

## CURRICULUM VITAE

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Name: Temple F. Smith

Address: BioMolecular Engineering Research Center  
Boston University  
36 Cummington Street  
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Date of Birth: March 7, 1939

Place of Birth: Auburn, New York

**Education:** Ph.D., 1969: Physics Department, University of Colorado, Boulder.  
B.S., 1963: Physics Department, Purdue University, Lafayette, IN  
Postdoctoral Fellow, March 1969 - August 1971: Department of Biophysics and Genetics,  
University of Colorado Medical School, Boulder.

### Professional Experience

- 1969 - 1971: Postdoctoral Fellow, NIH with Dr. Stanislaw Ulam (Chairman, Math. Dept. Univ. of Colo.), Dr. T.T. Puck (Eleanor Roosevelt Institute for Cancer Research, Colorado Medical Center) and Dr. John R. Sadler (Colorado Medical School) in bacterial genetic regulation.
- 1975 - 1979: Visiting Staff Member, Applied Mathematics and Theoretical Biology Divisions, Los Alamos Scientific Laboratory, Los Alamos, NM, as one of the original organizers of GenBank (1979-1980).
- 1971 - 1984: Professor, Department of Physics, Northern Michigan University, Marquette, MI.
- 1975 - 1976: NMU-AAUP Faculty Union Vice-President and Union negotiator.
- 1978 - 1979: Sabbatical leave, Visiting Associate Professor, Dept. of Molecular Biophysics and Biochemistry, Yale University, New Haven, Connecticut.
- 1980 - 1981: Visiting Professor, Biology/Mathematics Dept, University of Southern California, Los Angeles.
- 1981 - 1982: Visiting Staff Member, National DNA Data Bank, Theoretical Biology Group, Los Alamos National Laboratory, Los Alamos, NM.
- 1986: Organizer, MacroMolecules, Genes and Computers International Symposium and Workshop, Waterville Valley, New Hampshire.
- 1987: Co-organizer, Santa Fe Matrix of Biological Knowledge Workshop (on the application of modern computer science to integration of various bioclinical data resources).
- 1988: Co-organizer, computer protein structure workshop, Protein Society Symposium, San Diego, CA.
- 1989: Organizer, 1989 MacroMolecules, Genes and Computers: Chapter Two, International Symposium and Workshop, Waterville Valley, N.H.
- 1985 - 1991: Director, Molecular Biology Computer Research Resource, Dana-Farber Cancer Institute, Harvard Medical School and the Harvard School of Public Health.
- 1991 - Director, BioMolecular Engineering Research Center and Professor, Departments of Biomedical Engineering, Boston University and Pharmacology, Boston University School of Medicine.
- 1993: Organizer, 1993 MacroMolecules, Genes and Computers: Chapter Three, International Symposium and Workshop, Waterville Valley, N.H.
- 1995 - Senior Consultant and acting Bioinformatics division head, INCYTE Pharmaceuticals, Inc., Palo Alto, California.
- 1999: Co-organizer, 1999 Institute for the Academic Advancement of Youth *Discovering Biotechnology Day*.
- 2000: Co-Founder and Chief Information Officer, Modular Genetics, Inc.
- 2004 - 2005: Director, Graduate Program in Bioinformatics, Boston University

**Committee Service:**

- 1979 - 1986: NIH/DRR and NIH/IGMS Grant Review Committee Chairman, special study sessions on computer analyses in molecular biology.
- 1984 - Editorial board of Molecular Biology and Evolution.
- 1985 - 1987: DOE Human Genome project advisory committee.
- 1987 - 1989: Howard Hughes Medical Institutes Human Gene Mapping Library review and advisory panel.
- 1987 - 1988: National Science Foundation Science Center's program review panel.
- 1988: NIH Director's Ad Hoc Program Advisory Committee on Complex Genomes (Human Genome Initiative planning committee).
- 1988: National Library of Medicine IAIMS summer symposium planning committee.
- 1988 - 1989: Woods Hole Marine Biological Laboratory Library Planning Committee.
- 1990 - 1992: National Research Council Scientific and Technical Information Board.
- 1990: Elected to International Human Genome Organisation (HUGO).
- 1991: Tenure Committee (Chairman), College of Engineering, Boston University
- 1994: Editorial board of The Journal of Computational Biology.
- 1994-96: Graduate Committee, Department of Biomedical Engineering
- 1996-7: Tenure Committee, Boston University
- 1996-present: Undergraduate Committee, Department of Biomedical Engineering
- 1998-present: Advisory Board member for the Flybase Project, Harvard University
- 2002-present: Curriculum Committee, Bioinformatics Program, Boston University
- 2000-present: Advisory Committee Member, Resource for Biocomputing, Visualization and Informatics, U. of California, San Francisco

