Yanan Feng, Ph.D.

Email: feng@stanford.edu

EXPERIENCE

Jan. 2019-present: Senior Research Scientist, Genetics Department, Stanford University, Stanford, CA94305.

- Research project: the studying of the gene modifiers of Fragile X symptom in regulating the transcription and translation level of mutant FMR1 expression.
- Collaboration project: In vitro study of the mode of action of the transcriptional elongation factors SUPT4H/5H in transcribing trinucleotide repeat nucleotides.

May. 2017- Jan. 2019: Director, Huntington's Disease Research, Nuredis Inc. Menlo Park, CA 94025

Nov. 2016 -Apr. 2017 Principal Scientist, Nuredis Inc .

Lead a research team for SAR drug discovery of Huntington's Disease.

- Develop and supervise high throughput assays for pipeline compounds validation.
- S with CROs for in vitro assay platforms of biomarker quantitation aiming for future clinical applications.

Principal Scientist, Nuredis Inc. Menlo Park, CA 94025. Nov. 2016 - present

- Drug discovery for Huntington's disease
- Assay development for clinical applications

Senior Research Scientist, Genetics Department, Stanford University, Stanford, CA94305. May, 2009-Jan 2018

- High throughput screening of small molecules as therapeutic agents of neurodegenerative diseases resulted from nucleotide repeats disorder
- Functional studies of human cellular genes essential for C. difficile toxin cytotoxicity
- Study of the effect of human genetic variations of candidate CGEPs (cellular gene exploited by pathogen) to the toxin susceptibility of C. difficile

Research Associate, Genetics Department, Molecular Genetics Laboratory, Stanford University, Stanford, May, 2000-2009

- Genome-wide searching for CGEPs (cellular gene exploited by pathogen) that are involved in the cytotoxic effect of C. difficile.
- Genome-wide searches for genes that control the degradation of RNA containing AU-rich element 3' in human cell lines using Random-Homozygous Knock-out method and then using cDNA microarray and genomic walking technologies in

identifying the candidate genes as well as characterizing the corresponding mutant phenotype.

- Using siRNA knock-down and cDNA microarray technologies to study the specific genes that are associated with RNA stability control in mammalian cells.
- Collaboration on the DARPA (the Defense Advanced Research Projects Agency) funded project – "Genetic Mechanisms for host cell resistance to viral pathogens" with scientists from USDA, Plum Island Animal Disease Center.
- Collaborating with Dr. Dave McKay, who supervises the Structure Biology Laboratory at Stanford, to solve the protein structures of RNase E and RNase E homologs from other microorganisms.
- Collaborating with ISIS Pharmaceutics in a study that apply a novel approach involved synthetic RNA oligonucleotides to characterize a essential bacterial endoribonuclease mode of action.
- Collaborating with colleague scientists on E. coli mutants that have various point mutation in rne gene to study the mechanism of the essentiality of RNase E protein.

Research Assistant and Ph.D. candidate, Cancer Biology Program and Molecular Genetic Laboratory, Stanford University, Stanford, CA. Sep. 1994- May 2000

- Studies on the catalytic and binding activities of RNase E, a major ribonuclease which has global effect in controlling bacteria RNA stability.
- Discovery of the trans- and cis- elements which determine the polyadenylation efficiency of PAP I in E. coli.
- Discovery of the poly(A) binding proteins and studies of the physiological functions of such protein/protein association.

Research Assistant, Department of Pathology, University of Florida, Gainesville, FL. Aug.1993-May 1994

- Designing and developing the method for fast detecting polymorphism of human MHC class II gene locus.
- Studying the expression patterns of GAD antibody from patients with type I diabetes and the possible application of using such antibody in predicting children who may develop diabetes.

Research Assistant, Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan. 1992-1993

- Studies of the destabilizing effect of eukaryotic RNA AU-rich element in E. coli and the possible enzymes that involves in decaying such message.

Research Assistant, Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan. 1990-1992

- Evaluating the RFLP of human endogenous retroviral-like sequence in genetic linkage of different cancers, including liver cancer and paranasal sinus cancer that are prevalence in Asia ethnic group.

EDUCATION

Doctor of Philosophy in Cancer Biology, School of Medicine, Stanford University, Stanford, CA, 2000.
Dissertation: Protein/RNA interactions in RNA Decay Mediated by Escherichia coli poly(A) Polymerase I and RNase E.

Bachelor of Science in Medical Technology, School of Medical Technology, National Yang-Ming University, Taipei, Taiwan, 1990

SELECTED PUBLICATIONS

1. Kramer NJ, Carlomagno Y, Zhang YJ, Almeida S, Cook CN, Gendron TF, Prudencio M, Van Blitterswijk M, Belzil V, Couthouis J, Paul JW 3rd, Goodman LD, Daughrity L, Chew J, Garrett A, Pregent L, Jansen-West K, Tabassian LJ, Rademakers R, Boylan K, Graff-Radford NR, Josephs KA, Parisi JE, Knopman DS, Petersen RC, Boeve BF, Deng N, Feng Y, Cheng TH, Dickson DW, CohenSN, Bonini NM, Link CD, Gao FB, Petrucelli L, Gitler AD.
   Spt4 selectively regulates the expression of C9orf72 sense and antisense mutant transcripts
   Science, 2016, August; 353(6300): 708-712
2. Cheng HM, Chern Y, Chen IH, Liu CR, Li SH, Chun SJ, Rigo F, Bennett CF, Deng N, Feng Y, Lin CS, Yan YT, Cohen SN, Cheng TH
   Effects on Murine Behavior and Lifespan of Selectively Decreasing Expression of Mutant Huntingtin Allele by Supt4h Konckdown
   PLoS Genet. 2015 March; 11(3)
3. Feng Y, Cohen SN
   Upregulation of the Host SLC11A1 Gene by Clostridium difficile Toxin B Facilitates Glucosylation of Rho GTPases and Enhances Toxin Lethality
   Infection and Immunity 2013 Augst; 81(8): 2724-32
4. Feng Y , Piccone ME, Chang ACY, Mosser Ri, Lu Q, Kutish GF, Lu Z, Burrage TG, Gooch G, Rock DL, and Cohen SN
   Identification of Cellular Genes Affecting the Infectivity of Foot-and-Mouth Disease VirusJournal of Virology, 2009, July; 83(13): 6681–6688.
5. Feng Y, Caruthers JM, McKay DB, Cohen SN
   Retention of core catalytic functions by a conserved minimal ribonuclease E peptide that lacks the domain required for tetramer formation.
   Journal of Biological Chemistry, 2006 Sep. 15, 281(37):27046-51
6. Feng Y, Vickers TA, Cohen SN

The catalytic domain of RNase E shows inherent 3' to 5' directionality in cleavage site selection. Proceedings of the National Academia of Sciences of the United States of America, 2002, November 12, 99(23): 14746-14751

7. Feng Y, Huang H, Liao J, Cohen SN
   Escherichia coli poly(A)-binding proteins that interact with components of degradosomes or impede RNA decay mediated by polynucleotide phosphorylase and RNase E.
   Journal of Biological Chemistry, 2001 Aug. 24, 276(34):31651-6
8. Feng Y and Cohen SN
   Unpaired terminal nucleotides and 5' mono phosphorylation govern 3' polyadenylation by Escherichia coli poly(A) polymerase I.
   Proceedings of the National Academia of Sciences of the United States of America, 2000 June 6, 97(12): 6415-6420.