BIOGRAPHICAL SKETCH

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NAME Brutlag, Douglas L.	POSITION TITLE Professor of Biochemistry, Medical Informatics,
eRA COMMONS USER NAME brutlag.douglas	& Computer Science (by courtesy)

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
Calif. Institute of Technology, Pasadena, CA	B.S.	1968	Biology
Stanford University, Stanford, CA	Ph.D.	1972	Biochemistry

A. Positions and Honors.

Positions and Honors:
6/72 - 6/74	Research Scientist at the CSIRO, Canberra Australia.
9/74 - 1980	Assistant Professor of Biochemistry, Stanford University.
9/80 – 9/97	Associate Professor of Biochemistry, Stanford University.
9/97 – present	Professor of Biochemistry, Stanford University
9/96 – present	Professor of Medicine (by courtesy) Stanford University
9/2001-present	Honorary Professor of Bioinformatics, Keio University
1975	Elected to Federation of American Societies for Experimental Biology
1976	Member, American Society of Biological Chemists
1981	Guggenheim Fellowship, (declined).
1981 - 82	NIH Senior Fogarty International Fellow
1986	Elected Fellow of the American Assoc. for the Advancement of Science
1992	Computerworld-Smithsonian Award for Best Computer Application in Science

Public Service:
5/1978	National Institutes of Health, Cell Biology Study Section
5/1979	National Institutes of Health, Molecular Cytology Section
1982 - 1986	National Institutes of Health, Genetics Study Section
1985 - 1986	National Library of Medicine, Long-range Planning Committee
1989 - 1993	National Library of Medicine, Board of Scientific Counselors
1985 - 1989	BIONET National Computer Resource for Molecular Biology, Investigator
1987 - 1992	Consultant to NIH GenBank Database
1989 - 1992	Course organizer, Computer Applications in Molecular Biology, UNIDO
1993 - 1995	Course organizer, Computer Applications in Molecular Biology, ANGIS
1993	Editorial Board, Journal of Computational Biology
6/96 - pres.	Cofounder *International Society for Computational Molecular Biology*
9/97 - pres.	Chairman Scientific Advisory Board of TimeLogic Inc.
3/03 – 6/06	Scientific Advisory board, Pathwork Informatics
6/03 – 6/09	Presidential Scientific Advisory Board, Max Planck Institutes

B. Selected peer-reviewed publications (in reverse chronological order).

Huang, X., & Brutlag, D. L. (2007). Dynamic use of multiple parameter sets in sequence alignment. *Nuc. Acids Res, 35*, 678-68

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.

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

Saxonov, S., Berg, P., & Brutlag, D. L. (2006). A genome-wide analysis of CpG dinucleotides in the human genome distinguish

two distinct classes of promoters. *Proc Natl Acad Sci U S A, 103*(5), 1412-1417.

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.

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.

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

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

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

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.

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.

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.

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

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.

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.

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

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.

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.

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.

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