**Grant Support:**

- 1974 - 1976: Lac Operator Characterization, \$46,000 (NIH).
- 1979 - 1981: Molecular Sequence Analysis, \$47,500 (NIH).
- 1982 - 1984: Genetic Information Analysis (with Dr. M.S. Waterman), \$320,000 (Systems Development Foundation, Palo Alto, CA).
- 1983 - 1986: Molecular Sequence Analysis, \$160,000 (NIH).
- 1985 - 1989: Molecular Biology Computer Research Resource, \$1,725,000 (NIH).
- 1986 - 1988: Symposium grants from NIH/DRR, IBM, Digital Corp., NEC, National Library of Medicine, Sloan Foundation, and Sun Microsystems, \$200,000.
- 1988 - 1991: Protein Functional Domain Identification, \$545,000 (NSF).
- 1990 - 1995: Molecular Biology Computer Research Resource, \$4,000,000 (NIH).
- 1990: Predicting Protein Overall Structural Class, \$42,500 (NSF).
- 1990 - 1993: Isolation and Characterization of Rodent Lentiviruses (with R. Ruprecht), \$254,831 (NIH).
- 1993: Symposium travel award grant, \$30,000 - Sloan Foundation.
- 1994 - 1995: Sponsored Research agreement, \$174,000 (INCYTE Pharmaceuticals, Inc.)
- 1995 - 1999: BioMolecular Engineering Research Center, \$2,546,757 (NIH).
- 1995 - 2000: Institutional Training Grant in Genomic Science, \$700,988 (NIH).
- 1998-2001: Microbial protein and regulatory function analysis and database program, \$1,082,042 (DOE).
- 1998-2001: The inverse folding approach to protein structure prediction, \$400,000 (NSF).
- 1999-2000: Sponsored research agreement, \$150,000 (Genetics Institute).
- 2000-2004: Subcontract with Massachusetts General Hospital under NIH prime grant, "Activation of inflammation stress response pathways" (B. Seed PI), \$878,414.
- 2000-2005: Consortium with U. of Texas Southwest Med. Ctr. Under NIH prime grant, "Alliance for Cellular Signaling" (A. Gilman PI), \$75,000.
- 2001-2006: Automated protein fold model generation, \$450,000 (NIH).
- 2002-2008: The Eukaryotic core. \$1,700,000 (NSF).

**Teaching Experience:**

- 1964: U.S. Air Force, Lowry Training Center, Denver, Colorado.  
 1967: Instructor, Physics Department, University of Colorado, Denver Extension.  
 1969: Instructor, University of Colorado Medical School, University of Colorado.  
 1971 - 1984: Professor, Department of Physics, Northern Michigan University, Marquette, Michigan.  
 1978 - 1979: Visiting Associate Professor, Department of Molecular Biophysics and Biochemistry, Yale University.  
 1985 - Biostatistics Department, Harvard School of Public Health and Biochemistry and Molecular Pharmacology Department, Harvard Medical School.  
 1992 – 2002: Pharmacology, Boston University School of Medicine  
 1992 - Biomedical Engineering, Boston University

**Courses Taught, 1971 to present:**

Finite Mathematics of Molecular Biology (graduate)  
 Molecular Biology  
 Microcomputer Architecture and Programming  
 Biochemistry/Protein Structure  
 Introductory Engineering Physics  
 Numerical Taxonomy (graduate)  
 Advanced Biochemistry Techniques, Laboratory  
 Physics for premeds and biology majors  
 Quantum Mechanics  
 Introductory Computer Programming  
 Medical Physics  
 Statistical Mechanics  
 Modern Physics Laboratory  
 Introduction to Modern Physics  
 A cytogenetics laboratory course  
 Medical statistics  
 Introduction to Engineering  
 Molecular Pharmacology (graduate)  
 Molecular Architecture (graduate)  
 Signals & Systems in Biomedical Engineering  
 Biological Database Analysis

