

RICHARD H. LATHROP

Current Position: Professor, University of California, Irvine

Current Address: Department of Computer Science

4224 Donald Bren Hall

University of California, Irvine

Irvine, CA 92697-3435

949-824-4021 (voice); 949-824-4056 (fax); rickl@uci.edu (email)

EDUCATION, ACADEMIC POSITIONS:

July 2003–present: Professor. **University of California, Irvine.**

July 1997–June 2003: Associate Professor. **University of California, Irvine.**

July 1995–June 1997: Assistant Professor. **University of California, Irvine.**

Oct. 1993–June 1995: Research Scientist. **Massachusetts Institute of Technology.**

Oct. 1990–Oct. 1993: Post-doctoral Research Associate. **Massachusetts Institute of Technology.**
(Prof. Patrick Winston).

Sept. 1980–June 1990: Ph.D., Artificial Intelligence. **Massachusetts Institute of Technology.**

GPA: Cumulative 4.94/5.0; major 5.0/5.0; minor 5.0/5.0 (Philosophy of Mind and Knowledge).

Other Degrees: S.M., Computer Science, Feb. 1983. Electrical Engineer, June 1983.

Ph.D. Thesis: *Efficient Methods for Massively Parallel Symbolic Induction.* (Prof. Patrick Winston)

S.M. Thesis: *Parallelism in Arms and Legs.* (Prof. Marvin Minsky)

Jan. 1976–May 1978: B.A., Mathematics. **Reed College**, Portland, OR.

GPA: Cumulative 3.83/4.0; junior & senior years 3.93/4.0.

Senior Thesis: *Markov Chains on Finite Groups.* (Prof. Jack Dudman)

Jan. 1974–May 1975: (part-time) **Anchorage Community College**, Anchorage, AK.

Sept. 1972–May 1973: **New College**, Sarasota, FL.

HONORS AND ACCOMPLISHMENTS:

May 2009: UCI Professor of the Year, annual Celebration of Teaching awards.

Feb. 2009: Dean's Award for Undergraduate Teaching.

Jan. 2006: Appreciation Award, Equity Advisor, UCI Advance Program for gender equity among the faculty.

Nov. 2005: Innovation Award, UCI Office of Technology Alliances.

Apr. 2004: Co-founding scientist and Scientific Advisory Board of CODA Genomics, Inc., a company dedicated to applying information technology to gene design and synthetic biology. I was a co-inventor of US Patent No. 7,262,031 ("Method for Producing a Synthetic Gene or Other DNA Sequence").

Jan. 2004: Finalist, U.S. National Science Foundation Distinguished Teaching Scholar award.

May 2003: UCI Chancellor's Award for Excellence in Fostering Undergraduate Research.

Mar. 2002: Editorial Board of *IEEE Intelligent Systems*.

Jan. 2002: Biography listed in *Who's Who in the World'2002*.

Dec. 2001: Best Paper Award, International Conference on Genome Informatics (first author).

Oct. 2001: Editorial Board of *J. Molecular and Cellular Proteomics*.

June 2001: Scientific Advisory Board of University of Colorado, Denver, Center for Computational Biology.

May 2001: Scientific Advisory Board of GeneFormatics, Inc., a proteomics drug discovery company. The company merged with Structural Bioinformatics, Inc., in March, 2003, to form Cengent, Inc.

Nov. 1999: Biography listed in *Who's Who in America'2001*.

Apr. 1999: Cover article, *AI Magazine*, (first author).

July 1998: Innovative Application Award, AAAI/IAAI Conference, (first author). Estimated current and nearby HIV drug resistant mutants and recommended drug combination treatments to avoid both. The research appeared on the cover of *AI Magazine* in Spring, 1999.

June 1998: UCI Excellence in Teaching Award for undergraduate teaching.

July 1997: Scientific Advisory Board of CombiChem, Inc., a computational analysis and combinatorial chemistry drug discovery company. The company went public with 78 full-time employees in May, 1998, and was bought by Dupont Co. for \$95 million in Dec., 1999.

Feb. 1997: UCI/ICS Departmental Outstanding Faculty Award for teaching and research.

Oct. 1996: CAREER grant award from National Science Foundation.

