Douglas L. Brutlag

Professor of Biochemistry, Emeritus

NIH Biosketch available Online   Curriculum Vitae available Online   Resume available Online

Bio

ACADEMIC APPOINTMENTS

- Emeritus Faculty, Acad Council, Biochemistry
- Member, Bio-X

HONORS AND AWARDS

- Honorary Professor, Keio University (2001)
- Fellow, American College of Medical Informatics (2001)
- Best Computer Application in Science, Computerworld-Smithsonian Award (1992)
- Fellow, American Association for the Advancement of Science (1986)
- Teacher Scholar Award, Henry and Camille Dreyfus (1979)
- Young Investigator Award, Basil O'Conner National Foundation (1975)
- Ph.D. with Great Distinction, Stanford Biochemistry Department (1972)
- Henry M. Green Award for Undergraduate Research, California Institute of Technology (1968)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Board of Directors, IntelliCorp (1980 - 1985)
- Scientific Advisory Board, IntelliCorp (1980 - 1986)
- Board of Directors, IntelliGenetics (1986 - 1991)
- Editorial Board, Journal of Computational Biology (1993 - 1998)
- CoFounder, International Society for Computational Biology (1996 - present)
- Chairman, Scientific Advisory Board, Time Logic (1997 - 2003)
- Scientific Advisory Board, DoubleTwist (2000 - 2002)
- Chairman, Scientific Advisory Board, Pathwork Informatics (2003 - 2006)
- Presidential Advisory Board, Max Planck Institutes (2003 - 2011)

PROFESSIONAL EDUCATION

- B.S. with Honors, California Inst. of Technology , Biology (1968)
- Ph.D. with Great Distinction, Stanford University , Biochemistry (1972)

COMMUNITY AND INTERNATIONAL WORK

- Gordon Conference Organizer, Ventura, California
- Presidential Advisor, Max Planck Institute, Germany
- Dagstuhl Seminar on Bioinformatics, Dagstuhl, Germany
- International Conferences on Intelligent Systems in Molecular Biology
- Imperial Cancer Research Fund, London, England
- Course on Computer Applications in Molecular Biology, Sydney, Australia
- UNIDO Workshop on Computer Applications in Molecular Biology, Moscow, Russia
- Genbank Symposium, the first 15 years, Bethesda, Md
- UNIDO Course on Computational Biology, Trieste, Italy
- National Library of Medicine, Board of Scientific Counselors, Bethesda, Md
- GenBank Database, Bethesda, Md
- BIONET Resource for Computational Biology, Palo Alto, CA
- National Library of Medicine, Long Range Planning Panel, Bethesday, Md.
- NIH Genetics Study Section, Bethesda, Md

LINKS

- My Lab Site: http://brutlag.stanford.edu/
- Doug Brutlag's Resumé: http://cmgm.stanford.edu/~brutlag/
- Doug Brutlag's Research: http://brutlag.stanford.edu/

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

My primary interest is to understand the flow of information from the genome to the phenotype of an organism. This interest includes predicting the structure and function of molecules from their primary sequence, predicting function from structure and finally simulating protein folding and protein-ligand docking. These goals are the same as the goals of molecular biology, however, we use primarily computational approaches.

Teaching

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biochemistry (Phd Program)
- Biomedical Data Science (Phd Program)
- Biomedical Data Science (Masters Program)
- Biophysics (Phd Program)

Publications

PUBLICATIONS

- **Using Stochastic Roadmap Simulation to predict experimental quantities in protein folding kinetics: Folding rates and phi-values** *10th Annual International Conference on Research in Computational Molecular Biology*
  Chiang, T., Apaydin, M. S., Brutlag, D. L., Hsu, D., Latombe, J.
  MARY ANN LIEBERT INC.2007: 578–93

