

## CURRICULUM VITAE

### Brooke Lustig

#### *Contact Information*

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#### *Education*

- 1987                      Ph.D., Biophysical Chemistry  
University of California, Santa Cruz, Santa Cruz, CA 95064  
Research Advisor: Professor Anthony Fink  
Thesis: Application of Circular Dichroism and  
Complementary Techniques to the Folding of Ribonuclease A  
in Aqueous-Methanol Solvents
- 1976, 1977              B.A., Joint Degree in Molecular Biology and Biochemistry,  
University of Colorado at Boulder, Boulder, CO 80302  
Undergraduate Research Advisor: Professor Kurt  
Schlesinger; characterization of tyrosine hydroxylation in  
seizure-prone mice

#### *Professional Preparation*

- 2004-present              Lecturer in Chemistry at San Jose State University; Chemical  
& Materials Engineering; Electrical Engineering  
Courses: Chem100W (Writing Workshop: Chemical  
Communications), Chem291C (Divisional Seminar),  
Chem131B (Biochemistry Laboratory) Lecture (Fall 2011),  
ChE293 (Applied Bioinformatics); EE196B (Molecular  
Bioengineering)  
Curriculum-Based Research Activities: Development of  
graduate Bioinformatics courses that include seedbed class  
research projects
- 1995-2004              Lecturer in Chemistry at San Jose State University; Chemical  
& Materials Engineering
- 1989-94                  IRTA Fellow at NIH/NCI/LMMB Bethesda, MD 20892  
Supervisor: Dr. Robert Jernigan
- 1988-89                  Lecturer in Chemistry at San Jose State University

Research Areas: Lattice and other coarse-grained modeling of RNA and proteins; development of DNA-related statistical potentials and their application

1989 Staff Scientist Applied Sciences Consultants, NIH-SBIR GM36180, "Computer Folding of RNA Molecules Using Monte Carlo Methods," current address: Palo Alto, CA 94301

1988 Research Associate at University of California Santa Cruz  
Supervisor: Professor Anthony Fink  
Research Area: Application of dynamic light scattering to the characterization of protein folding intermediates

***Professional and University Service (since 2004)***

*Proposal Review*

California State University Program for Education and Research in Biotechnology, Grants Review (2005, 2007, 2008)

*Manuscript Review*

Journal of Biomolecular Structure and Dynamics (2010)

Entropy (2008)

Journal of Applied Crystallography (2008)

*Reading Committee Member M.S. in Chemistry, Chemical & Materials Engineering, Computer Engineering*

Chun-Jung Chu (CME, Thesis-2005), Prema Ghangadhar (CHEM, Thesis-2011)  
Parul Gupta (CME, Project-2006), Kam Hon Hoi (CME, Project-2009), Nada Khouderchah (CHEM, Thesis-2008), Yong Lee (CMPE, Project-2007), Brendan Mar (CHEM, Thesis-2011), Vasudha Narula (CHEM, Thesis-2008), Sree Rajeshwari (CME, Project-2010), Dipti Sukul (CHEM, Thesis-2008), Min Zhang (CHEM, Thesis-2010)

*College of Science Research Day Poster Presentations*

Nepal, R., Rose, D., Gholizadeh, S., Lau, R. Radhika Mishra, Kimberly Uweh **Novel Application of Statistical Predictors: First Stage Calculation of Solvent Accessible Protein Residues** (2011).

Nguyen, T., Do, S., Radhika Mishra, M. & Lustig, B. **Sequence Homology Calculations for Proteins and Relevant DNA Indicate Specific Limitations for a Gap-Based Parameter** (2010).

Mishra, R., Do, S., Le, T., Khan-Van Tu, K.-V. & Lustig, B. **Unusual Patterns of Protein Packing Corresponding to Specific Clusters of Surface Accessible Residues** (2009).

Do, S., Lakkaraju, H., Potluri, S., Pham, K., Kantardjieff, K. & Lustig, B. **Protein Sequence Homology Parameters Applied to the Prediction of Solvent Accessible Residues** (2008).

