

# CURRICULUM VITAE

9/9/2017

**NAME:** Leng Han, Ph.D.

**PRESENT TITLE:** Assistant Professor and CPRIT Scholar

**WORK ADDRESS:** McGovern Medical School at UTHealth  
The University of Texas Health Science Center at Houston  
Department of Biochemistry and Molecular Biology  
6431 Fannin St. MSB 6.166, Houston, TX 77030

**BIRTHDATE:** 9/26/1982

**CITIZENSHIP:** China

## **UNDERGRADUATE EDUCATION:**

B.S. in Biotechnology, Wuhan University, China

## **GRADUATE EDUCATION:**

Ph.D. in Genetics, Chinese Academy of Sciences, China

## **POSTGRADUATE TRAINING:**

Stanford University, Stanford, CA  
The University of Texas MD Anderson Cancer Center, Houston, TX

## **ACADEMIC & ADMINISTRATIVE APPOINTMENTS:**

Assistant Professor, 2015-Present  
Department of Biochemistry and Molecular Biology  
McGovern Medical School at UTHealth

## **PROFESSIONAL ORGANIZATIONS:**

### **NATIONAL**

Co-chair of Local Organization Committee, International Conference on Intelligent Biology and Medicine (ICIBM 2016), December 8-10, 2016, Houston, TX, USA

## **HONORS AND AWARDS:**

- 2001-2004 Outstanding Undergraduate Scholarship, Wuhan University, China
- 2008 Zhuli Yuehua Scholarship, Kunming Institute of Zoology, CAS, China
- 2012 Excellent Doctoral Dissertation of Yunnan Province, China
- 2015 The Second Prize for Outstanding Performance and Excellence in Scientific Presentation, The 29th SCBA-Texas Chapter Annual Symposium, Houston, TX
- 2015 Ben F. Love Fellowship in Innovative Cancer Therapies, MDACC, Houston, TX
- 2015 Recruitment of First-Time, Tenure-Track Faculty Members, Cancer Prevention and Research Institute of Texas (CPRIT)
- 2016 Institutional nominee for Searle Scholar, UT Health
- 2017 Institutional nominee for Pew Scholar, UT Health

## **EDITORIAL POSITIONS:**

- 2012-2013 Lead Guest Editor, The Scientific World Journal
- 2012-Present Editorial Board, Computational Biology Journal
- 2012-Present Associate Editorial Board, American Journal of Cancer Genetics, Genomics and Proteomics
- 2012-Present Associate Editorial Board, American Journal of Cancer Science
- 2013-Present Advisory Board, International Journal of Genetics
- 2013-Present Editorial Board, Journal of Bioinformatics and Comparative Genomics
- 2013 Lead Guest Editor, BioMed Research International
- 2014 Lead Guest Editor, International Journal of Genomics
- 2014-Present Editorial Board, Scientific Journal of Bioinformatics & Computational Biology

2015                      Guest Editor, BioMed Research International  
2015-Present            Guest Editor, Cancer Informatics  
2016-Present            Guest Editor, International Journal of Genomics  
2017-Present            Guest Editor, Genes

**SERVICE ON THE UNIVERSITY OF TEXAS HEALTH SCIENCE CENTER AT HOUSTON COMMITTEES**

2017 – Present        Faculty Senate  
2017                    Faculty review committee for McGovern Medical School Dean's Award for Excellence in Postdoctoral Research

**SPONSORSHIP OF POSTDOCTORAL FELLOWS:**

Yu Xiang, 2016/1 – present  
Jing Gong, 2016/4- present  
Youqiong Ye, 2016/8-present  
Zhang Zhao, 2016/11-present  
Jing Xu, 2016/12-2016/5

**CURRENT TEACHING RESPONSIBILITIES:**

Co-lecturer in Current Methods in Structural and Molecular Biology at UTHealth GSBS (4/2017), 9 students, for 2 year

Co-lecturer in GS21 1017 Foundations of Biomedical Research at UTHealth GSBS (9/2017) 33 students, for 2 year

