annotations. *Nucleic Acids Research*, In Preparation.

105. Ben-hur, A., & Brutlag, D. L. (2004). *Protein Sequence motifs: highly predictive features of protein function.* Paper presented at the Neural Information Processing Systems, Vancouver British Columbia.

106. Liang, . M. P., Troyanskaya, O. G., Laederach, A., Brutlag, D. L., & Altman, R. B. (2004). Computational Functional Genomics. *IEEE Signal Processing*(November), 62-69.

107. Liu, Y., Wei, L., Batzoglou, S., Brutlag, D. L., Liu, J. S., & Liu, X. S. (2004). A suite of web-based programs to search for transcriptional regulatory motifs. *Nucleic Acids Res, 32*(Web Server issue), W204-207.

108. Shapiro, J., & Brutlag, D. (2004). FoldMiner and LOCK 2: protein structure comparison and motif discovery on the web. *Nucleic Acids Res, 32*(Web Server issue), W536-541.

109. Shapiro, J., & Brutlag, D. (2004). FoldMiner: structural motif discovery using an improved superposition algorithm. *Protein Sci, 13*(1), 278-294.

110. Wang, H., Segal, E., Ben-Hur, A., Koller, D., & Brutlag, D. (2004). *Identifying protein-protein interaction sites on a genome-wide scale.* Paper presented at the Neural Information Processing Systems (NIPS), Vancouver, British Columbia, Canada.

111. Bertaccini, E. J., Shapiro, J., Brutlag, D. L., & Trudell, J. R. (2005). Homology modeling of a human glycine alpha 1 receptor reveals a plausible anesthetic binding site. *J Chem Inf Model, 45*(1), 128-135.

112. Su, Q. J., Lu, L., Saxonov, S., & Brutlag, D. L. (2005). eBLOCKs: enumerating conserved protein blocks to achieve maximal sensitivity and specificity. *Nucleic Acids Res, 33*(Database issue), D178-182.

113. Wang, H., Segal, E., Ben-hur, A., Koller, D., & Brutlag, D. L. (2005). Identifying Protein-Protein Interaction Sites on a Genome-Wide Scale. In L.K. Saul, Y. Weiss & L. Bottou (Eds.), *Advances in Neural Information Processing Systems* (Vol. 17, pp. 1465-1472). Cambridge, MA: MIT Press.

114. Ben-Hur, A., & Brutlag, D. L. (2006). Protein sequence motifs: Highly predictive features of protein function. In I. Guyon, S. Gunn, M. Nikravesh & L. Zadeh (Eds.), *Feature extraction, foundations and applications* (pp. 625-645). New York: Springer Verlag.

115. Brutlag, D. L. (2006). Inferring protein function from protein sequence. In T. Lengauer (Ed.), *Bioinformatics - From Genomes to Drugs* (Second ed., pp. 1087-1119). Weinheim, Germany: Wiley-VCH.

116. Chiang, T. H., Apaydin, M. S., Brutlag, D. L., Hsu, D., & Latombe, J. C. (2006). Predicting experimental quantities in protein folding kinetics using Stochastic Roadmap Simulation *Research in Computational Molecular Biology, Proceedings* (Vol. 3909, pp. 410-424). Berlin: Springer-Verlag Berlin.

117. Ebert, J., & Brutlag, D. (2006). Development and validation of a consistency based multiple structure alignment algorithm. *Bioinformatics, 22*(9), 1080-1087.

118. Ebert, J., & Brutlag, D. L. (2006). Development and Validation of a Consistency Based Multiple Structure Alignment Algorithm Running title: Consistency Based Multiple Alignmen. *Bioinformatics, 22*, 1080-1087.

119. Fratkin, E., Naughton, B. T., Brutlag, D. L., & Batzoglou, S. (2006). MotifCut: regulatory motifs finding with maximum density subgraphs. *Bioinformatics, 22*(14), e150-157.

120. Naughton, B. T., Fratkin, E., Batzoglou, S., & Brutlag, D. L. (2006). A graph-based motif detection algorithm models complex nucleotide dependencies in transcription factor binding sites. *Nucleic Acids Res, 34*(20), 5730-5739.

121. Rhee, S. Y., Taylor, J., Wadhera, G., Ben-Hur, A., Brutlag, D. L., & Shafer, R. W. (2006). Genotypic predictors of human immunodeficiency virus type 1 drug resistance. *Proc Natl Acad Sci U S A*, 17355-17360.

122. Saxonov, S., Berg, P., & Brutlag, D. L. (2006). A genome-wide analysis of CpG dinucleotides in the human genome distinguishes two distinct classes of promoters. *Proc Natl Acad Sci U S A, 103*(5), 1412-1417.

123. Tellez, A. B., Crowder, S., Spagnolo, J. F., Thompson, A. A., Peersen, O. B., Brutlag, D. L., et al. (2006). Nucleotide channel of RNA-dependent RNA polymerase used for intermolecular uridylylation of protein primer. *J Mol Biol, 357*(2), 665-675.

124. Chiang, T. H., Apaydin, M. S., Brutlag, D. L., Hsu, D., & Latombe, J. C. (2007). Using stochastic roadmap simulation to predict experimental quantities in protein folding kinetics: folding rates and phi-values. *J Comput Biol, 14*(5), 578-593.

125. Huang, X., & Brutlag, D. L. (2007). Dynamic use of multiple parameter sets in sequence alignment. *Nucleic Acids Res, 35*(2), 678-686.