**Publications:**

- Smith, T.F. (1969). The genetic code, information density, and evolution. *Mathematical Biosciences* **4**, 179.
- Sadler, John R. and Smith, Temple F. (1971). Mapping of the lactose operator. *Journal of Molecular Biology* **62**, 139-169.
- Smith, Temple F. and Sadler, John R. (1971). The nature of lactose operator constitutive mutations. *Journal of Molecular Biology* **59**, 273-305.
- Beyer, William A., Stein, Myron L., Smith, Temple F. and Ulam, Stanislaw M. (1974). A molecular sequence metric and evolutionary trees. *Mathematical Biosciences* **19**, 9-25.
- Sadler, JR, Miwa, J, Maas P and Smith, T. (1974). Growth of high density bacterial cultures: a simple device. *Lab Pract.* **23**(11), 642-643.
- Smith, T.F., Grunwald, M., Artwich, R. and Hill, H.Z. (1975). A simple statistical analysis of indian muntjac Giemsa band patterns. *Cytogenetic Cell Genetics*, **15**, 153-165.
- Waterman, M.S., Smith, T.F., and Beyer, W.A. (1976). Some biological sequence metrics. *Advances in Mathematics* **20**, (3), 367-387.
- Smith, T.F., Sadler, J.R. and Goad, Walter. (1977). Statistical-Mechanical modeling of a regulatory protein: the lactose repressor. *Mathematical Biosciences* **36**, 61-86.
- Waterman, M.S., Smith, T.F., Singh, M. and Beyer, W.A. (1977). Additive evolutionary trees. *Journal of Theoretical Biology* **64**, 199-213.