**MENTORING ACTIVITIES:**

Dr. Jing Feng, visiting associate professor, 2016/8-2017/8  
Martha Czernuszenko, Pre-Baccalaureate Trainee, 2016/4-2016/7  
Chunjie Liu, visiting student, 2016/10-present

**CURRENT GRANT SUPPORT:**

Principal Investigator (Han)  
09/01/2015 – 08/31/2019  
Recruitment of First-Time, Tenure-Track Faculty Members,  
RR150085, \$2,000,000  
Cancer Prevention and Research Institute of Texas (CPRIT)

Co-Investigator (5%)  
11/01/2015 – 10/31/2018

UTHealth Pulmonary Center of Excellence Discovery Award Program  
\$300,000  
UTHealth (Internal)  
PI: Harry Karmouty-Quintana

Co-Investigator (5%)  
01/01/2017-12/31/2018  
UTHealth Pulmonary Center of Excellence Discovery Award Program  
\$300,000  
UTHealth (Internal)  
PI: Shyu

Co-Investigator (5%)  
07/01/17-06/30/22  
National Institutes of Health  
1R01 HL137990  
PI: Xia

Co-investigator (5%)  
National Institutes of Health  
1R01 HL138510  
PI: Karmouty-Quintana

Subcontract PI (5%)  
07/01/17-06/30/22  
National Institutes of Health  
PI: Lin

## **PUBLICATIONS:**

### **Refereed Original Articles in Journals**

1. Jiang C\*, Han L\*, Su B, Li WH, and Zhao Z: Features and trend of loss of promoter-associated CpG islands in the human and mouse genomes. **Molecular Biology and Evolution**, 2007. 24: 1991-2000.
2. Han L, Su B, Li WH, and Zhao Z: CpG island density and its correlations with genomic features in mammalian genomes. **Genome Biology**, 2008. 9: R79.
3. Han L, Yang R, Su B, and Zhao Z: An SVM-based algorithm for classifying promoter-associated CpG islands in the human and mouse genomes. **Lecture Notes in Artificial Intelligence**, 2008. 5227: 6.
4. Han L, and Zhao Z: Comparative analysis of CpG islands in four fish genomes. **Comparative and Functional Genomics**, 2008: 565631.
5. Han L, and Zhao Z: CpG islands or CpG clusters: how to identify functional GC-rich regions in a genome? **BMC Bioinformatics**, 2009. 10: 65.

6. Zhao Z, and Han L: CpG islands: algorithms and applications in methylation studies. **Biochemical and Biophysical Research Communications**, 2009. 382: 643-5.
7. Han L, and Zhao Z: Contrast features of CpG islands in the promoter and other regions in the dog genome. **Genomics**, 2009. 94: 117-24.
8. Sun J, Han L, and Zhao Z: Gene- and evidence-based candidate gene selection for schizophrenia and gene feature analysis. **Artificial Intelligence in Medicine**, 2010. 48: 99-106.
9. Han L, Zheng S, Sun S, Huang T, and Zhao Z: Genome-Wide DNA Methylation Profiling in 40 Breast cancer cell lines. **Lecture Notes in Computer Science**, 2010. 6215.
10. Su Z, Han L, and Zhao Z: Conservation and divergence of DNA methylation in eukaryotes. **Epigenetics**, 2011. 6: 134-140.
11. Lee AS, Xu D, Plews JR, Nguyen PK, Nag D, Lyons JK, Han L, Hu S, Lan F, Liu J, Huang M, Narsinh KH, Long CT, de Almeida PE, Levi B, Kooreman N, Bangs C, Pacharinsak C, Ikeno F, Yeung AC, Gambhir SS, Robbins RC, Longaker MT, and Wu JC: Preclinical derivation and imaging of autologously transplanted canine induced pluripotent stem cells. **Journal of Biological Chemistry**, 2011. 286: 32697-704.
12. Dey D, Inayathullah M, Lee AS, LeMieux MC, Zhang X, Wu Y, Nag D, De Almeida PE, Han L, Rajadas J, and Wu JC: Efficient gene delivery of primary human cells using peptide linked polyethylenimine polymer hybrid. **Biomaterials**, 2011. 32: 4647-58.
13. Gu M, Nguyen PK, Lee AS, Xu D, Hu S, Plews JR, Han L, Huber BC, Lee WH, Gong Y, de Almeida PE, Lyons J, Ikeno F, Pacharinsak C, Connolly AJ, Gambhir SS, Robbins RC, Longaker MT, and Wu JC: Microfluidic single-cell analysis shows that porcine induced pluripotent stem cell-derived endothelial cells improve myocardial function by paracrine activation. **Circulation Research**, 2012. 111: 882-93.
14. Du X\*, Han L\*, Guo AY, and Zhao Z: Features of methylation and gene expression in the promoter-associated CpG islands using human methylome data. **Comparative and Functional Genomics**, 2012. 2012: 598987.
15. Xia J\*, Han L\*, and Zhao Z: Investigating the relationship of DNA methylation with mutation rate and allele frequency in the human genome. **BMC Genomics**, 2012. 13 Suppl 8: S7.

