

# Zehua Chen, Ph.D.

<http://www.ccrnp.ncifcrf.gov/~chenze/>

*Broad Institute of MIT and Harvard Cambridge, MA 02141 Phone: 301-682-6623 Email: [zehua@mit.edu](mailto:zehua@mit.edu)*

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## Objective:

- Seeking a challenging position in computational biology, bioinformatics, genomics, environmental genomics, microbiology, systems biology or related discipline.

## Research Interests:

- Information theory based DNA binding site models; Protein-DNA recognition code; Gene transcription and translation regulation; Information analysis of synonymous codon usage and amino acid biases; Microarray gene expression analysis; Microbial genomic diversity and evolution, comparative genomics; Environmental genomics of bacteria and phages; Evolutionary analysis of gene families and genomes; Z curve based genome sequence analysis; Nucleotide and protein sequence analysis; Genomic data mining.

## Current Research:

- Information analysis of codon usage biases;
- Codon bias patterns related to tissue-specific gene expression;
- Codon bias evolution in closely and distantly related species;
- Microarray gene expression analysis;
- Malaria transcription factor binding site models, splice junction site models;
- Information models of mammalian transcription factor binding sites;
- Ribosome binding site (RBS) models for phages and their bacterial hosts;
- T7-like promoter models, T7 islands;
- Evolution of T7-like phages and their transcription systems;
- Comparative analysis of bacterial Fur binding site models.

## Education:

- Sep 1991 - July 1995, B.S., Major in Freshwater Fishery, Southwest Agricultural University, Chongqing, China.
- Sep 1995 - Feb 2001, Ph.D., Major in Molecular Biology, Shanghai Institute of Biochemistry and National Center for Gene Research, Chinese Academy of Sciences, Shanghai, China.  
Advisor: Prof. Guofan Hong,  
Work on rice genome mapping, sequencing and analysis.

Ph.D. thesis:

Sequence-ready contig map construction and sequence analysis of a 1.8 Mb region close to the distal telomere of rice chromosome 4.

## Brief Chronology of Employment:

- Feb 2001 - Oct 2001, Research Fellow,  
National Center for Gene Research,  
Chinese Academy of Sciences, Shanghai, China  
Work on rice genome mapping, sequencing and analysis.
- Nov 2001 - Oct 2006, Postdoctoral Fellow,  
Laboratory of Experimental and Computational Biology (LECB),  
(\* Since Aug, 2005, LECB has been renamed to CCRNP—  
Center for Cancer Research Nanobiology Program \*)  
NCI-Frederick, CCR, NIH, Frederick, MD.  
Work on molecular information theory based DNA binding site models.
- Dec 2006 - Jan 2008, Research Associate,  
Boston College — Biology Department,  
Chestnut Hill, MA.  
Work on codon usage bias and transcription regulation.
- Jan 2008 - Present, Bioinformatics Scientist,  
The Broad Institute of MIT and Harvard,  
Cambridge, MA.  
Work on prokaryotic and fungal genome annotation.

## Presentations:

- Poster (by **Chen Z** and Chuang J.): Selective optimization of codon usage detected by information theory based codon bias measurements, 2007 Oct 11-13, the RECOMB Regulatory Genomics, at the Broad Institute of MIT and Harvard:  
<http://compbio.mit.edu/recombsat/>
- Talk (by **Chen Z**): Information as a measure of codon usage biases, 2007 May 15, at the Boston College Biology retreat.
- Poster (by **Chen Z** and Chuang J.): Information as a measure of codon usage biases, 2007 May 8-12, at the Cold Spring Harbor Laboratory: The Biology of Genomes.  
<http://meetings.cshl.edu/meetings/genome07.shtml>
- Poster (by **Chen Z** and Chuang J.): Information as a measure of codon usage biases, 2007 Mar 29-Apr 1, at the Cold Spring Harbor Laboratory: Systems Biology, Global Regulation of Gene Expression: <http://meetings.cshl.edu/meetings/systems07.shtml>
- Talk (by **Chen Z**): Information theory based DNA binding site models, 2006 Aug 24, at the Computational Systems Biology Lab (CSBL): <http://csbl.bmb.uga.edu/index.html/>
- Talk (by **Chen Z**): Information theory based DNA binding site models, 2006 June 9, at the SuperArray Biosciences Corporation: <http://www.superarray.com/>, Host: Dr. Xiao Zeng.
- Talk (by **Chen Z**): Information theory analysis of T7-like phages, 2006 June 2, at the Biology Department of the Brookhaven National Laboratory: <http://www.biology.bnl.gov/>, Host: Dr. F. William Studier.