- Waterman, M.S. and Smith, T.F. (1978). On the similarity of dendrograms. *Journal of Theoretical Biology* **73**, 789-800.
- Waterman, M.S. and Smith, T.F. (1978). RNA secondary structure: a complete mathematical analysis. *Mathematical Biosciences* **42**, 257-266.
- Smith, T.F. and Ross, M. (1979). I.R.-stimulated catalysis (a potential spectral tool). *International Journal of Peptide Protein Research* **14**, 313-316.
- Bednarek, A.R. and Smith, Temple F. (1980). A taxonomic distance applicable to paleontology. *Mathematical Biosciences* **50**, 285-295.
- Howell, J.A., Smith, T.F. and Waterman, M.S. (1980). Computation of generating functions for biological molecules. *SIAM Journal of Applied Mathematics* **39**, (1), 119-133.
- Smith, Temple F. (1980). Comparative sequence analysis. *Comments on Molecular & Cell Biophysics* **1**, (1), 3-14.
- Smith, Temple F. and Waterman, Michael S. (1980). How alike are two trees? *The American Mathematical Monthly* **87**, (7), 552-553.
- Smith, Temple F. and Waterman, Michael S. (1980). New stratigraphic correlation techniques. *Journal of Geology* **88**, 451-457.
- Smith, Temple F. and Waterman, Michael S. (1980). Protein constraints induced by multiframe encoding. *Mathematical Biosciences* **49**, 17-26.
- Smith, Temple F. and Waterman, Michael S. (1981). Comparison of Biosequences. *Advances in Applied Mathematics* **2**, 482-489.
- Smith, T.F. and Waterman, M.S. (1981). Overlapping genes and information theory. *Journal of Theoretical Biology* **91**, 379-380.
- Smith, T.F. and Waterman, M.S. (1981). The identification of common molecular subsequences. *Journal of Molecular Biology* **147**, 195-197.
- Smith, T.F., Waterman, M.S. and Fitch, W.M. (1981). Comparative biosequence metrics. *Journal of Molecular Evolution* **18**, 38-46.
- Fitch, W.M. and Smith, T.F. (1982). Optimal sequence alignment. *Proceeding National Academy of Science* **80**, 1382-1386.
- Morowitz, H. and Smith, T.F. (1982). Between history and physics. *Journal of Molecular Evolution* **18**, 265-282.
- Smith, T.F., Waterman, M.S. and Sadler, J.R. (1982). Statistical characterization of nucleic acid sequence functional domains. *Nucleic Acids Research*, **11**, 2205-2220.
- Fitch, W.M., Smith, T.F. and Ralph, W.W. (1983). Efficient restriction map reconstruction. *Gene* **22**, 19-29.
- Sadler, J.R., Waterman, M.S. and Smith, T.F. (1983). Regulatory pattern identification in nucleic acid sequences. *Nucleic Acids Research* **11**, 2221-2231.
- Smith, T.F. and Burks, C. (1983). Searching for sequence similarities. *Nature* **301**, 194.
- Galas, D.J. and Smith, T.F. (1984). Codon boundaries and multiple reading frame preferences. *Molecular Biology and Evolution*, **3**, 260-268.
- Waterman, M.S., Smith, T.F. and Katcher, H.L. (1984). Algorithms for restriction map comparisons. *Nucleic Acids Research* **12**, 237-242.
- Smith, T.F., Waterman, M.S. and Burks, C. (1985). The statistical distribution of nucleic acid similarities. *Nucleic Acids Research* **13**, 645-656.
- Bruck, C., Co, M.S., Slaoui, M., Gauton, G.N., Smith, T.F., Field, B.N., Mullins, J.I. and Green, M.I. (1986). Nucleic acid sequence of an internal image-bearing monoclonal anti-idiotype and its comparison to the sequence of the external antigen. *Proceeding National Academy of Science (USA)* **83**, 6578-6582.
- Fitch, W.M., Smith, T.F. and Breslow, J.L. (1986). Detecting internally repeated sequences and inferring the history of duplication. *Methods in Enzymology* **128**, 773-788.
- Ruvolo, Maryellen and Smith, Temple F. (1986). Phylogeny and DNA-DNA hybridization. *Molecular Biology and Evolution* **3**(3), 285-289.
- Waterman, M. and Smith, T.F. (1986). Rapid dynamic programming algorithms for RNA secondary structure. *Advances in Applied Mathematics* **7**, 455-464.
- Bradley, M.K., Smith, T.F., Lathrop, R.H., Livingston, D.M. and Webster, T.A. (1987). Consensus topography in the ATP binding site of the simian virus 40 and polyoma virus large tumor antigens. *Proceeding National Academy Science* **84**, 4026-4030.
- Gruskin, K.D. and Smith, T.F. (1987). Molecular genetics and computer analyses. *Computer Applications in the BIOScience* **3**, 167-170.
- Gruskin, K.D., Smith, T.F. and Goodman, M. (1987). A question as to the origin of a reverse transcriptase calmodulin. *Proceeding National Academy of Science* **84**, 1605-1608.

