

610 W 113TH STREET
APT 3C
NEW YORK, NY 10025

PHONE 212-865-0682
FAX 530-686-7611
E-MAIL JL840@COLUMBIA.EDU

Jinfeng Liu

Education

Columbia University, New York, NY
Ph.D. (with distinction) in Pharmacology, 2004
M.Phil. in Pharmacology, 2002

University of Medicine and Dentistry of New Jersey, Piscataway, NJ
M.S. in Molecular Genetics and Microbiology, 1998

Peking University, Beijing, China
B.S. in Biochemistry and Molecular Biology, 1996

Research experience

2005-present
2004-2005

Dept. of Biochemistry & Molecular Biophysics/Center for Computational Biology and Bioinformatics, Columbia University, New York, NY

Associate research scientist

Postdoctoral research scientist

- Developed a sequence based protein domain boundary prediction method using neural network
- Maintained target selection pipeline for Northeast Structural Genomics Consortium
- Participated in functional annotation of mouse cDNAs project (FANTOM) headed by RIKEN Institute, Japan.
- Developed a support vector machine based method to distinguish coding and non-coding RNAs.

1999-2004

Dept. of Pharmacology/Center for Computational Biology and Bioinformatics, Columbia University, New York, NY

Thesis research for Ph.D. degree/Research Assistant

- Characterized and compared genome-wide structural and functional features of entirely sequenced genomes using various bioinformatics tools
- Demonstrated functional importance of proteins with long regions without regular secondary structures by analyzing evolutionary conservation and protein-protein interaction patterns from large data set
- Established automatic target selection procedure for structural genomics, selected more than 12,000 target proteins for structural determination in Northeast Structural Genomics Consortium
- Built web based (HTML, PERL/CGI) Bioinformatics tools including a server for predicting Non-Regular Secondary Structure (NORSp) and an SRS-based database of *Predictions for Entire Proteomes* (PEP)
- Participated in *Methanosarcina acetivorans* sequencing and annotation project headed by Whitehead Institute (MIT) by providing annotation of transmembrane proteins.

1997-1998

University of Medicine and Dentistry of New Jersey, Piscataway, NJ

Thesis research for M.S. degree/Research Assistant

Conducted research on cell cycle checkpoint control in fission yeast.

Honors

Dissertation with distinction, Columbia University, 2004
Travel fellowship for The 10th International Conference on Intelligent Systems for Molecular Biology, 2002
Columbia University Faculty Fellowship, 1998-1999
Rutgers University Departmental Fellowship, 1997-1998
Excellent Graduation Thesis Award of Peking University, 1996
Pratthana Life Science Scholarship, 1994
Peking University Scholarship, 1993

Professional Activities

Member: International Society for Computational Biology
Member: New York Academy of Science

Member: programming committee, International Conference on Intelligent Systems for Molecular Biology (ISMB), 2004-2005
Member: programming committee, European Conference on Computational Biology, 2005

Journal Reviewer: Nature Reviews Genetics; Bioinformatics; BMC Structural Biology; ChemBioChem; Journal of Bioinformatics and Computational Biology; PLoS Computational Biology; Proteins

President, Columbia University Medical Center Chinese Students & Scholars Association (CUMC-CSSA), 2001