- Talk (by **Chen Z**): Discovery of T7 Islands Using Information Theory Based T7-like Promoter Models, 2006 May 15, at the 2006 Texas, Evergreen Phage and Virus Genomics and Ecology Meeting: [http://www.biochem.uthscsa.edu/~hs\\_lab/phage\\_meeting/](http://www.biochem.uthscsa.edu/~hs_lab/phage_meeting/)
- Poster (by **Chen Z** and Schneider TD): Takeover Pressure Explains Excess Information at T7-like Promoters, 2006, May 12-15, at the 2006 Texas, Evergreen Phage and Virus Genomics and Ecology Meeting:  
[http://www.biochem.uthscsa.edu/~hs\\_lab/phage\\_meeting/](http://www.biochem.uthscsa.edu/~hs_lab/phage_meeting/)
- Poster (by **Chen Z** and Schneider TD): Takeover Pressure Explains Excess Information at T7-like Promoters, 2005 Oct, at the 2005 NIH Research Festival:  
<http://researchfestival.nih.gov/>
- Talk (by **Chen Z**): Information Theory Based T7-like Promoter Models: Evolution of T7-like Transcription Systems and Detection of a Novel Group of Genomic Islands Containing Tandem T7-like Promoters. 16th International Phage Biology Meeting:  
<http://www.evergreen.edu/phage/meetings/2005meeting.htm>
- Poster (by **Chen Z** and Schneider TD): Comparative Analysis of T7-like Promoter Bearing Regions in Bacterial Genomes Reveals a Novel Group of Islands. TIGR's GSAC XVI:  
<http://www.tigr.org/conf/gsac/>
- Poster (by **Chen Z** and Schneider TD): Comparative Analysis of T7-like Promoter Bearing Regions in Bacterial Genomes Reveals a Novel Group of Islands. 2004 NIH Research Festival: <http://researchfestival.nih.gov/festival04/default.htm>
- Poster (by **Lyakhov IG**, Chen Z and Schneider TD): A Novel Bacteriophage Lambda Cro Responsive Element in the oop RNA Promoter. 2004 NIH Research Festival:  
<http://researchfestival.nih.gov/festival04/default.htm>
- Poster (by **Chen Z** and Schneider TD): Excess Information at T7-like Promoters and Classification of T7-like Phages. The Eighth Annual International Conference on Research in Computational Molecular Biology (RECOMB2004, <http://recomb04.sdsc.edu/>). Abstract (poster number K23) is available at:  
<http://recomb04.sdsc.edu/cgi-admin/posterabstracts.cgi>
- Abstracts for the RGP Rice Genome Workshop:  
<http://rgp.dna.affrc.go.jp/rgp/rgm7/Workshop.html>  
<http://rgp.dna.affrc.go.jp/rgp/rgm6/rgm6ws.html>
- Abstracts for the International Plant & Animal Genome Conference (PAG):  
<http://www.intl-pag.org/pag/7/abstracts/pag7189.html>  
<http://www.intl-pag.org/pag/8/abstracts/pag8080.html>  
[http://www.intl-pag.org/pag/9/abstracts/W52\\_01.html](http://www.intl-pag.org/pag/9/abstracts/W52_01.html)

## Professional Associations:

- International Society for Computational Biology: <http://www.iscb.org/>
- American Society for Microbiology: <http://www.asm.org/>
- Sigma Xi: <http://www.sigmaksi.org/>

- Bacteriophage Ecology Group:  
[http://www.mansfield.ohio-state.edu/~sabedon/beg\\_members.htm](http://www.mansfield.ohio-state.edu/~sabedon/beg_members.htm)
- IEEE: the Institute of Electrical and Electronics Engineers,  
<http://www.ieee.org/>

## Referee for Peer-reviewed Journals:

- Nucleic Acids Research, <http://nar.oxfordjournals.org/>
- Bioinformatics, <http://bioinformatics.oxfordjournals.org/>

## Manuscripts in Preparation:

- **Chen Z** and Chuang J. **Selective optimization of codon usage detected by information theory based codon bias measurements.** 2008, *in preparation.*
- **Chen Z** and Schneider TD. **Takeover pressure explains excess information at T7-like promoters.** 2008, *in preparation.*