Lakkaraju, H., Potluri, S., Hardin, A. & Lustig, B. **Sequence Signatures and Packing for Multimeric Proteins** (2007).

### *Other Positions and Honors*

2010-2011	Faculty Mentor, Scholars in Science, NSF-SJSU
2008-2009	Co-PI CSU California State University General Research Grant
2007	Co-PI Intel Education Grant 32553, Chemistry Computing Cluster and Workstations
2004	PI Research Contract Extension, Sage-N Research Bioinformatics Algorithm Development
2004	PI Research Contract, Sage-N Research Bioinformatics Algorithm Development
2000-2001	Co-PI California State University Program for Education and Research in Biotechnology: Development of an Integrated Bioinformatics Infrastructure and Curriculum
1998-1999	PI NIH SBIR GM39372, Selection and Structure of Peptides Binding HIV-1 TAR.

### *Current Research Interests*

Ongoing development of computational methods to further characterize entropy and related properties of proteins and RNA for the prediction of structure as well as the binding of other molecules. This includes applying novel sequence and homology-based methods to characterize the surface and buried regions of protein chains and their interfaces. Collaborators include Profs. Katherine Kantardjieff (CSU, Pomona) and Prof. Thomas Young (Lehman-CUNY). And the implementation of these sorts of approaches includes the design of potential anti-HIV agents, specifically modified Tat peptides binding to TAR RNA. This continues work with an experimental collaborator, Prof. Elaine Collins (SJSU).

### ***Recent Student and Postdoctoral Researchers (2009-Present)***

Sylvia Do (MBT, M.S.); currently NSF Graduate Fellow ISU), Jocelyn Fuentecilla (undergrad-BIOL), Shabnam Gholzideh (CME, M.S.-Project), Aarthi Jankiraman (M.S.-CME, Res. Assoc.), Robert Lau (undergrad-BIOL), Tuan Le (undergrad-CHEM), Jared May (undergrad-CMPE), Radhika Mishra (CHEM, M.S.-Thesis), Reecha Nepal (CHEM), Frank Nguyen (undergrad-BIOL), Trung Nguyen (CHEM), John Resngit (undergrad-BIOL), Daniel Rose (Postdoc., currently Drucker School of Management/Claremont College) Euclid Sun (undergrad-BIOL, Scholars in Science), Angela Tao (MSE), Kimberly Uweh (undergrad-PHIL), Khan-Van Tu (undergrad-CHEM)

### ***Research Students (2004-2008)***

Sridhar Busani (CME, M.S.-Project), Santhoshi Caringula (CME, M.S.-Project), Sowjanya Kalakoti (CME, Thesis-Project), Hema Lakkaraju (CME, M.S., currently Roche), Haihong Liao (CHEM, M.S.-Thesis), Shalini Potluri (CME, M.S., currently Prosetta), Siddharth Potnis (CME, M.S.-Project), William Yeh (CME, M.S.-Thesis)

### ***Publications and Proceedings (Peer Reviewed)***

1. Rose, D., Nepal, R., Gholizadeh, S., Mishra, R., Lau, R. and **Lustig, B.** "Novel application of query-based qualitative predictors for characterization of solvent accessible residues in conjunction with protein sequence homology" (2011) Proceedings of the 22nd International Workshop on Database and Expert Systems Applications, 70-74.
2. Liao, H., Yeh, W., Chiang, D., Jernigan, R. L. and **Lustig, B.** "Protein sequence entropy is closely related to packing density and hydrophobicity" (2005) *Prot. Engr.* 18, 59-64.
3. Wander, D. S., Yang, F., McNeil, M and **Lustig, B.** "Scoring DNA sequence alignment using energetics of hybridization" (2003) Proceedings of Annual Meeting of American Institute of Chemical Engineers, 555b(1-8).
4. Hsieh, M., Collins, E. D., Blomquist, T. and **Lustig, B.** "Flexibility of BIV TAR-Tat: Models of peptide binding" (2002) *J. Biomol. Struct. Dyn.* 20, 243-247.
4. **Lustig, B.** and **Jeang K.-T.** "Biological applications of hammerhead ribozymes as anti-viral molecules" (2001) *Curr. Med. Chem.* 8, 1181-1187.
5. **Lustig, B.**, Bahar, I. and Jernigan, R. L. "RNA bulge entropies correlate with peptide binding strengths for HIV-1 and BIV TAR RNA because of improved conformational access" (1998) *Nucleic Acids Res.* 26, 5212-5217.
6. **Lustig, B.**, Arora, S. and Jernigan, R. L. "RNA base-amino acid interaction strengths derived from structures and sequences" (1997) *Nucleic Acids Res.* 25, 2562-2565.