Publications

1. Liu J, Gough J, and Rost B (2005) Distinguish Protein-Coding from Non-Coding RNAs Using Support Vector Machines. *PLoS Genetics*: submitted.
2. Powers R, Mirkovic N, Goldsmith-Fischman S, Acton TB, Chiang Y, Huang YJ, Ma L, Rajan PK, Cort JR, Kennedy MA, Liu J, Rost B, Honig B, Murray D, and Montelione GT (2005) Solution structure of srchaeglobus fulgidis peptidyl-tRNA hydrolase (Pth2) provides evidence for an extensive conserved family of pth2 enzymes in archea, bacteria and eukaryotes. *Proteins*: in press.
3. Snyder DA, Chen Y, Denissova NG, Acton TB, Aramini JM, Ciano M, Karlin R, Liu J, Manor P, Paranjli R, Rossi P, Swapna GVT, Xiao R, Rost B, Hunt JF, and Montelione GT (2005) Lack of correlation between NMR spectral quality and success in crystallization demonstrates that NMR and x-ray crystallography are complementary methods for small protein structure determination. *J. Am. Chem. Soc.*: in press.
4. Carninci P, Kasukawa T, Katayama S, ..., Liu J, ... (193 co-authors) ..., Kawai J and Hayashizaki Y (2005) The transcriptional landscape of the mammalian genome. *Science*. 309(5740): 1559-1563.
5. Benach J, Edstrom WC, Lee I, Das K, Cooper B, Xiao R, Liu J, Rost B, Acton TB, Montelione GT, and Hunt JF (2005) The 2.35 Å structure of the TenA homolog from Pyrococcus furiosus supports an enzymatic function in thiamine metabolism. *Acta Crystallogr D Biol Crystallogr*. 61(Pt 5): 589-598.
6. Powers R, Acton TB, Chiang Y, Rajan PK, Cort JR, Kennedy MA, Liu J, Ma L, Rost B, and Montelione GT (2004) (1)H, (13)C and (15)N assignments for the Archaeoglobus fulgidis protein AF2095. *J Biomol NMR*. 30(1): 107-108.
7. Liu J and Rost B (2004) CHOP proteins into structural domain-like fragments. *Proteins*. 55(3): 678-688.
8. Liu J and Rost B (2004) CHOP: parsing proteins into structural domains. *Nucleic Acids Res*. 32(Web Server issue): W569-571.

9. Rost B, Yachdav G, and Liu J (2004) The PredictProtein server. *Nucleic Acids Res.* 32(Web Server issue): W321-326.
10. Liu J, Hegyi H, Acton TB, Montelione GT, and Rost B (2004) Automatic target selection for structural genomics on eukaryotes. *Proteins.* 56(2): 188-200.
11. Wunderlich Z, Acton TB, Liu J, Kornhaber G, Everett J, Carter P, Lan N, Echols N, Gerstein M, Rost B, and Montelione GT (2004) The protein target list of the Northeast Structural Genomics Consortium. *Proteins.* 56(2): 181-187.
12. Bigelow HR, Petrey DS, Liu J, Przybylski D, and Rost B (2004) Predicting transmembrane beta-barrels in proteomes. *Nucleic Acids Res.* 32(8): 2566-2577.
13. Liu J and Rost B (2004) Sequence-based prediction of protein domains. *Nucleic Acids Res.* 32(12): 3522-3530.
14. Liu J and Rost B (2003) NORSp: Predictions of long regions without regular secondary structure. *Nucleic Acids Res.* 31(13): 3833-3835.
15. Rost B and Liu J (2003) The PredictProtein server. *Nucleic Acids Res.* 31(13): 3300-3304.
16. Carter P, Liu J, and Rost B (2003) PEP: Predictions for Entire Proteomes. *Nucleic Acids Res.* 31(1): 410-413.
17. Liu J and Rost B (2003) Domains, motifs and clusters in the protein universe. *Curr Opin Chem Biol.* 7(1): 5-11.
18. Aramini JM, Huang YJ, Cort JR, Goldsmith-Fischman S, Xiao R, Shih LY, Ho CK, Liu J, Rost B, Honig B, Kennedy MA, Acton TB, and Montelione GT (2003) Solution NMR structure of the 30S ribosomal protein S28E from *Pyrococcus horikoshii*. *Protein Sci.* 12(12): 2823-2830.
19. Rost B, Liu J, Nair R, Wrzeszczynski KO, and Ofran Y (2003) Automatic prediction of protein function. *Cell Mol Life Sci.* 60(12): 2637-2650.
20. Rost B, Liu J, Przybylski D, Nair R, Wrzeszczynski KO, Bigelow H, and Ofran Y (2003) Predict protein structure through evolution, in '*Chemoinformatics - From Data to Knowledge*', Gasteiger J and Engel T (eds), Wiley, 1789-1811.
21. Liu J, Tan H, and Rost B (2002) Loopy proteins appear conserved in evolution. *J Mol Biol.* 322(1): 53-64.
22. Liu J and Rost B (2002) Target space for structural genomics revisited. *Bioinformatics.* 18(7): 922-933.
23. Galagan JE, Nusbaum C, Roy A, ..., Liu J, ... (54 co-authors)..., Metcalf WW, and Birren B (2002) The genome of *M. acetivorans* reveals extensive metabolic and physiological diversity. *Genome Res.* 12(4): 532-542.
24. Liu J and Rost B (2001) Comparing function and structure between entire proteomes. *Protein Sci.* 10(10): 1970-1979.
25. Xiao J, Li Y, Zhang J, Liu J, and Chen Z (1998) [Nucleotide and protein sequence analysis of rice dwarf virus replicase(segment S1)]. *Wei Sheng Wu Xue Bao.* 38(5): 348-358.