July 1996: Constructive proof that the Halting Problem is formally learnable from examples, to arbitrarily high accuracy with arbitrarily high confidence, under any probability distribution (sole author, *Proc. Intl. Conf. Machine Learning*).

June 1996: Member of Founding Board of Directors, and Founding Treasurer, International Society for Computational Biology.

Feb. 1996: Cover article, *J. Molecular Biology*, (first author). Found global optimum protein “threading” with speed-ups exceeding 10^{25} over best previously published result using the same formalism.

Sep. 1994: Published NP-completeness proof (sole author, *Protein Engineering*).

May 1990: MIT EE&CS George M. Sprowl award for excellence in Ph.D. thesis (\$1,250). My thesis was nominated by MIT for the ACM Distinguished Doctoral Dissertation award.

Sept. 1989: Co-founding scientist of Arris Pharmaceutical Corp., a company dedicated to drug discovery by integrating machine learning with advanced biology and chemistry. I was a co-inventor of US Patent No. 5,526,281 (“Machine Learning Approach to Modeling Biological Activity for Molecular Design and to Modeling Other Characteristics”). Arris went public with 59 full-time employees and a valuation of approximately \$60 million in Nov., 1993. It merged with Sequana to form AxyS Pharmaceuticals in Jan., 1998, which was acquired by Celera Therapeutics for \$188 million in Nov., 2001.

Nov. 1987: Cover article, *Communications of the ACM*, (first author). The program later was integrated into the commercial package PROTEAN for molecular biologists by DNASTAR under an NIH/SBIR grant.

July 1987: Best Paper Award, ACM/IEEE International Design Automation Conference (first author).

June 1986: Elected to Sigma Xi (the national scientific research honor society).

April 1986: First published $\mathcal{O}(n)$ algorithm for sequential fully-constrained tree-structured robot forward dynamics (sole author, *IEEE Intl. Conf. Robotics and Automation*).

Summer 1985: First published $\mathcal{O}(\log n)$ algorithm for parallel unconstrained single-chain robot inverse dynamics (sole author, *Intl. J. Robotics Research*).

Fall 1980: National Science Foundation Graduate Fellowship.

June 1978: Elected to Phi Beta Kappa (the national academic honor society).

April 1977: Licensed as a Nuclear Reactor Operator by the U.S. Nuclear Regulatory Commission.

PROFESSIONAL MEMBERSHIPS:

American Association for Artificial Intelligence (AAAI; Life Member).

Association for Computing Machinery (ACM).

Institute of Electrical and Electronic Engineers (IEEE).

International Society for Computational Biology (ISCB).

INVITED PRESENTATIONS

(excludes conference papers, session moderating, tutorials, etc.)

Dec. 2007: Keynote address, Rocky Mountain Bioinformatics Conf., Snowmass, CO (Larry Hunter).

Feb. 2007: UCI Entrepreneurs Forum, invited talk (invited by Dave Schetter).

Dec. 2006: Inter-Nano-Science, 21st Center of Excellence Japanese Government Project Symposium, Awaji, Japan, Invited Talk (Takashi Washio).

Nov. 2006: Human Proteome Organization Conf., Invited Talk (Cindi Lilly).

Aug. 2006: World Congress on Biomedical Engineering and Medical Physics, Seoul, Korea, Invited Talk (Tatsuya Akutsu).

Apr. 2006: UCI CAL-IT2, invited talk at Knobbe Martens Olsen & Bear program series on "synthetic biology/bioinformatics and the CODA Genomics story. (Debbie Nielsen).

Mar. 2006: University of California, Merced, Research Seminar (Masa Watanabe).

Feb. 2006: UCI CAL-IT2, invited presentation to David Crane, Gov. Schwarzenegger's special advisor for jobs and economic growth; and Mindy Fletcher, deputy chief of staff for internal affairs in the governor's office, on their visit to evaluate the economic impact and job development aspect of CAL-IT2 as one of the California Institutes for Science and Innovation (Albert Yee).

May 2005: University of Pittsburgh, PA, Research Seminar (Takis Benos).

Aug. 2004: 8th Pacific Rim International Conference on Artificial Intelligence, Conference Keynote Speech (Hans Guesgen).