- **Dynamic use of multiple parameter sets in sequence alignment** *NUCLEIC ACIDS RESEARCH*
  Huang, X., Brutlag, D. L.
  2007; 35 (2): 678-686
- **Genotypic predictors of human immunodeficiency virus type 1 drug resistance** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Rhee, S., Taylor, J., Wadhera, G., Ben-Hur, A., Brutlag, D. L., Shafer, R. W.
  2006; 103 (46): 17355-17360
- **A graph-based motif detection algorithm models complex nucleotide dependencies in transcription factor binding sites** *NUCLEIC ACIDS RESEARCH*
  Naughton, B. T., Fratkin, E., Batzoglou, S., Brutlag, D. L.
  2006; 34 (20): 5730-5739
- **MotifCut: regulatory motifs finding with maximum density subgraphs** *14th Conference on Intelligent Systems for Molecular Biology*
  Fratkin, E., Naughton, B. T., Brutlag, D. L., Batzoglou, S.
  OXFORD UNIV PRESS.2006: E150–E157
- **Development and validation of a consistency based multiple structure alignment algorithm** *BIOINFORMATICS*
  Ebert, J., Brutlag, D.
  2006; 22 (9): 1080-1087
- **Nucleotide channel of RNA-dependent RNA polymerase used for intermolecular uridylylation of protein primer** *JOURNAL OF MOLECULAR BIOLOGY*
  Tellez, A. B., Crowder, S., Spagnolo, J. F., Thompson, A. A., Peersen, O. B., Brutlag, D. L., Kirkegaard, K.
  2006; 357 (2): 665-675
- **A genome-wide analysis of CpG dinucleotides in the human genome distinguishes two distinct classes of promoters** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Saxonov, S., Berg, P., Brutlag, D. L.
  2006; 103 (5): 1412-1417
- **Predicting experimental quantities in protein folding kinetics using Stochastic Roadmap Simulation** *10th Annual International Conference on Research in Computational Molecular Biology*
  Chiang, T., Apaydin, M. S., Brutlag, D. L., Hsu, D., Latombe, J.
  SPRINGER-VERLAG BERLIN.2006: 410–424
- **eBLOCKs: enumerating conserved protein blocks to achieve maximal sensitivity and specificity** *NUCLEIC ACIDS RESEARCH*
  Su, Q. J., Lu, L., Saxonov, S., Brutlag, D. L.
  2005; 33: D178-D182
- **Homology modeling of a human glycine alpha 1 receptor reveals a plausible anesthetic binding site** *JOURNAL OF CHEMICAL INFORMATION AND MODELING*
  Bertaccini, E. J., Shapiro, J., Brutlag, D. L., Trudell, J. R.
  2005; 45 (1): 128-135
- **Computational functional genomics** *IEEE SIGNAL PROCESSING MAGAZINE*
  Liang, M. P., Troyanskaya, O. G., Laederach, A., Brutlag, D. L., Altman, R. B.
  2004; 21 (6): 62-69
- **A suite of web-based programs to search for transcriptional regulatory motifs** *NUCLEIC ACIDS RESEARCH*
  Liu, Y. Y., Wei, L. P., Batzoglou, S., Brutlag, D. L., Liu, J. S., Liu, X. S.
  2004; 32: W204-W207
- **FoldMiner and LOCK 2: protein structure comparison and motif discovery on the web** *NUCLEIC ACIDS RESEARCH*
  Shapiro, J., Brutlag, D.
  2004; 32: W536-W541
- **FoldMiner: Structural motif discovery using an improved superposition algorithm** *PROTEIN SCIENCE*
  Shapiro, J., Brutlag, D.

2004; 13 (1): 278-294

- **3MATRIX and 3MOTIF: a protein structure visualization system for conserved sequence motifs** *NUCLEIC ACIDS RESEARCH*
  Bennett, S. P., Lu, L., Brutlag, D. L.
  2003; 31 (13): 3328-3332
- **Remote homology detection: a motif based approach** *BIOINFORMATICS*
  Ben-Hur, A., Brutlag, D.
  2003; 19: i26-i33
- **WebFEATURE: an interactive web tool for identifying and visualizing functional sites on macromolecular structures** *NUCLEIC ACIDS RESEARCH*
  Liang, M. P., Banatao, D. R., Klein, T. E., Brutlag, D. L., Altman, R. B.
  2003; 31 (13): 3324-3327
- **3MOTIF: visualizing conserved protein sequence motifs in the protein structure database** *BIOINFORMATICS*
  Bennett, S. P., Nevill-Manning, C. G., Brutlag, D. L.
  2003; 19 (4): 541-542
- **Automated construction of structural motifs for predicting functional sites on protein structures.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
  Liang, M. P., Brutlag, D. L., Altman, R. B.
  2003: 204-215
- **Stochastic conformational roadmaps for computing ensemble properties of molecular motion** *5th International Workshop on Algorithmic Foundations of Robotics*
  Apaydin, M. S., Brutlag, D. L., Guestrin, C., Hsu, D., Latombe, J. C.
  SPRINGER-VERLAG BERLIN.2003: 131–147
- **Automatic construction of 3D structural motifs for protein function prediction** *2nd International Computational Systems Bioinformatics Conference*
  Liang, M. P., Brutlag, D. L., Altman, R. B.
  IEEE COMPUTER SOC.2003: 613–614
- **Stochastic roadmap simulation: An efficient representation and algorithm for analyzing molecular motion** *6th Annual International Conference on Computational Biology (RECOMB 2002)*
  Apaydin, M. S., Brutlag, D. L., Guestrin, C., Hsu, D., Latombe, J. C., Varma, C.
  MARY ANN LIEBERT INC.2003: 257–81
- **Stochastic roadmap simulation for the study of ligand-protein interactions** *European Conference on Computational Biology (ECCB 2002)*
  Apaydin, M. S., Guestrin, C. E., Varma, C., Brutlag, D. L., Latombe, J. C.
  OXFORD UNIV PRESS.2002: S18–S26
- **Using robotics to fold proteins and dock ligands** *European Conference on Computational Biology (ECCB 2002)*
  Brutlag, D., Apaydin, S., Guestrin, C., Hsu, D., Varma, C., Singh, A., Latombe, J. C.
  OXFORD UNIV PRESS.2002: S74–S74
- **An algorithm for finding protein-DNA binding sites with applications to chromatin-immunoprecipitation microarray experiments** *NATURE BIOTECHNOLOGY*
  Liu, X. S., Brutlag, D. L., Liu, J. S.
  2002; 20 (8): 835-839
- **BioProspector: discovering conserved DNA motifs in upstream regulatory regions of co-expressed genes.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
  Liu, X., Brutlag, D. L., Liu, J. S.
  2001: 127-138
- **Capturing molecular energy landscapes with probabilistic conformational roadmaps** *IEEE International Conference on Robotics and Automation*
  Apaydin, M. S., SINGH, A. P., Brutlag, D. L., Latombe, J. C.
  IEEE.2001: 932–939

