



Feng-Chi chen, PhD

Investigator

+886-37-246166 ext. 36111

+886-37-586467

fcchen@nhri.org.tw

Education

- 1992
B.S. in Biology,
National Taiwan Normal University, Taiwan
- 2001
Ph.D. in Life Sciences,
National Tsing-Hua University, Taiwan

Professional Experiences

- 2016/04-present
Institute of Population Health Sciences, National Health Research Institutes, Taiwan
Investigator
- 2016/09-present
Department of Biological Science and Technology, National Chiao-Tung University, Taiwan
Adjunct Professor
- 2011/10-2016/03
Institute of Population Health Sciences, National Health Research Institutes, Taiwan
Associate Investigator
- 2011/08-2016/07
Department of Biological Science and Technology, National Chiao-Tung University, Taiwan
Adjunct Associate Professor
- 2006/06-2011/09
Division of Biostatistics and Bioinformatics, National Health Research Institutes, Taiwan
Assistant Investigator
- 2008/02-2011/07
Department of Biological Science and Technology, National Chiao-Tung University, Taiwan
Adjunct Associate Professor
- January 2009 – March 2009
Department of Bioengineering, University of California at San Diego, USA
Visiting Scholar

Research Interests

Comparative genomics and transcriptomics; molecular evolution; bioinformatics; patent informatics.

Research Activities & Accomplishment

Over 50 scientific articles in international journals.

Selected Publications

- **Chen FC*** and Guo-Liang Yeh. 2016. Invalidation of atorvastatin patent highlights complex Chinese patent law. *Trends in Pharmacological Sciences* (Epub ahead of print).
- **Chen FC***. 2016. Divided infringement in the limelight of the patent battle field. *Trends in Biotechnology* 34 (10): 771-773.
- Hsu MK, Pan CL, and **Chen FC***. 2016. Functional divergence and convergence between the transcript network and gene network in lung adenocarcinoma. *OncoTargets and Therapy* 9: 335-347.
- Hsu MK, Wu IC, Cheng CC, Su JL*, Hsieh CH, Lin YS, and **Chen FC***. 2015. Triple-layer dissection of the lung adenocarcinoma transcriptome – regulation of the gene, transcript, and exon levels. *Oncotarget* 6(30):28755-73.
- **Chen FC***. 2015. Alternative RNA structure-coupled translational regulations in tumorigenesis. *International Journal of Molecular Sciences* 16(1): 452-475. (invited review).
- **Chen FC***, Chuang TJ*, Lin HY, and Hsu MK. 2014. The evolution of the coding exome of the Arabidopsis species - the influences of DNA methylation, relative exon position, and exon length. *BMC Evolutionary Biology* 14: 145.
- **Chen FC***, Liao YC, Huang JM, Lin CH, Chen YY, Dou HY, and Hsiung CA*. 2014. Pros and cons of the tuberculosis drugome approach – an empirical analysis. *Plos One* 9(6): e100829.
- Chuang TJ* and **Chen FC***. 2014. DNA methylation is associated with an increased level of conservation at nondegenerate nucleotides in mammals. *Molecular Biology and Evolution* 31(2):387-96.
- **Chen FC*** 2014. Are all of the human exons alternatively spliced? *Briefings in Bioinformatics* 15 (4): 542-551.
- Wang TC and **Chen FC***. 2013. The evolutionary landscape of the *Mycobacterium tuberculosis* genome. *Gene* 518(1):187-93.
- Hsu MK and **Chen FC***. 2012. Selective constraint on the upstream open reading frames that overlap with coding sequences in animals. *Plos One* 7(11): e48413.
- Chuang TJ*, **Chen FC***, and Chen YZ. 2012. Position-dependent correlations between the level of DNA methylation and the evolutionary rates of mammalian coding exons. *Proceedings of the National Academy of Sciences* 109(39):15841-6.
- Gelly J-C, Lin HY, de Brevern A.G. *, Chuang TJ*, and **Chen FC***. 2012. Selective Constraint on Human Pre-mRNA Splicing by Protein

Structural Properties. *Genome Biology and Evolution* 4(9):966-75.