Mar. 2003: University of Minnesota, Minneapolis, MN, Bioinformatics Symposium "Bioinformatics: Building Bridges," Invited Talk (Lynda Ellis).

Dec. 2002: Conference on Genome Informatics, Tokyo, Conference Opening Address (Satoru Miyano).

May 2002: Workshop on Post-Genomic Knowledge Discovery, National University of Singapore, Invited Talk (Limsoon Wong).

May 2002: SIAM Conf. on Optimization, Toronto, Ontario, Canada, Invited Talk (Harvey Greenberg).

June 2001: Rigel Pharmaceuticals, Research Seminar (Kunbin Qu).

Dec. 2000: Oncotech, Research Seminar (Shubra Mittal).

Aug. 2000: Intelligent Systems and Molecular Biology Conf., San Diego, CA, Invited Panelist on Lisp in Bioinformatics (Sheng-Chuan Wu).

July 2000: ICML-2000 Workshop on Machine Learning of Spatial Knowledge, Stanford, CA, Invited Panelist (David Page, Diane Cook).

June 2000: DARPA Computation, Biology, and Language Workshop, Arlington, VA, Invited Panelist (Bob Berwick, Simon Kasif).

Jan. 2000: Pacific Symposium on Biocomputing, Oahu, HI, Invited Panelist on Data Mining in Biological Databases (Janice Glasgow).

Dec. 1999: University of Wisconsin, Madison, WI, Distinguished Lecture Series in Biomedical Informatics (Mark Craven, David Page).

Nov. 1999: University of Chicago, Chicago, IL, Research Seminar (Ridg Scott).

Oct. 1999: Montana State University, Bozeman, MT, Research Seminar (Marcella McClure).

May 1999: Conf. on Data Mining in Crystallography, Erice, Sicily, Italy, Invited Lecturer (Suzanne Fortier).

Oct 1998: Harvey Mudd College, Claremont, CA, Research Seminar (Margaret Fleck).

May 1998: Information Sciences Institute, Marina del Rey, CA, Research Seminar (Kevin Knight).

Jan. 1998: Pacific Symposium on Biocomputing, Kapalua, HI, Invited Panelist on Challenges in Annotating Genomes (Ying Xu).

Nov. 1997: Washington University at St. Louis, MO, Research Seminar (David States).

June 1997: Intelligent Systems and Molecular Biology Conf., Halkidiki, Greece, Conference Keynote Speaker (Alfonso Valencia).

May 1997: Symposium on Bioinformatics, Structure, and Function, Urbana, IL, Invited Talk (Shankar Subramaniam).

Feb. 1997: Intl. Congress on Gene Function Determination, Washington, D.C., Invited Talk (Thom Bliss).

Sept. 1996: UC Irvine Life Science Research and Technology Showcase, Irvine, CA, Invited Talk (David Schetter).

Aug. 1996: Stanford University, Stanford, CA, Research Seminar (Russ Altman).

Aug. 1996: Innovative Applications of Artificial Intelligence Conf., Portland, OR, Conference Invited Survey Talk (Howard Shrobe).

June 1996: University of Bergen, Norway, First Opponent of Inge Jonassen doctoral thesis defense (Ingrid Eidhammer).

June 1996: Intelligent Systems and Molecular Biology Conf., St. Louis, MO, Conference Banquet After-dinner Speaker (David States).

Mar. 1996: Workshop on Prediction and Modelling of Protein Structures, EMBO/European Bioinformatics Institute, Hinxton, England, Invited Talk (Gerrit Vriend).

Sept. 1995: Washington State University, Pullman, WA, Research Seminar (Keith Dunker).

July 1995: American Crystallographic Association Meeting, Montreal, Invited Talk (Suzanne Fortiers).

Mar. 1995: Workshop on Global Minimization of Nonconvex Energy Functions, DIMACS, Rutgers University, Piscataway, NJ, Invited Talk (Panos Pardalos).

Mar. 1995: Symposium on Genome Project and Computer Science, Tokyo, Invited Talk (Toshihisa Takagi).

Jan. 1995: Santa Fe Institute, Santa Fe, NM, Research Seminar (Stuart Kauffman).

