

CURRICULUM VITAE

KUO-BIN LI (李國彬)

ADDRESS

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PERSONAL DETAILS

Gender: Male
Date of birth: May 8, 1966
Citizenship: Taiwan

EDUCATION

- 10/1984–06/1988 B.S., Department of chemistry, National Taiwan University, Taipei, Taiwan.
- 01/1992–10/1996 Ph.D., Department of chemistry, McGill University, Montréal, Québec, Canada.
Specialization: NMR spectral analysis, protein structure determination, cheminformatics
Thesis: *Development of Computer-Assisted Resonance Assignment Methods for Protein Heteronuclear 3D NMR Spectra*
Supervisor: Prof. B. C. Sanctuary
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EMPLOYMENT

- 02/1997–08/1999 Postdoctoral fellow, Rowland Institute at Harvard, Harvard University, Cambridge, Massachusetts, USA. (<http://www.rowland.harvard.edu>)
Supervisor: Dr. Jeff C. Hoch
Specialization: NMR spectral analysis, distributed parallel programming
- 01/2000–11/2000 Research fellow, Bioinformatics division, Biomedical Engineering Center, Industrial Technology Research Institute. (工業技術研究院生醫中心生物資訊組)
Principle Investigator: Dr. Adam Yao (姚文萱博士)
Specialization: pairwise sequence homology comparison, PC/workstation cluster computing

11/2000–09/2001	Bioinformatics project manager, DigiGenomics Inc., Taipei, Taiwan. (基因數碼科技公司) Specialization: management of biological database, sequence annotation, DNA microarray
12/2001–present	Research Scientist and Team Leader, Bioinformatics Institute, Singapore.
07/2003–present	Adjunct assistant professor, Department of biochemistry, National University of Singapore.

RESEARCH INTERESTS

Non-coding RNA: microRNAs and their targets; phylogenetic footprinting and gene regulation by *cis*- and *trans*-acting RNA interactions; antisense transcripts as regulators of alternative splicing.

Protein functional analyses: protein family classification and functional prediction using amino acid properties (opposed to using homology comparison) and signal processing techniques.

Mutation analysis: determine a missense mutation in amino acid level is deleterious or not; connection between single nucleotide polymorphism and protein function.

Transcription factor binding sites: *ab initio* discovery of transcription factor binding sites using DNA-protein binding models and machine learning techniques.

Distributed Parallel Computing: MPI programming and its application to bioinformatics applications

TEACHING EXPERIENCES

Computational biology 1 and 2: master level one year course, subjects include pairwise alignment, multiple alignment, profile analysis, hidden Markov models, computational gene findings, molecular evolution, building phylogenetic trees, protein-protein interactions.

(<http://web.bii.a-star.edu.sg/~kuobin/lectures/>)

PUBLICATIONS

1. *Automated extraction of amino acid spin systems in proteins using 3D HCCH-COSY/TOCSY spectroscopy and Constrained Partitioning Algorithm(CPA)*, Kuo-Bin Li and Bryan C. Sanctuary, *J. Chem. Inf. Comput. Sci.*, **1996**, 36(3), 585–593.
2. *Automated assignment of proteins using heteronuclear 3D NMR. 1: Backbone spin systems extraction and creation of polypeptides*, Kuo-Bin Li and Bryan C. Sanctuary, *J. Chem. Inf. Comput. Sci.*, **1997**, 37(2), 359–366.
3. *Automated assignment of proteins using heteronuclear 3D NMR. 2: Side chain and sequence-specific assignment*, Kuo-Bin Li and Bryan C. Sanctuary, *J. Chem. Inf. Comput. Sci.*, **1997**, 37(3), 467–477.
4. *Distributed Parallel Processing for Multidimensional Maximum Entropy Reconstruction*, Kuo-Bin Li, Alan S. Stern and Jeffrey C. Hoch, *J. Mag. Reson.*, **1998**, 134(1), 161–163.

