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EDUCATION

- 2003-present** Postdoctoral Fellow, Yale University
Research in **computational biology and bioinformatics**
Advisor: Mark Gerstein, Department of Molecular Biophysics and Biochemistry
- 1995-2002** Ph.D. degree in **Chemistry**, Stanford University
Thesis research in **computational structural biology**
Advisor: Michael Levitt, Department of Structural Biology
GPA: 4.1 / 4.0
- 1991-1995** B.Sc. degree in **Chemistry**, Minor in **Computer Science**, Peking University
Undergraduate thesis research in **chemical physics**
Advisor: Xincheng Zhao, Department of Chemistry
GPA: 4.2 / 4.0

SELECTED AWARDS AND HONORS

- 2005** Finalist, Career Awards at the Scientific Interface, Burroughs Wellcome Fund
(Interview to be conducted in October, 2005)
- 2004-present** Fellowship of the Jane Coffin Childs Memorial Fund for Medical Research
- 2004** James Hudson Brown – Alexander Brown Coxe Postdoctoral Fellowship (declined)
- 1996-2001** Howard Hughes Predoctoral Fellowship in Biological Sciences
- 1995** Award for Excellent B.Sc. Thesis, Peking University
- 1993** Baosteel Scholarship (awarded to three best students of Peking University)
- 1992** Guanghua Scholarship, Peking University
- 1991-1995** Excellent Student Scholarships, Peking University
- 1990** The Gold Medal of the 22nd International Chemistry Olympiad held in Paris
- 1989** Winner's Medal, Chinese Mathematics Olympiad

PROFESSIONAL SERVICE

Referee for manuscripts: *Proceedings of the National Academy of Sciences; Journal of Molecular Biology; Proteins: Structure, Function, Genetics; Bioinformatics; Genome Biology; FEBS Letters; Proceedings of the Pacific Symposium on Biocomputing; Proceedings of the IEEE Computer Society Bioinformatics Conference; etc.*

RESEARCH EXPERIENCE

- 2003-present** Postdoctoral research at Yale University, with Professor Mark Gerstein in the Department of Molecular Biophysics and Biochemistry. Research projects: integrated statistical modeling of sequence, structural, and functional genomic data;

genome-wide prediction and analysis of bio-molecular networks; integrating genomic and proteomic data for cellular modeling and simulation.

- 1996-2002** Doctoral research at Stanford University, with Professor Michael Levitt in the Department of Structural Biology. Research projects: a hierarchical method for *ab initio* protein tertiary structure prediction; a rigorous approach for optimally deriving and assessing knowledge-based energy functions; large-scale organization and evolution of protein folding thermodynamics and kinetics in sequence space.
- 1995-1996** Graduate research at Stanford University, with Professor Harden M. McConnell in the Department of Chemistry. Research projects: high resolution comparative modeling of MHC-peptide complex; systematic cross-comparison between molecular models and dissociation kinetics of MHC-peptide complex.
- 1995** Undergraduate thesis research at Peking University, with Professor Xinsheng Zhao in the Department of Chemistry. Research projects: photodissociation dynamics of CH_3N_3 ; observation of triplet methylnitrene radical; new method for analyzing the fluorescence time profile using Fourier transform; deducing kinetic mechanism of chemical reaction networks.

TEACHING EXPERIENCE

- 1999** Teaching Assistant, "Structural Biology 228: Computational Structural Biology", Department of Structural Biology, Stanford University.
- 1995-1996** Teaching Assistant, "Chemistry 135: Physical Chemistry Principles", and "Chemistry 36: Chemical Separations", Department of Chemistry, Stanford University.

THESES

- (1) **Xia Y.** Physical, organizational and evolutionary principles of protein sequence-structure relationships. Ph.D. Thesis, Stanford University (December 2002). 170 pages.
- (2) **Xia Y.** Photodissociation dynamics of methylazide. B.Sc. Thesis, Peking University (August 1995). In Chinese. 76 pages.

MANUSCRIPTS IN PREPARATION

- (1) **Xia Y**, Gerstein M. Sequence, structural and functional genomic determinants of protein evolutionary rate.
- (2) McClellan AJ, **Xia Y**, Gerstein M, Frydman J. Condition-specific yeast Hsp90 chaperone subnetworks revealed by chemical synthetic lethality.
- (3) Dunn AY, **Xia Y**, Gerstein M, Frydman J. Large-scale identification and analysis of cellular substrates of the eukaryotic chaperonin TRiC/CCT.