COMMUNITY SERVICE:

2002, 2007-2009: Senior Area Chair, Intl. Conf. on Intelligent Systems for Molecular Biology.

2001-present: Grant proposal review panel, National Institutes of Health (Chair, 2003-2004; Auxiliary Chair, 2005-present; BDMA, MSFD).

Apr. 2005: Program Committee, Intl. Conf. on Machine Learning.

Apr. 2005: Program Committee, European Conf. on Computational Biology.

1993-2004: Program Committee, Intl. Conf. on Intelligent Systems for Molecular Biology.

2000-2004: Program Committee, Intl. Conf. on Genome Informatics.

Mar. 2003: Program Committee, Intl. Conf. on Knowledge Discovery and Data Mining.

Dec. 2002: Co-Chair of Program Committee, Intl. Conf. on Genome Informatics.

Dec. 2002, Jan. 2000: Grant proposal review panel, National Science Foundation

Sept. 2002, Sept. 2000: Symposium Organizer, Structural Genomics at UCI.

May 2002: Organizing Committee, Workshop on Post-Genomic Knowledge Discovery, National University of Singapore.

2001-2002: Advisory Board, University of Colorado, Denver, Center for Computational Biology.
Aug. 1999 – Dec. 2001: Site Selection Coordinator, Intl. Conf. on Intelligent Systems for Molecular Biology.
June 2001: Session Co-Organizer, Informatics and the New Biology, Pacific Division meeting of the AAAS.
Jan. 2001: Co-chair, DNA Structure, Interactions, and Expression, at Pacific Symposium on Biocomputing.
May 2000: Member, Bioinformatics Working Group of the National Advisory Research Resources Council, National Institutes of Health.
Apr. 1999: Program Committee, Intl. Conf. on Computational Molecular Biology.
1996-1999: Chair and Co-chair, Protein Structure Prediction Session, at Pacific Symposium on Biocomputing.
Jul. 1998: Tutorial, Computational Molecular Biology, at Natl. Conf. on Artificial Intelligence.
Jun. 1998, Aug. 1994: Organizing Committee, Intl. Conf. on Intelligent Systems for Molecular Biology.
Dec. 1997: Program Committee, Workshop on Genome Informatics.
Jun. 1996: Member of Founding Board of Directors, and Founding Treasurer, Intl. Society for Computational Biology.
1993-1995: Chair and Co-chair, Protein Structure Prediction Session, at Hawaii Intl. Conf. on System Sciences.
Jan. 1994: Tutorial, Protein Structure Prediction, at Hawaii Intl. Conf. on System Sciences.
Aug. 1993: Program Committee, AI and Genome Workshop, at Intl. Joint Conf. on Artificial Intelligence.
Aug. 1993: Organizing Committee, Macromolecules, Genes and Computers Conf.
Jul. 1993: Tutorial, Intro. to AI for Biologists, at Intl. Conf. on Intelligent Systems for Molecular Biology.
Jul. 1990: Program Committee, Conf. on Bioinformatics, Integration of Organismic and Molecular Data Bases, and Use of Expert Systems in Biology; and Chair, Protein Sequence Functional Analysis.
Jul.–Aug. 1987: Organizing Committee, Workshop on the Matrix of Biological Knowledge; and Co-Chair, Framework Group; and tutorial, Introduction to Artificial Intelligence for Biologists.

REVIEWING (since 1996):

Organizations

Review panel, site visits (BDMA, MSFD; Chair, Auxiliary Chair), National Institutes of Health (NIH).
Review panel, National Science Foundation (NSF).
U.S. Civilian Research and Development Foundation (CRDF)
National Science, Education, and Research Commission (NSERC, Canada)
Australian Research Council (Australia)
Montana State NSF-EPSCoR (University of Montana)

Journals

ACM J. on Experimental Algorithmics
Bioinformatics
CABIOS (Computer Applications in the BioSciences)
IEEE Intelligent Systems
J. of Artificial Intelligence Research
J. of Bioinformatics and Computational Biology
J. of Computational Biology
J. of Constraints
J. of Molecular Biology
J. of New Generation Computing