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

- **The EMOTIF database** *NUCLEIC ACIDS RESEARCH*
  Huang, J. Y., Brutlag, D. L.
  2001; 29 (1): 202-204

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

- **Bayesian segmentation of protein secondary structure** *JOURNAL OF COMPUTATIONAL BIOLOGY*
  Schmidler, S. C., Liu, J. S., Brutlag, D. L.
  2000; 7 (1-2): 233-248

- **Minimal-risk scoring matrices for sequence analysis** *JOURNAL OF COMPUTATIONAL BIOLOGY*
  Wu, T. D., Nevill-Manning, C. G., Brutlag, D. L.
  1999; 6 (2): 219-235

- **A motion planning approach to flexible ligand binding.** *Proceedings. International Conference on Intelligent Systems for Molecular Biology*
  SINGH, A. P., Latombe, J. C., Brutlag, D. L.
  1999: 252-261

- **Regression analysis of multiple protein structures** *JOURNAL OF COMPUTATIONAL BIOLOGY*
  Wu, T. D., Schmidler, S. C., Hastie, T., Brutlag, D. L.
  1998; 5 (3): 585-595

- **Directions for clinical research and genomic research into the next decade: Implications for informatics** *JOURNAL OF THE AMERICAN MEDICAL INFORMATICS ASSOCIATION*
  Rindfleisch, T. C., Brutlag, D. L.
  1998; 5 (5): 404-411

- **Genomics and computational molecular biology** *CURRENT OPINION IN MICROBIOLOGY*
  Brutlag, D. L.
  1998; 1 (3): 340-345

- **Highly specific protein sequence motifs for genome analysis** *Colloquium on Computational Biomolecular Science*
  Nevill-Manning, C. G., Wu, T. D., Brutlag, D. L.
  NATL ACAD SCIENCES.1998: 5865–71

- **Modeling and superposition of multiple protein structures using affine transformations: analysis of the globins.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
  Wu, T. D., Schmidler, S. C., Hastie, T., Brutlag, D. L.
  1998: 509-520

- **Enumerating and ranking discrete motifs** *5th International Conference on Intelligent Systems for Molecular Biology (ISMB-97)*
  Nevill-Manning, C. G., SETHI, K. S., Wu, T. D., Brutlag, D. L.
  AMER ASSOC ARTIFICIAL INTELLIGENCE.1997: 202–209

- **Hierarchical protein structure superposition using both secondary structure and atomic representations** *5th International Conference on Intelligent Systems for Molecular Biology (ISMB-97)*
  SINGH, A. P., Brutlag, D. L.
  AMER ASSOC ARTIFICIAL INTELLIGENCE.1997: 284–293

- **Introns and reading frames: Correlation between splicing sites and their codon positions** *MOLECULAR BIOLOGY AND EVOLUTION*
  Tomita, M., Shimizu, N., Brutlag, D. L.
  1996; 13 (9): 1219-1223