- Jurka, J. and Smith, T.F. (1987). Beta-turns in early evolution: Chirality, genetic code, and biosynthetic pathways. *Cold Spring Harbor Symposia on Quantitative Biology* **LII**, 407-410.
- Jurka, J. and Smith, T.F. (1987). Beta-turn driven early evolution: The genetic code and bio-synthetic pathways. *Journal of Molecular Evolution* **25**, 15-19.
- Lathrop, R.H., Webster, T.A. and Smith, T.F. (1987). ARIADNE: Pattern-directed inference and hierarchical abstraction in protein structure recognition. *Communications of the ACM* **30** (11), 909-921.
- Mengeritsky, Galina and Smith, Temple F. (1987). Recognition of characteristic patterns in sets of functionally equivalent DNA sequences. *Computer Applications in the BIOScience* **3** (3), 223-227.
- Ralph, W.W., Webster, T.A. and Smith, T.F. (1987). A modified Chou and Fasman protein structure algorithm. *Computer Applications in the BIOScience* **3** (3), 211-216.
- Semon, D., Movva, N. R., El Alama, M., Smith, T.F. and Davies, J. (1987). Plasmid-determined bleomycin resistance in staphylococcus aureus. *Plasmid* **17**, 46-53.
- Webster, T.A., Lathrop, R.H. and Smith, T.F. (1987). Prediction of a common structural domain in aminoacyl-tRNA synthetases through use of a new pattern-directed inference system. *Biochemistry* **26**, 6950-6957.
- Chin, David T., Goff, Stephen A., Webster, Teresa A., Smith, Temple F. and Goldberg, Alfred L. (1988). Sequence of the *lon* gene in *Escherichia Coli*. *Journal of Biological Chemistry* **263** (24), 11718-11728.
- Figge, James, Webster, Teresa, Smith, Temple F. and Paucha, Eva. (1988). Prediction of similar transforming regions in simian virus 40 large T, adenovirus E1A, and myc oncoproteins. *Journal of Virology* **62**(5), 1814-1818.
- Figge, James and Smith, Temple F. (1988). Cell-division sequence motif. *Nature* **334**, 109.
- Jurka, Jerzy, Smith, Temple F. and Labuda, Damian. (1988). Small cytoplasmic Ro RNA pseudogene and an Alu repeat in the human alpha-1 globin gene. *Nucleic Acids Research* **16**(2), 766.
- Jurka, Jerzy and Smith, Temple F. (1988). A fundamental division in the Alu family of repeated sequences. *Proceeding National Academy of Sciences* **85**, 4775-4778.
- Smith, T.F., Srinivasan, A., Schochetman, G., Marcus, M. and Myers, G. (1988). The phylogenetic history of immunodeficiency viruses. *Nature* **333**, 573-575.
- Webster, Teresa A., Lathrop, Richard H. and Smith, Temple F. (1988). Predicted unidentified reading frame 6 human mtDNA dinucleotide-binding site. *PROTEINS* **3**(2), 97-101.
- Mengeritsky, Galina and Smith, Temple F. (1989). New analytical tool for analysis of splice site sequence determinants. *Computer Applications in the Biosciences* **5**(2), 97-100.
- Smith, Randall F. and Smith, Temple F. (1989). Identification of new kinase related genes in three herpesviruses, herpes simplex virus, varicella-Zoster virus, and Epstein-Barr virus. *Journal of Virology* **63**(1), 450-455.
- Smith, T.F. (1989). Genetic sequence semantic and syntactic patterns. In *Computers and DNA, SFI Studies in the Sciences of Complexity*, vol. **VII**. Eds. G. Bell and T. Marr, Addison-Wesley.
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- Webster, T.A., Patarca, R., Lathrop, R. and Smith, T.F. (1989). Potential structural motifs for reverse transcriptases. *Molecular Biology and Evolution* **6** (3), 317-320.
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- Gonzalez, I.L., Sylvester, J.E., Smith, T.F., Stamboulion, D. and Schmickel, R.D. (1990). Ribosomal RNA gene sequences and hominoid phylogeny. *Molecular Biology and Evolution* **7** (3), 203-219.
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- Lathrop, R.H., Webster, T.A., Smith, T.F. and Winston, P.H. (1990). ARIEL: a massively parallel symbolic learning assistant for protein structure/function. In *Artificial Intelligence at MIT: Expanding Frontiers*, ed. Patrick H. Winston with Sarah A. Shellard, MIT Press, Cambridge, MA, 70-103.
- Smith, R.F. and Smith, T.F. (1990) Automatic generation of primary sequence patterns from sets of related proteins. *Proceeding National Academy of Sciences (USA)* **87**, 118-122.
- Smith, T.F. (1990) The history of the genetic sequence databases. *Genomics* **6**, 701-707.
- Vega, Miguel A., Guigó, Roderic and Smith, Temple F. (1990). Autoimmune response in AIDS? *Nature* **345**, 26.
- Zhu, Q-L., Smith, T.F., Lathrop, R.H. and Figge, J. (1990). The acid helix-turn activator motif. *PROTEINS* **8**, 156-163.