J. of Theoretical Biology
Mathematical Biosciences
Machine Learning
Molecular and Cellular Proteomics
Proceedings of the National Academy of Sciences
Protein Science
Protein Engineering
Proteins: Structure, Function, and Genetics

Conferences

Conference on Information, Statistics, and Induction in Science (ISIS)
Conference on Intelligent Systems for Molecular Biology (ISMB)
Genome Informatics Conference (GIW)
Pacific Symposium on Biocomputing (PSB)
Research in Computational Molecular Biology (RECOMB)
Symposium on Discrete Algorithms (SODA)

INDUSTRIAL EXPERIENCE:

Apr. 2004: **Co-Founder, Scientific Advisory Board, Consultant.**

CODA Genomics, inc. (Irvine, CA).

The company is dedicated to applying information technology to synthetic biology. I was a co-inventor of US Patent No. 7,262,031 (“Method for producing a synthetic gene or other DNA sequence”).

July 2001–Dec. 2002: **Scientific Advisory Board.**

GeneFormatics, Inc. (San Diego, CA).

The company is dedicated to a proteomics approach to drug discovery. The company merged with Structural Bioinformatics, Inc., in March, 2003, to form Cengent, Inc.

April 1997–Dec. 1999 (part-time): **Scientific Advisory Board, Consultant.**

CombiChem, Inc. (San Diego, CA).

The company is dedicated to drug discovery by computational analysis and combinatorial chemistry. CombiChem went public with 78 full-time employees in May, 1998, and was bought by Dupont Co. for \$95 million in Dec. 1999.

May 1989–Dec. 1993 (part-time): **Co-Founder, Senior Scientist, Consultant.**

Arris Pharmaceutical Corp., (South San Francisco, CA).

The company is dedicated to drug discovery by integrating artificial intelligence and machine learning with advanced biology and chemistry. It went public in Nov., 1993, with 59 full-time employees and a valuation of approximately \$60 million. Human clinical trials of a novel asthma drug began in Jan., 1994. I was a co-inventor of US Patent No. 5,526,281 (“Machine Learning Approach to Modeling Biological Activity for Molecular Design and to Modeling Other Characteristics”). Arris merged with Sequana to form AxyS Pharmaceuticals in Jan., 1998, which was acquired by Celera Therapeutics for \$188 million. in Nov., 2001.

June 1984–Aug. 1991 (summers): **Software Engineer, Consultant.**

Gould/A.M.I. VLSI CAD Research Laboratory, (Twain Harte, CA).

Researched relation of structure to function in VLSI. Designed and implemented a mixed-mode functional simulator, a structural circuit optimizer, and a functional abstraction from structure prototype.

June 1982–Sept. 1983 (summers): **Summer Staff.**

Hewlett-Packard Engineering Productivity Division (Cupertino, CA).

Assisted the design and implementation of a silicon compiler (DPG, the Data-Path Generator).

Jan.–May 1980: **Business Software Consultant.**

Solid State Equipment Ltd. (Lower Hutt, New Zealand).

Developed inventory control/job status monitoring package for small businesses.

Aug. 1978–April 1979: **Data Telecommunications Programmer/Analyst.**

Progress Electronics (Portland, OR).

Wrote entire assembler telecommunications sub-system for the master controller of a remote water-level telemetry system for the National Oceanic and Atmospheric Administration, and a remote air quality and meteorological sensor system for Oregon Department of Environmental Quality.

May–Sept. 1977: **Chief Programmer.**

NSF-SOS research project (Portland OR).

Designed and implemented complete system for gamma spectra analysis and statistical processing of data.

May–Oct. 1975, May–Sept. 1976: **Business Programmer/Analyst.**

Alaskan Data Systems (Anchorage AK).

Designed and implemented all programs for each phase of internal bookkeeping system.

April 1974–May 1975: **Programmer and production control supervisor.**

U.S. Postal Service (Anchorage, AK).

Wrote numerous programs pertaining to productivity analysis and manpower utilization. Developed a computer-assisted training system later adopted by Western Region HQ.

EDITED VOLUMES:

Proceedings, Genome Informatics 2002, eds. Lathrop, R., Nakai, K., Miyano, S., Takagi, T., Kanehisa, M. Universal Academy Press, Tokyo, 2002.