PUBLICATIONS

- (1) Yu H*, **Xia Y***, Trifonov V, Gerstein M. Organizational themes of molecular networks revealed by global comparisons. *Nature Biotechnology*. Submitted. (* Joint first authors)
- (2) **Xia Y**, Lu LJ, Gerstein M. Integrated prediction of helical membrane protein interactions in yeast. *Journal of Molecular Biology*. In revision.
- (3) Lu LJ, **Xia Y**, Paccanaro A, Yu H, Gerstein M. Assessing the limits of genomic data integration for predicting protein networks. *Genome Research* **15**: 945-953 (2005). (Highlighted by the *Faculty of 1000*)
- (4) Lu LJ*, **Xia Y***, Yu H*, Rives A, Lu H, Schubert F, Gerstein M. Protein interaction prediction by integrating genomic features and protein interaction network analysis. In Azuaje F, Dopazo J, eds. *Data Analysis and Visualization in Genomics and Proteomics* 61-81 (2005). (* Joint first authors)
- (5) Huber D, Boyd D, **Xia Y**, Olma MH, Gerstein M, Beckwith J. Use of thioredoxin as a reporter to identify a subset of *Escherichia coli* signal sequences that promote signal recognition particle-dependent translocation. *Journal of Bacteriology* **187**: 2983-2991 (2005).
- (6) Balasubramanian S, **Xia Y**, Freinkman E, Gerstein M. Sequence variation in G-protein-coupled receptors: analysis of single nucleotide polymorphisms. *Nucleic Acids Research* **33**: 1710-1721 (2005).
- (7) Lehnert U*, **Xia Y***, Royce TE, Goh CS, Liu Y, Senes A, Yu H, Zhang Z, Engelman DM, Gerstein M. Computational analysis of membrane proteins: genomic occurrence, structure prediction and helix interactions. *Quarterly Review of Biophysics* **37**: 121-146 (2004). (* Joint first authors)
- (8) **Xia Y***, Yu H*, Jansen R*, Seringhaus M, Baxter S, Greenbaum D, Zhao H, Gerstein M. Analyzing cellular biochemistry in terms of molecular networks. *Annual Review of Biochemistry* **73**: 1051-1087 (2004). (* Joint first authors)
- (9) Yu H, Luscombe NM, Lu HX, Zhu X, **Xia Y**, Han JJ, Bertin N, Chung S, Vidal M, Gerstein M. Annotation transfer for genomics: assessing the transferability of protein-protein and protein-DNA interactions between organisms. *Genome Research* **14**: 1107-1118 (2004).
- (10) Freeman-Cook LL, Dixon AM, Frank JB, **Xia Y**, Ely L, Gerstein M, Engelman DM, DiMaio D. Selection and characterization of small random transmembrane proteins that bind and activate the platelet-derived growth factor β receptor. *Journal of Molecular Biology* **338**: 907-920 (2004).
- (11) **Xia Y**, Levitt M. Simulating protein evolution in sequence and structure space. *Current Opinion in Structural Biology* **14**: 202-207 (2004).

- (12) **Xia Y**, Levitt M. Funnel-like organization in sequence space determines the distributions of protein stability and folding rate preferred by evolution. *Proteins: Structure, Function, Bioinformatics* **55**: 107-114 (2004).
- (13) **Xia Y**, Levitt M. Roles of mutation and recombination in the evolution of protein thermodynamics. *Proceedings of the National Academy of Sciences of the United States of America* **99**: 10382-10387 (2002). (Highlighted by the *Faculty of 1000*)
- (14) Fain B, **Xia Y**, Levitt M. Design of an optimal Chebyshev-expanded discrimination function for globular proteins. *Protein Science* **11**: 2010-2021 (2002).
- (15) Fain B, **Xia Y**, Levitt M. Determination of optimal Chebyshev-expanded hydrophobic discrimination function for globular proteins. *IBM Journal of Research and Development* **45**: 525-531 (2001).
- (16) **Xia Y**, Levitt M. Extracting knowledge-based energy functions from protein structures by error rate minimization: Comparison of methods using lattice model. *Journal of Chemical Physics* **113**: 9318-9330 (2000).
- (17) **Xia Y**, Huang ES, Levitt M, Samudrala R. *Ab initio* construction of protein tertiary structures using a hierarchical approach. *Journal of Molecular Biology* **300**: 171-185 (2000).
- (18) Samudrala R, **Xia Y**, Levitt M, Cotton NJ, Huang ES, Davis R. Probing structure-function relationships of the DNA polymerase alpha-associated zinc-finger protein using computational approaches. In Altman R, Dunker K, Hunter L, Klein T, Lauderdale K, eds. *Proceedings of the Pacific Symposium on Biocomputing* 179-189 (2000).
- (19) Samudrala R, **Xia Y**, Huang ES, Levitt M. *Ab initio* protein structure prediction using a combined hierarchical approach. *Proteins: Structure, Function, Genetics* **3S**: 194-198 (1999). (Highlighted in *Modern Drug Discovery* **3**: 41-42, 45-46, Nov/Dec 2000)
- (20) Samudrala R, **Xia Y**, Levitt M, Huang ES. A combined approach for *ab initio* construction of low resolution protein tertiary structures from sequence. In Altman R, Dunker K, Hunter L, Klein T, Lauderdale K, eds. *Proceedings of the Pacific Symposium on Biocomputing* 505-516 (1999).
- (21) Liang MN, Lee C, **Xia Y**, McConnell HM. Molecular modelling and design of invariant chain peptides with altered dissociation kinetics from class II MHC. *Biochemistry* **35**: 14734-14742 (1996).
- (22) Ying L, **Xia Y**, Shang H, Zhao X, Tang Y. Photodissociation of methylazide: Observation of triplet methylnitrene radical. *Journal of Chemical Physics* **105**: 5798-5805 (1996).
- (23) Ying L, **Xia Y**, Shang H, Zhao X, Tang Y. Photodissociation of CH₃N₃ – Spectral evidences for the formation of triplet CH₃N radical. *Acta Phys.-Chim. Sinica* **11**: 961-964 (1995).

REFERENCES

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