- Breese, K., Friedrich, T., Andersen, T.T., Smith, T.F. and Figge, J. (1991). Structural Characterization of a 14-Residue Peptide Ligand of the Retinoblastoma Protein: Comparison with a Nonbinding Analog. *Peptide Research* **4** (4), 220-226.
- Guigó, R., Johansson, A. and Smith, T.F. (1991). Automatic evaluation of protein sequence functional patterns. *CABIOS* **7** (3), 309-315.
- Guigó, Roderic and Smith, Temple F. (1991). A common pattern between the TGF- $\beta$  family and glutaredoxin. *Biochem. J.* **280**, 829-836.
- Morowitz, Harold J., Deamer, David W. and Smith, Temple. (1991). Biogenesis as an evolutionary process. *Journal of Molecular Evolution* **33**, 207-208.
- Guigó, Roderic, Knudsen, Steen, Drake, Neil and Smith, Temple. (1992). Prediction of gene structure. *Journal of Molecular Biology* **226**, 141-157.
- Lamperti, Edward D., Kittelberger, J. Matthew, Smith, Temple F. and Villa-Komaroff, Lydia. (1992). Corruption of genomic databases with anomalous sequence. *Nucleic Acids Research* **20** (11), 2741-2747.
- Smith, Randall F. and Smith, Temple F. (1992). Pattern-induced multi-sequence alignment (PIMA) algorithm employing secondary structure-dependent gap penalties for use in comparative protein modelling. *Protein Engineering* **5** (1), 35-41.
- Smith, Temple F. and Waterman, Michael S. (1992). The continuing case of the Florida dentist. *Science* **256**, 1155-1156.
- Figge, James, Breese, Kimberly, Vajda, Sandor, Zhu, Qing-lin, Eisele, Leslie, Andersen, Thomas T., MacColl, Robert, Friedrich, Thomas, and Smith, Temple F. (1993). The binding domain structure of retinoblastoma-binding proteins. *Protein Science* **2**, 155-164.
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- Guigó, Roderic and Smith, Temple F. (1993). Inferring correlation between database queries: analysis of protein sequence patterns. *IEEE Transactions on Pattern Analysis and Machine Intelligence* **15** (10), 1030-1041.
- Kister, Alexander, Muchnik, Ilya, Bouzida, Djamel, Reinherz, Ellis and Smith, Temple. (1993). Efficient pattern comparative method for selecting functionally important motifs in protein sequences: Application to zinc enzymes. *Biosystems* **30**, 233-240.
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- Lathrop, Richard H., Webster, Teresa A., Smith, Temple F. and Winston, Patrick H. (1993). Massively parallel symbolic induction of protein structure/function relationships. In *Machine Learning, From Theory to Applications*, ed. Hanson, S. Remmele, W. Rivest, R.L., Springer-Verlag (forthcoming); reprinted from *Proc. 24th Hawaii Intl. Conf. on System Sciences* (1991), pp. 585-594, IEEE Computer Soc. Press, Los Alamitos, CA.
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- Luidens, Mary Koeppe, Aks, Carolyn S., Zhu, Qing-lin, Smith, Temple F., MacColl, Robert, and Figge, James. (1993). Environmental effects on the folding of functional peptide segments from steroid hormone receptors. *Peptide Research* **6** (3), 134-139.
- Neer, Eva J., Schmidt, Carl J. and Smith, Temple F. (1993). LIS is more. *Nature Genetics* **4**, 1-4.
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- Zhang, You-xun, Fox, James G., Ho, Yu, Zhang, Li, Stills, Harold F., Jr., and Temple F. Smith. (1993). Comparison of the major outer membrane protein (MOMP) gene of mouse pneumonitis (MoPn) and hamster SFPD strains of *Chlamydia trachomatis* with other chlamydial strains. *Molecular Biology and Evolution* **10** (6), 1327-1342.
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- Lathrop, Richard H. and Smith, Temple F. (1994). A branch-and-bound algorithm for optimal protein threading with pairwise (contact potential) amino acid interactions. *Proceedings of the 27th Hawaii International Conference on System Sciences*, Jan. 1994, IEEE Computer Soc. Press, Los Alamitos, CA, 365-374.
- Neer, Eva J., Schmidt, Carl J., Nambudripad, Raman and Smith, Temple F. (1994). WD repeat proteins: an ancient family of regulatory proteins. *Nature* **371**, 297-300.
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- White, James, Stultz, Collin and Smith, Temple F. (1994). Protein classification by stochastic modeling and optimal filtering of amino-acid sequences. *Mathematical BioSciences* **119**, 35-75.
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