(Guest Editor of Special Issue of Journal). “Intelligent Systems in Biology II,” ed. Lathrop, R.H., *IEEE Intelligent Systems*, 17(2), March/April, 2002.

(Guest Editor of Special Issue of Journal). “Intelligent Systems in Biology,” ed. Lathrop, R.H., *IEEE Intelligent Systems*, 16(6), November/December, 2001.

Proceedings, Sixth Intl. Conf. on Intelligent Systems for Molecular Biology, eds. Glasgow, J., Lathrop, R., Littlejohn, T., Major, F., Peitsch, M., Sankoff, D., Sensen, C., AAAI Press, Menlo Park, 1998.

Proceedings, Second Intl. Conf. on Intelligent Systems for Molecular Biology, eds. Altman, R., Brutlag, D., Karp, P., Lathrop, R., Searls, D., AAAI Press, Menlo Park, 1994.

BOOK CHAPTERS:

“Protein Threading,” Bienkowska, J., and Lathrop, R.H., in *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics*, ed. Jorde, L., John Wiley & Sons, Hoboken, New Jersey, 2005.

“Analysis and Algorithms for Protein Sequence-Structure Alignment,” Lathrop, R.H., Rogers, R.G. Jr., Bienkowska, J., Bryant, B.K.M., Buturović, L.J., Gaitatzes, C., Nambudripad, R., White, J.V., and Smith, T.F., in *Computational Methods in Molecular Biology*, eds. Salzberg, S., Searls, D., Kasif, S., Elsevier Science, Amsterdam, 1998.

“Predicting Protein Structure with Probabilistic Models,” Stultz, C.M., Nambudripad, R., Lathrop, R.H., and White, J.V., in *Protein Structural Biology in Biomedical Research*, eds. Allewell, N., Woodward, C., Vol. 22B of *Advances in Molecular and Cell Biology, 1997*, series ed. Bittar, E.E., JAI Press, Greenwich, CT, USA, 1997.

“The Identification of Protein Functional Patterns,” Smith, T.F., Lathrop, R.H. and Cohen, F.E., in *Integrative Approaches to Molecular Biology*, eds. Collado-Vides, J., Magasanik, B., and Smith, T.F., MIT Press, Cambridge, MA, 1996.

“Massively Parallel Symbolic Induction of Protein Structure / Function Relationships,” Lathrop, R.H., Webster, T.A., Smith, T.F., and Winston, P.H., pp. 157–173 in *Machine Learning: From Theory to Applications*, eds. Hanson, S., Remmele, W., and Rivest, R., Springer-Verlag, Berlin, 1993; also appeared in *Proc. 27th Hawaii Intl. Conf. on System Sciences*, IEEE Computer Soc. Press, 1991.

“Integrating AI With Sequence Analysis,” Lathrop, R.H., Webster, T.A., Smith, R., Winston, P.H., and Smith, T.F., pp. 210–258 in *Artificial Intelligence and Molecular Biology*, ed. Hunter, L., AAAI Press, Menlo Park, 1993.

“ARIEL: A Massively Parallel Symbolic Learning Assistant for Protein Structure / Function,” Lathrop, R.H., Webster, T.A., Smith, T.F., and Winston, P.H., in *Artificial Intelligence at MIT: Expanding Frontiers*, eds. Winston, P.H., and Shellard, S., MIT Press, Cambridge, MA, 1990.

REFEREED JOURNAL ARTICLES:

“Novel TUTase associates with an editosome-like complex in mitochondria of *Trypanosoma brucei*,” Aphasizheva, I., Ringpis, G.-E., Weng, J., Gershon, P.D., Lathrop, R.H., Aphasizhev, R., *RNA*, in press, 2009.

“Computationally Optimized DNA Assembly of synthetic genes,” Larsen, L.S.Z., Wassman, C.D., Hatfield, G.W., Lathrop, R.H., *Intl. J. Bioinformatics Research and Applications*, 4(3):324-336, 2008.

“Genome wide screens in yeast to identify potential binding sites and target genes of DNA binding proteins,” Zheng J., Yan J., Wang T., Mosbrook-Davis D., Dolan K., Christensen R., Stormo G., Haussler D., Lathrop R.H., Brachmann R., Burgess S., *Nucleic Acids Research*, Jan; 36(1):e8, 2008.