- **Sequences and topology - Challenges for algorithms and experts - Editorial overview** *CURRENT OPINION IN STRUCTURAL BIOLOGY*
  Brutlag, D. L., STERNBERG, M. J.
  1996; 6 (3): 343-345
- **Discovering empirically conserved amino acid substitution groups in databases of protein families.** *Proceedings / ... International Conference on Intelligent Systems for Molecular Biology ; ISMB. International Conference on Intelligent Systems for Molecular Biology*
  Wu, T. D., Brutlag, D. L.
  1996; 4: 230-240
- **Identification of protein motifs using conserved amino acid properties and partitioning techniques.** *Proceedings / ... International Conference on Intelligent Systems for Molecular Biology ; ISMB. International Conference on Intelligent Systems for Molecular Biology*
  Wu, T. D., Brutlag, D. L.
  1995; 3: 402-410
- **DISCOVERING STRUCTURAL CORRELATIONS IN ALPHA-HELICES** *PROTEIN SCIENCE*
  Klingler, T. M., Brutlag, D. L.
  1994; 3 (10): 1847-1857
- **On near-optimal alignments of biological sequences.** *Journal of computational biology*
  Naor, D., Brutlag, D. L.
  1994; 1 (4): 349-366
- **Discovering side-chain correlation in alpha-helices.** *Proceedings / ... International Conference on Intelligent Systems for Molecular Biology ; ISMB. International Conference on Intelligent Systems for Molecular Biology*
  Klingler, T. M., Brutlag, D. L.
  1994; 2: 236-243
- **BLAZE (TM) - AN IMPLEMENTATION OF THE SMITH-WATERMAN SEQUENCE COMPARISON ALGORITHM ON A MASSIVELY-PARALLEL COMPUTER** *2ND INTERNATIONAL WORKSHOP ON OPEN PROBLEMS OF COMPUTATIONAL MOLECULAR BIOLOGY*
  Brutlag, D. L., DAUTRICOURT, J. P., Diaz, R., FIER, J., MOXON, B., Stamm, R.
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- **Detection of correlations in tRNA sequences with structural implications.** *Proceedings / ... International Conference on Intelligent Systems for Molecular Biology ; ISMB. International Conference on Intelligent Systems for Molecular Biology*
  Klingler, T. M., Brutlag, D. L.
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- **SEARCHING GENE AND PROTEIN-SEQUENCE DATABASES** *M D COMPUTING*
  BARSALOU, T., Brutlag, D. L.
  1991; 8 (3): 144-149
- **KNOWLEDGE-BASED SIMULATION OF DNA METABOLISM - PREDICTION OF ENZYME ACTION** *COMPUTER APPLICATIONS IN THE BIOSCIENCES*
  Brutlag, D. L., Galper, A. R., MILLIS, D. H.
  1991; 7 (1): 9-19
- **IMPROVED SENSITIVITY OF BIOLOGICAL SEQUENCE DATABASE SEARCHES** *COMPUTER APPLICATIONS IN THE BIOSCIENCES*
  Brutlag, D. L., DAUTRICOURT, J. P., Maulik, S., RELPH, J.
  1990; 6 (3): 237-245
- **CONVERSION AND RECIPROCAL EXCHANGE BETWEEN TANDEM REPEATS IN DROSOPHILA-MELANOGASTER** *MOLECULAR & GENERAL GENETICS*
  HIPEAUJACQUOTTE, R., Brutlag, D. L., Bregegere, F.
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- **IS THERE A RELATIONSHIP BETWEEN DNA-SEQUENCES ENCODING PEPTIDE LIGANDS AND THEIR RECEPTORS** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Goldstein, A., Brutlag, D. L.
  1989; 86 (1): 42-45
- **EXPRESSION OF THE DROSOPHILA TYPE-II TOPOISOMERASE IS DEVELOPMENTALLY REGULATED** *BIOCHEMISTRY*