5. *Modern Spectrum Analysis in Multidimensional NMR Spectroscopy: Comparison of Linear-Prediction Extrapolation and Maximum-Entropy Reconstruction*, Alan S. Stern, Kuo-Bin Li, and Jeffrey C. Hoch, *J. Am. Chem. Soc.*, **2002**, 124(9), 1982–1993.
6. *ClustalW-MPI: ClustalW Analysis Using Distributed and Parallel Computing*, Kuo-Bin Li, *Bioinformatics*, **2003**, 19(12), 1585–1586.
7. *Multiple sequence alignment using tabu search*, Tariq Riaz, Yi Wang and Kuo-Bin Li, *Proceedings of the second Asia-Pacific Bioinformatics Conference*, Dunedin, New Zealand, **2004**.
8. *Rapid motif detection in protein sequences using wavelet transform*, Arun Krishnan, Kuo-Bin Li and Praveen Issac, *in silico Biology*, **2004**, 4, 0013.
9. *An adaptive iterative algorithm for refining multiple sequence alignment*, Yi Wang and Kuo-Bin Li, *Computational Biology and Chemistry*, **2004**, 28(2), 141–148.
10. *Predicting allergenic proteins using wavelet transform*, Kuo-Bin Li, Praveen Issac and Arun Krishnan, *Bioinformatics*, **2004**, 20, 2572-2578.
11. *G-PRIMER, a greedy algorithm for selecting minimal primer set*, Jiren Wang, Kuo-Bin Li, and Wing-Kin Sung, *Bioinformatics*, **2004**, 20, 2473-2475.
12. *From genomes to drugs with bioinformatics*, Kuo-Bin Li, in *Novel compounds from Natural Products in the New Millennium, Potential and Challenges*, Ed. Benny K. H. Tan, B. H. Bay and Y. Z. Zhu, World Scientific, Singapore, **2004**.
13. *A tabu search algorithm for post-processing multiple sequence alignment*, Tariq Riaz, Yi Wang and Kuo-Bin Li, *Journal of Bioinformatics and Computational Biology*, **2005**, 3(1), 145-156.
14. *Immunohistochemical detection of Ki67 in breast cancer correlates with transcriptional regulation of genes related to apoptosis and cell death*, Puay Hoon Tan, Boon Huat Bay, George Yip, Sathiyamoorthy Selvarajan, Patrick Tan, Jeanne Wu, Chee How Lee and Kuo-Bin Li, *Modern Pathology*, **2005**, 18(3), 374-381.
15. *Y-box binding protein, YB-1, as a marker of tumor aggressiveness and response to adjuvant chemotherapy in breast cancer*, Jingxiang Huang, Puay Hoon Tan, Kuo-Bin Li, Ken Matsumoto, Masafumi Tsujimoto and Boon Huat Bay, *International Journal of Oncology*, **2005**, 26(3), 607-613.
16. *A Position-specific and consistency-based objective function for iterative multiple sequence Alignment*, Yi Wang, Tariq Riaz, Espen Enerly, Sheng Zeng and Kuo-Bin Li, in the *Proceedings of the 6th WSEAS International Conference on Mathematics and computers in biology and chemistry*, Buenos Ayres, Argentina, March 1-3, **2005**.
17. *Multiple sequence alignment using an exhaustive and greedy algorithm*, Yi Wang and Kuo-Bin Li, *Journal of Bioinformatics and Computational Biology*, **2005**, 3(2), 243-255.
18. *WebAllergen: a web server for predicting allergenic proteins*, Tariq Riaz, Hen Ley Hor, Arun Krishnan, Francis Tang and Kuo-Bin Li, *Bioinformatics*, **2005**, 21(10), 2570-2571.
19. *The quality of a multiple sequence alignment can be evaluated by a position-specific and consistency-based objective function*, Yi Wang, Tariq Riaz, Espen Enerly, Sheng Zeng and Kuo-Bin Li, *WSEAS Transactions on Mathematics and Computers in Biology and Biomedicine*, **2005**, 2(2), 147-157.
20. *Natural antisense as potential regulator of alternative initiation, splicing and termination*, Espen Enerly, Zeng Sheng and Kuo-Bin Li, *in silico Biology*, **2005**, 5, 0033.

21. *pSLIP: SVM based protein subcellular localization prediction using multiple physicochemical properties*, Deepak Sarda, Gek-Huey Chua, **Kuo-Bin Li**, and Arun Krishnan, *BMC Bioinformatics*, **2005**, 6, 152.
22. *Protein subcellular localization prediction for Gram-negative bacteria using amino acid subalphabets and a combination of multiple support vector machines*, Jiren Wang, Wing-Kin Sung, Arun Krishnan and **Kuo-Bin Li**, *BMC Bioinformatics*, **2005**, 6, 174.
23. *CMDWave: conserved motifs detection using wavelets*, Tariq Riaz, **Kuo-Bin Li**, Francis Tang and Arun Krishnan, *in silico Biology*, **2005**, 5, 0038.