“Choosing where to look next in a mutation sequence space: Active Learning of informative p53 cancer rescue mutants,” Danziger SA, Zeng J, Wang Y, Brachmann RK, Lathrop RH, *Bioinformatics*, Jul 1;23(13), 2007; co-published in *2007 Proc. Intl. Conf. on Intelligent Systems for Molecular Biology*.

“A fine-grain statistical phylogeography of influenza A H5N1,” Wallace, R.G., HoDac, H., Lathrop, R.H., Fitch, W.M., *Proc. Natl. Acad. Sci., USA*, Mar 13;104(11):4473-8, 2007.

“DNA Deformation Energy as an Indirect Recognition Mechanism in Protein-DNA Interactions,” Aeling, K., Steffen, N.R., Johnson, M., Hatfield, G.W., Lathrop, R.H., Senear, D.F., *IEEE Trans. on Computational Biology and Bioinformatics*, Jan-Mar;4(1):117-25, 2007.

“GRA1 protein vaccine confers better immune response compared to codon-optimized GRA1 DNA vaccine,” Doskaya M., Kalantari-Dehaghi M., Walsh C.M., Hiszczynska-Sawicka E., Davies D.H., Felgner P.L., Larsen L.S., Lathrop R.H., Hatfield G.W., Schulz J.R., Guruz Y., Journak F., *Vaccine*, 25(10):1824-37, Feb. 26, 2007. Epub Nov. 20, 2006.

“Functional census of mutation sequence spaces: The example of p53 cancer rescue mutants,” Danziger, S.A., Swamidass, S.J., Zeng, J., Dearth, L.R., Lu, Q., Chen, J.H., Cheng, J., Hoang, V.P., Saigo, H., Luo, R., Baldi, P., Brachmann, R.K., and Lathrop, R.H., *IEEE Transactions on Computational Biology and Bioinformatics*, 3(2):114-25, Apr.-Jun., 2006.

“Hybrid Biomedical Database Integration: A p53 cancer research database,” Bichutskiy, V., Colman, R., Brachmann, R.K., Lathrop, R.H., *Cancer Informatics*, 2:277-287, 2006.

“Indirect recognition in sequence-specific DNA binding by Escherichia coli integration host factor: the role of DNA deformation energy,” Aeling, K.A., Opel, M.L., Steffen, N.R., Tretyachenko-Ladokhina, V., Hatfield, G.W., Lathrop, R.H., Senear, D.F., *J. Biol. Chem.*, 281(51):39236-48, Dec. 22, 2006. Epub 2006 Oct 11.

“HB tag modules for PCR-based gene tagging and tandem affinity purification in *Saccharomyces cerevisiae*,” Tagwerker, C., Zhang, H., Wang, X., Larsen, L.S., Lathrop, R.H., Hatfield, G.W., Auer, B., Huang, L., Kaiser, P., *Yeast*, 23(8):623-32, Jun., 2006.

“Predicting Oligonucleotide-Directed Mutagenesis Failures in Protein Engineering,” Wassman, C.D., Tam,

P.Y., Lathrop, R.H., Weiss, G.A., *Nucleic Acids Research*, 32(21):6407–6413, 2004.

“DNA Sequence and Structure: Direct and Indirect Recognition in Protein-DNA Binding,” Steffen, N.R., Murphy, S.D., Toller, L., Hatfield, G.W., Lathrop, R.H., *Bioinformatics*, 18 Suppl 1:S22-S30, 2002.

“Information-Theoretic Dissection of Pairwise Contact Potentials,” Cline, M.S., Karplus, K., Lathrop, R.H., Smith, T.F., Rogers, R.G. Jr., Haussler, D., *Proteins: Structure, Function, Genetics*, 49(1):7-14, 2002.

“An Anytime Local-to-Global Optimization Algorithm for Protein Threading in Theta (m^2n^2) Space,” Lathrop, R.H., *J. Computational Biology*, Fall-Winter, 6(3-4):405-18, 1999.

“Combinatorial Optimization in Rapidly Mutating Drug-Resistant Viruses,” Lathrop, R.H., Pazzani, M.J., *J. Combinatorial Optimization*, 3:301–320, 1999.