## Publications:

- **Chen Z**, Lewis KA, Shultzaberger RK, Lyakhov IG, Zheng M, Doan B, Storz G and Schneider TD. **Discovery of Fur binding site clusters in *Escherichia coli* by information theory models.** *Nucleic Acids Res*, 2007, 35(20):6762-77.
- Shultzaberger RK, **Chen Z**, Lewis KA and Schneider TD. **Anatomy of *Escherichia coli* sigma 70 promoters.**, *Nucleic Acids Res*, 2007, 35:771-788.
- **Chen Z** and Schneider TD. **Comparative analysis of tandem T7-like promoter containing regions in enterobacterial genomes reveals a novel group of genetic islands.** *Nucleic Acids Res*, 2006, 34(4):1133-1147.
- **Chen Z** and Schneider TD. **Information theory based T7-like promoter models: classification of bacteriophages and differential evolution of promoters and their polymerases.** *Nucleic Acids Res*, 2005, 33(19):6172-6187.
- **Chen Z** and Schneider TD. **Excess information at T7-like promoters and classification of T7-like phages.** *RECOMB: Currents in Computational Molecular Biology*. 2004, 492-3.
- Feng Q, Zhang Y, Hao P, Wang S, Fu G, Huang Y, Li Y, Zhu J, Liu Y, Hu X, Jia P, Zhang Y, Zhao Q, Ying K, Yu S, Tang Y, Weng Q, Zhang L, Lu Y, Mu J, Lu Y, Zhang LS, Yu Z, Fan D, Liu X, Lu T, Li C, Wu Y, Sun T, Lei H, Li T, Hu H, Guan J, Wu M, Zhang R, Zhou B, **Chen Z**, Chen L, Jin Z, Wang R, Yin H, Cai Z, Ren S, Lv G, Gu W, Zhu G, Tu Y, Jia J, Zhang Y, Chen J, Kang H, Chen X, Shao C, Sun Y, Hu Q, Zhang X, Zhang W, Wang L, Ding C, Sheng H, Gu J, Chen S, Ni L, Zhu F, Chen W, Lan L, Lai Y, Cheng Z, Gu M, Jiang J, Li J, Hong G, Xue Y, Han B. **Sequence and analysis of rice chromosome 4.** *Nature*. 2002 Nov 21;420(6913):316-20.

- Zhao Q, Zhang Y, Cheng Z, Chen M, Wang S, Feng Q, Huang Y, Li Y, Tang Y, Zhou B, **Chen Z**, Yu S, Zhu J, Hu X, Mu J, Ying K, Hao P, Zhang L, Lu Y, Zhang LS, Liu Y, Yu Z, Fan D, Weng Q, Chen L, Lu T, Liu X, Jia P, Sun T, Wu Y, Zhang Y, Lu Y, Li C, Wang R, Lei H, Li T, Hu H, Wu M, Zhang R, Guan J, Zhu J, Fu G, Gu M, Hong G, Xue Y, Wing R, Jiang J, Han B. **A fine physical map of the rice chromosome 4.** *Genome Res.* 2002 May;12(5):817-23.  
\*Note: My name (Zehua Chen) in this paper was misspelled as “Zhehua Chen”.
- **Chen ZH**, Zhou B, Han B, Qian YM, Hong GF. **Structural Analysis of a Gene Cluster Encoding Two Cationic and Three Anionic Peroxidases from Rice Chromosome 4.** *Sheng Wu Hua Xue Yu Sheng Wu Wu Li Xue Bao* (Shanghai). 2001; 33(2):163-172.
- Zhou B, **Chen ZH**, Han B, Hong GF. **Identification and Structural Analysis of a class of Potentially Transposable Solo-LTR in Rice Genome.** *Sheng Wu Hua Xue Yu Sheng Wu Wu Li Xue Bao* (Shanghai). 2001;33(2):158-162.
- Liu ST, Chang WZ, Cao HM, Hu HL, **Chen ZH**, Ni FD, Lu HF, Hong GF. **A HU-like protein binds to specific sites within nod promoters of *Rhizobium leguminosarum*.** *J Biol Chem.* 1998 Aug 7;273(32):20568-74.

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 \* version=1.42 of cvs.txt 2008 Jan 12  
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