7. Lustig, B. and **Jernigan, R. L.** "Consistencies of individual DNA base-amino acid interactions in structures and sequences" (1995) *Nucleic Acids Res.* 23, 4707-4711.
8. Lustig, B., Lin, N. H., Smith, S. M., Jernigan, R. L. and **Jeang, K.-T.** "A small modified hammerhead ribozyme and its conformational characteristics determined by mutagenesis and lattice calculation" (1995) *Nucleic Acids Res.* 23, 3531-3538.
9. Lustig, B., Covell, D. G. and **Jernigan, R. L.** "Conformations of t-RNA: Base pairing and stacking" (1994) *J. Biomol. Struct. Dyn.* 12, 145-161.
10. Lustig, B. and Fink, A. L. "Secondary structure formation precedes tertiary structure in the refolding of ribonuclease A" (1992) *Biochim. Biophys. Acta.* 1121, 229-233.
11. Lustig, B. and **Fink, A. L.** "The thermal denaturation of ribonuclease A in aqueous-methanol solvents" (1992) *Biochim. Biophys. Acta.* 1119, 205-210.
12. **Fink, A. L.**, Anderson, W. D., Hattersly, J. E. and Lustig, B. "The effect of methanol and temperature on the kinetics of refolding of ribonuclease A" (1988) *FEBS Lettr.* 236, 190-194.

***Selected Presentations, Including Invited Seminars (since 2004)***

Do, S., Lakkaraju, H., Potluri, S., Pham, K., Kantardjieff, K. and **Lustig, B.** "Protein Sequence Homology Parameters Applied to the Prediction of Solvent Accessible Residues" (2008) 52nd Biophysical Society Meeting Abstracts. Biophys. J. 94, Supplement, Abstract, 3280-Pos.

Nepal, R., Rose, D., Gholizadeh, S., Lau, R., Mishra, R., Uweh, K. and **Lustig, B.** "Novel Application of Statistical Predictors: First Stage Calculation of Solvent Accessible Protein Residues" (2011) N. California ACS Undergraduate Research Symposium, San Jose, CA. (poster)

Lustig, B. "Sequence Homology and Protein Structure: Is That All There Is?" Chemistry Departmental Seminar, San Jose State University (October 2010).

Lustig, B. "CSU Cyberinfrastructure: How Much is Enough" Twentieth CSU Biotechnology Symposium (2008).

Lustig, B. "Sequence Entropy and Related Methods in Computational Sequence Analysis" Chemistry Departmental Seminar, San Jose State University (April 2006).

***Other Presentations (Since 2004)***

Tao, A., Sun, E., May, J., Lustig, B. and **Young, T.** "Novel Application of Molecular Dynamics Methods to Identify Unique Structural Features That Enhance Protein Binding" (2011) Twenty-third CSU Biotechnology Symposium, Anaheim, CA, Poster 195.