Abstracts

1. Liu J, Gough J, and Rost B (2005) Distinguishing protein-coding from non-coding RNAs through SVM. The Thirteenth International Conference on Intelligent Systems for Molecular Biology (*ISMB 2005*, Detroit, Michigan, 6/2005).
2. Liu J, Hegyi H, Acton TB, Montelione GT, and Rost B (2004) Automatic target selection for structural genomics on eukaryotes. (*Pacific Symposium on Biocomputing*, Big Island, Hawaii, 1/2004).
3. Carter P, Liu J, and Rost B (2002) The PEP Database: Proteins of Entire Proteomes. The Tenth International Conference on Intelligent Systems for Molecular Biology (*ISMB 2002*, Edmonton, Canada, 8/2002).
4. Liu J and Rost B (2002) Target Space for structural genomics revisited. The Tenth International Conference on Intelligent Systems for Molecular Biology (*ISMB 2002*, Edmonton, Canada, 8/2002).

5. **Liu J** and Rost B (2002) Target Space for structural genomics revisited. **Keystone Symposia** (Structural Genomics: From Gene Sequence to function, Breckenridge, Colorado, 1/2002).
6. **Liu J** and Rost B (2000) Non-structured Regions in Genomic Proteins: Junk or Functional? The Eighth International Conference on Intelligent Systems for Molecular Biology (**ISMB 2000**, San Diego, California, 8/2000).
7. **Liu J**, Shi L, and Grundy WN (2000) Comparative Analysis of Yeast Microarray Gene Expression Data: Hierarchical Clustering and Self-organizing Maps. The Eighth International Conference on Intelligent Systems for Molecular Biology (**ISMB 2000**, San Diego, California, 8/2000).

References

Dr. Burkhard Rost
Department of Biochemistry and Molecular Biophysics
Center for Computational Biology and Bioinformatics
Columbia University
1130 St. Nicholas Avenue
New York, NY 10032
Phone: (212) 851-4668
E-mail: rost@columbia.edu

Dr. Barry Honig
Department of Biochemistry and Molecular Biophysics
Center for Computational Biology and Bioinformatics
Columbia University
1130 St. Nicholas Avenue
New York, NY 10032
Phone: (212) 851-4651
E-mail: bh6@columbia.edu

Dr. Gaetano T. Montelione
Center for Advanced Biotechnology and Medicine
Rutgers, The State University of New Jersey
679 Hoes Lane
Piscataway, New Jersey 08854
Phone: (732) 235-5321
E-mail: guy@cabm.rutgers.edu

Dr. Nancy C. Walworth
Department of Pharmacology
UMDNJ-Robert Wood Johnson Medical School
675 Hoes Lane
Piscataway, NJ 08854
Phone: (732) 235-5661
E-mail: walworna@umdnj.edu