Fairman, R., Brutlag, D. L.
1988; 27 (2): 560-565

- **IDENTICAL SATELLITE DNA-SEQUENCES IN SIBLING SPECIES OF DROSOPHILA** *JOURNAL OF MOLECULAR BIOLOGY*
  Lohe, A. R., Brutlag, D. L.
  1987; 194 (2): 161-170
- **ADJACENT SATELLITE DNA SEGMENTS IN DROSOPHILA - STRUCTURE OF JUNCTIONS** *JOURNAL OF MOLECULAR BIOLOGY*
  Lohe, A. R., Brutlag, D. L.
  1987; 194 (2): 171-179
- **MULTIPLE FORMS AND CELLULAR-LOCALIZATION OF DROSOPHILA DNA TOPOISOMERASE-II** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Heller, R. A., Shelton, E. R., Dietrich, V., Elgin, S. C., Brutlag, D. L.
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- **PROXIMITY-DEPENDENT ENHANCEMENT OF SGS-4 GENE-EXPRESSION IN DROSOPHILA-MELANOGASTER** *CELL*
  Kornher, J. S., Brutlag, D.
  1986; 44 (6): 879-883
- **MULTIPLICITY OF SATELLITE DNA-SEQUENCES IN DROSOPHILA-MELANOGASTER** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Lohe, A. R., Brutlag, D. L.
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- **BIONET - NATIONAL COMPUTER RESOURCE FOR MOLECULAR-BIOLOGY** *NUCLEIC ACIDS RESEARCH*
  Smith, D. H., Brutlag, D., FRIEDLAND, P., Kedes, L. H.
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- **A FAMILY OF DISPERSED REPETITIVE EXTRAGENIC PALINDROMIC DNA-SEQUENCES IN ESCHERICHIA-COLI** *EMBO JOURNAL*
  Gilson, E., Clement, J. M., Brutlag, D., Hofnung, M.
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- **SIMILARITIES IN STRUCTURE AND FUNCTION OF CALF THYMUS AND DROSOPHILA CASEIN KINASE-II** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Dahmus, G. K., Glover, C. V., Brutlag, D. L., Dahmus, M. E.
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- **RAPID SEARCHES FOR COMPLEX PATTERNS IN BIOLOGICAL MOLECULES** *NUCLEIC ACIDS RESEARCH*
  ABARBANEL, R. M., WIENEKE, P. R., Mansfield, E., Jaffe, D. A., Brutlag, D. L.
  1984; 12 (1): 263-280
- **DNA TOPOISOMERASE-II FROM DROSOPHILA-MELANOGASTER - RELAXATION OF SUPERCOILED DNA** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Osheroff, N., Shelton, E. R., Brutlag, D. L.
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- **DNA TOPOISOMERASE-II FROM DROSOPHILA-MELANOGASTER - PURIFICATION AND PHYSICAL CHARACTERIZATION** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Shelton, E. R., Osheroff, N., Brutlag, D. L.
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- **PURIFICATION AND CHARACTERIZATION OF A TYPE-II CASEIN KINASE FROM DROSOPHILA-MELANOGASTER** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Glover, C. V., Shelton, E. R., Brutlag, D. L.
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- **MAXAMIZE - A DNA SEQUENCING STRATEGY ADVISOR** *NUCLEIC ACIDS RESEARCH*
  Bach, R., FRIEDLAND, P., Brutlag, D. L., Kedes, L.
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- **SEQ - A NUCLEOTIDE-SEQUENCE ANALYSIS AND RECOMBINATION SYSTEM** *NUCLEIC ACIDS RESEARCH*

Brutlag, D. L., CLAYTON, J., FRIEDLAND, P., Kedes, L. H.
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- **GENESIS, A KNOWLEDGE-BASED GENETIC-ENGINEERING SIMULATION SYSTEM FOR REPRESENTATION OF GENETIC DATA AND EXPERIMENT PLANNING** *NUCLEIC ACIDS RESEARCH*
  FRIEDLAND, P., Kedes, L., Brutlag, D., Iwasaki, Y., Bach, R.
  1982; 10 (1): 323-340
- **RIBONUCLEIC-ACID AND OTHER POLYANIONS FACILITATE CHROMATIN ASSEMBLY INVITRO** *BIOCHEMISTRY*
  Nelson, T., Wiegand, R., Brutlag, D.
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- **HISTONE ACETYLASE FROM DROSOPHILA-MELANOGASTER SPECIFIC FOR H-4** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  WIEGAND, R. C., Brutlag, D. L.
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  Hsieh, T. S., Brutlag, D.
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- **MOLECULAR ARRANGEMENT AND EVOLUTION OF HETEROCHROMATIC DNA** *ANNUAL REVIEW OF GENETICS*
  Brutlag, D. L.
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  Carlson, M., Brutlag, D.
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- **EXTRACTS OF DROSOPHILA EMBRYOS MEDIATE CHROMATIN ASSEMBLY INVITRO** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Nelson, T., Hsieh, T. S., Brutlag, D.
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  Fry, K., Brutlag, D.
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  Carlson, M., Brutlag, D.
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- **GENE ADJACENT TO SATELLITE DNA IN DROSOPHILA-MELANOGASTER** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Carlson, M., Brutlag, D.
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  Carlson, M., Brutlag, D.
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  Brutlag, D., Carlson, M., Fry, K., Hsieh, T. S.
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  Rubenstein, J. L., Brutlag, D., Clayton, D. A.
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