Nguyen, T., Do, S., Mishra, R. and **Lustig, B.** "Sequence Homology Calculations for Proteins and Relevant DNA Indicate Specific Limitations for a Gap-Based Parameter" (2010) Sixth Annual College of Science Student Research Day, San Jose State University. (poster)

Arora, S., Kalakoti, S., Mishra, R., Do, S., Kantardjieff, K. and **Lustig, B.** "Characterization of Protein Tertiary Contacts Using Homology-Based Parameters" (2009) Twenty-first CSU Biotechnology Symposium, A165. (poster)

Pham, K., Do, S., Lakkaraju, H., Lustig, B. and **Kantardjieff, K. A.** "Extracting Protein Structural Features for Sequence-Homology Calculations" (2008) Twentieth CSU Biotechnology Symposium, Oakland, CA, A141. (poster)

**Posterkhin, Y.**, Courellis, S., Kantardjieff, K. A., Chun, R., Cousins, K., Fleming, P., Kioussis, N., Lustig, B., Petkovic, D., Sharma, S., Thibault, W., and Valafar, F. "Enabling Biocomputational Applications to Provide and Consume Services within CSU's Grand Grid" (2008) Twentieth CSU Biotechnology Symposium, Oakland, CA, A137. (poster)

Lakkaraju, H., Hardin, A., Potluri, S., Fowler, R., Potnis, S., Busani, S. and **Lustig, B.** "Characterizing Features of Protein Structure by Sequence Entropy and Related Methods" (2007) Nineteenth CSU Biotechnology Symposium, Los Angeles, CA, A110. (poster)

Yeh, W., Potluri, S. and **Lustig, B.** "Protein Structure Characterization Using Sequence Entropy" (2006) Eighteenth CSU Biotechnology Symposium, San Jose, CA, A113. (poster)

Wang, J., Yang, F., Nair, J. and **Lustig, B.** (2005) "Evaluation of an Energy-Based Smith-Waterman Algorithm for Sequence Alignment in a Parallelized Computation Setting" Seventeenth CSU Biotechnology Symposium, Los Angeles, CA, A117. (poster)

### ***Theses and Thesis Project Reports (Research Advisor)***

1. Gholizadeh, S. "Exploring Sequence Space Parameters for Characterization of Protein Topology" M.S. Thesis-Project, San Jose State University (2011). CME
2. Mishra R. "Characterization of Protein Residue Structural Accessibility Using Sequence Entropy" **M.S. Thesis**. San Jose State University, 2010. **CHEM**
3. Kalakoti, S. "Sequence Variability and Its Application to the Characterization of Three-Dimensional Structure" M.S. Thesis-Project, San Jose State University (2008). CME
4. Caringula, S., "Characterization of Function and Structure Using DNA Sequence Hybridization Method" M.S. Thesis-Project, San Jose State University (2008). CME
5. Lakkaraju, H. "Protein Structure Prediction Using Homology-Based

- Parameters" M.S. Thesis-Project, San Jose State University (2008). MSE
6. Potluri, S. "Exploring the Viability of Protein Structure Prediction Using Sequence Entropy" **M.S. Thesis** (2007). CME
  7. Potnis, S., "Characterization Signatures of Protein and Related Species" M.S. Thesis-Project, San Jose State University (2007). CME
  8. Busani, S., "Energy Based Evaluation of Protein Sequences and Other Sequence Information" M.S. Thesis-Project, San Jose State University (2007). CME
  9. Nair, J. "Alignment Shift Analysis Using Hybridization Energy Analysis" **M.S. Thesis**, San Jose State University (2006). CME
  10. Liao, H. "Flexibility and Sequence Variability in Proteins" **M.S. Thesis**, San Jose State University (2005). **CHEM**
  11. Yeh, W. "Detailed Analysis of Protein Sequence Entropy, Hydrophobicity and Flexibility" **M.S. Thesis**, San Jose State University (2005). MSE
  12. Imaaya, Y. "Developing and Testing of Revised Energy-Based Smith Waterman Algorithm" M.S. Thesis-Project, San Jose State University (2005). CMPE
  13. Wander, D. S. "RNA Structure Energies Applied to Genome Sequence Search" **M.S. Thesis**, San Jose State University (2002). CME