

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 Citzenships

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

Douglas L. Brutlag

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 satellite 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 topoisomerase 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.

Douglas L. Brutlag

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). MAXIMIZE. 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

Douglas L. Brutlag

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., & Bregere, 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 AAI 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

Douglas L. Brutlag

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),

Douglas L. Brutlag

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 Automotons 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.

Douglas L. Brutlag

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.

Douglas L. Brutlag

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., Wadhwa, 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.

Douglas L. Brutlag

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.