“A Bayes-Optimal Probability Theory that Unifies Protein Sequence-Structure Recognition and Alignment.” Lathrop, R.H., Rogers, R.G. Jr., Smith, T.F., White, J.V., *Bull. Math. Biol.*, 60:1039–1071, 1998.

“Current Limitations to Protein Threading Approaches,” Smith, T.F., Lo Conte, L., Bienkowska, J., Gaiatzes, C., Rogers, R.G. Jr., and Lathrop, R.H., *J. Computational Biol.*, 4(3):217–225, 1997.

“Solving the Multiple-Instance Problem with Axis-Parallel Rectangles,” Dietterich, T.G., Lathrop, R.H., Lozano-Perez, T., *Artificial Intelligence*, 89:31-71, 1997.

“Global Optimum Protein Threading with Gapped Alignment and Empirical Pair Potentials,” Lathrop, R.H. and Smith, T.F., *J. Mol. Biol.* (cover article), 255:641–665, Feb., 1996.

“Compass: A Shape-Based Machine Learning Tool for Drug Design,” Jain, A.N., Dietterich, T.G., Lathrop, R.H., Chapman, D.E., Critchlow, R.E., Bauer, B.E., Webster, T.A., Lozano-Perez, T., *J. Computer-Aided Molecular Design*, 8:635–652, Dec., 1994.

“The Protein Threading Problem With Sequence Amino Acid Interaction Preferences Is NP-Complete,” Lathrop, R.H., *Protein Engineering*, 7(9):1059–1068, Sept., 1994.

“Acid Helix-Turn Activator Motif,” Zhu, Q.-L., Smith, T.F., Lathrop, R.H., and Figge, J., *Proteins: Structure, Function, and Genetics*, 8:156-163, 1990.

“Potential Structural Motifs for Reverse Transcriptases”, Webster, T.A., Patarca, R., Lathrop, R.H., Smith, T.F., *Molecular Biology and Evolution*, 6(3):317–320, 1989.

“Pattern Descriptors and the Unidentified Reading Frame 6 Human mtDNA Dinucleotide-Binding Site”, Webster, T.A., Lathrop, R.H., Smith, T.F., *Proteins: Structure, Function, and Genetics*, 3:97–101, 1988.

“ARIADNE: Pattern-Directed Inference and Hierarchical Abstraction in Protein Structure Recognition”, Lathrop, R.H., Webster, T.A., Smith, T.F., *Communications of the ACM*, (cover article) 30(11):909–921, Nov., 1987.

“Prediction of a Common Structural Domain in Aminoacyl-tRNA Synthetases through Use of a New Pattern-Directed Inference System”, Webster, T.A., Lathrop, R.H., Smith, T.F., *Biochemistry*, 26:(22)6950–6957, Nov., 1987.

“Consensus Topography in the ATP Binding Site of the Simian Virus 40 and Polyomavirus Large Tumor Antigens”, Bradley, M.K., Smith, T.F., Lathrop, R.H., Livingston, D.M., Webster, T.A., *Proc. National Academy of Science (PNAS)*, 84:4026–4030, June, 1987.

“Parallelism in Manipulator Dynamics”, Lathrop, R.H., *Intl. J. of Robotics Research*, Summer, 1985, pp. 80–102; also appeared in *Proc. IEEE Intl. Conf. on Robotics and Automation*, pp. 772–778, St. Louis, MO, March 25–28, 1985.

JOURNAL ARTICLES, OTHER:

“Knowledge-based Avoidance of Drug-Resistant HIV Mutants,” Lathrop, R.H., Steffen, N.R., Raphael, M., Deeds-Rubin, S., Pazzani, M.J., Cimoch, P.J., See, D.M., Tilles, J.G., (cover illustration; invited article from IAAI Conference paper of same title, below), *AI Magazine*, 20(1):13–25, Spring, 1999.

“ ‘Functional Abstraction’ Anticipates Timing Glitches,” Lathrop, R.H., Hall, R.J., Duffy, G., Alexander, K.M., and Kirk, R.S., *IEEE Spectrum*, 27(4):41–42, April, 1990.

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