- **Chen FC***, Liao BY*, Pan CL, Lin HY, and Chang AYF. 2012. Assessing determinants of exonic evolutionary rates in mammals. *Molecular Biology and Evolution* 29(10):3121-9.
- **Chen FC***, Pan CL, and Lin HY. 2012. Independent effects of alternative splicing and structural constraint on the evolution of mammalian coding exons. *Molecular Biology and Evolution* 29(1):187-93.
- Lin CH, Hsiung CA*, and **Chen FC***. 2011. Changes in transcriptional orientation are associated with increases in evolutionary rates of enterobacterial genes. *BMC Bioinformatics* 12 (Suppl 9):S19.
- Chen CH, Lin HY, Pan CL, and **Chen FC***. 2011. Exploring the selective constraint on the sizes of insertions and deletions in 5' untranslated regions in mammals. *BMC Evolutionary Biology* 11: 192
- **Chen FC**, Chen CJ, Li WH, and Chuang TJ. 2010. Gene family size conservation is a good indicator of evolutionary rates. *Molecular Biology and Evolution* 27(8):1750-8.
- Chen CH, Chuang TJ, Liao BY, and **Chen FC***. 2009. Scanning for the signatures of positive selection for human-specific insertions and deletions. *Genome Biology and Evolution* 1: 415-9
- Lin FK, Pan CL, Chuang TJ*, and **Chen FC***. 2009. CAPIH: A Web interface for comparative analyses and visualization of host-HIV protein-protein interactions. *BMC Microbiology* 9: 164.
- **Chen FC**, **Chen YZ**, and **Chuang TJ**. 2009. CNVVdb: a database of copy number variations across vertebrate genomes. *Bioinformatics* 25(11):1419-21.
- Huang YT, **Chen FC***, and Chuang TJ*. 2008. Identification and analysis of ancestral hominoid transcriptome inferred from cross-species transcripts and processed pseudogene comparisons. *Genome Research* 18(7):1163-70.
- **Chen FC** and Chuang TJ. Nucleotide sequence divergence between humans and chimpanzees. 2008 (Invited review) *Encyclopedia of Life Sciences*. DOI: 10.1002/9780470015902.a0020751.
- **Chen FC** and Chuang TJ. 2007. Different alternative splicing patterns are subject to opposite selection pressure for protein reading frame preservation. *BMC Evolutionary Biology* 7: 179.
- **Chen FC**, Chen CJ, and Chuang TJ. 2007. INDELSCAN: a web server for comparative identification of species-specific and non-species-specific insertion/deletion events. *Nucleic Acids Research* (Web Server Issue): W633-8.
- **Chen FC**, Chaw SM, Tzeng YH, Wang SS, and Chuang TJ. 2007. Opposite evolutionary effects between different alternative splicing patterns. *Molecular Biology and Evolution* 24: 1443-6.

- **Chen FC**, Wang SS, Chaw SM, Huang YT, and Chuang TJ. 2007. Plant Gene and Alternatively Spliced Variant Annotator. A plant genome annotation pipeline for rice gene and alternatively spliced variant identification with cross-species expressed sequence tag conservation from seven plant species. *Plant Physiology* 143:1086-95.
- **Chen FC**, Chen CJ, Li WH, and Chuang TJ. 2007. Human-specific insertions and deletions inferred from mammalian genome sequences. *Genome Research* 17: 16-22.
- **Chen FC**, Chen CJ, Ho JY and Chuang TJ. 2006. Identification and evolutionary analysis of novel exons and alternative splicing events using cross-species EST-to-genome comparisons. *BMC Bioinformatics* 7: 136
- **Chen FC**, Wang SS, Chen CJ, Li WH and Chung TJ. 2006. Alternatively and constitutively spliced exons are subject to different evolutionary forces. *Molecular Biology and Evolution* 23:675-682.
- **Chen FC** and TJ Chuang. 2005. ESTViewer: a Web interface for visualizing mouse, rat, cattle, pig, and chicken conserved ESTs in human genes and human alternatively spliced variants. *Bioinformatics* 21: 2510-2513.
- Chuang TJ, **Chen FC** and MY Chou. 2004. A comparative method for identification of gene structures and alternatively spliced variants. *Bioinformatics* 20: 3064-3079.
- **Chen FC** and Li WH. 2001. Genomic divergences between humans and other hominoids and the effective population size of the common ancestor of humans and chimpanzees. *American Journal of Human Genetics* 68: 444-456.

Patent

None