16. Sun N, Yazawa M, Liu J, Han L, Sanchez-Freire V, Abilez OJ, Navarrete EG, Hu S, Wang L, Lee A, Pavlovic A, Lin S, Chen R, Hajjar RJ, Snyder MP, Dolmetsch RE, Butte MJ, Ashley EA, Longaker MT, Robbins RC, and Wu JC: Patient-specific induced pluripotent stem cells as a model for familial dilated cardiomyopathy. **Science Translational Medicine**, 2012. 4: 130ra47.
17. Liu J, Narsinh KH, Lan F, Wang L, Nguyen PK, Hu S, Lee A, Han L, Gong Y, Huang M, Nag D, Rosenberg J, Chouldechova A, Robbins RC, and Wu JC: Early stem cell engraftment predicts late cardiac functional recovery: preclinical insights from molecular imaging. **Circulation Cardiovascular Imaging**, 2012. 5: 481-90.
18. Lan F, Liu J, Narsinh KH, Hu S, Han L, Lee AS, Karow M, Nguyen PK, Nag D, Calos MP, Robbins RC, and Wu JC: Safe genetic modification of cardiac stem cells using a site-specific integration technique. **Circulation**, 2012. 126: S20-8.
19. Samuels DC\*, Han L\*, Li J, Quanghu S, Clark TA, Shyr Y, and Guo Y: Finding the lost treasures in exome sequencing data. **Trends in Genetics**, 2013. 29: 593-9.
20. Lan F, Lee AS, Liang P, Sanchez-Freire V, Nguyen PK, Wang L, Han L, Yen M, Wang Y, Sun N, Abilez OJ, Hu S, Ebert AD, Navarrete EG, Simmons CS, Wheeler M, Pruitt B, Lewis R, Yamaguchi Y, Ashley EA, Bers DM, Robbins RC, Longaker MT, and Wu JC: Abnormal calcium handling properties underlie familial hypertrophic cardiomyopathy pathology in patient-specific induced pluripotent stem cells. **Cell Stem Cell**, 2013. 12: 101-13.
21. Hu S, Wilson KD, Ghosh Z, Han L, Wang Y, Lan F, Ransohoff KJ, Burridge P, and Wu JC: MicroRNA-302 increases reprogramming efficiency via repression of NR2F2. **Stem Cells**, 2013. 31: 259-68.
22. Erdogan B, Bosompem A, Peng D, Han L, Smith E, Kennedy ME, Alford CE, Wu H, Zhao Z, Mosse CA, El-Rifai W, and Kim AS: Methylation of promoters of microRNAs and their host genes in myelodysplastic syndromes. **Leukemia & Lymphoma**, 2013. 54: 2720-7.
23. Dey D\*, Han L\*, Bauer M, Sanada F, Oikonomopoulos A, Hosoda T, Unno K, De Almeida P, Leri A, and Wu JC: Dissecting the molecular relationship among various cardiogenic progenitor cells. **Circulation Research**, 2013. 112: 1253-62.
24. Cancer Genome Atlas Research Network (Including Han L), Weinstein JN, Collisson EA, Mills GB, Shaw KR, Ozenberger BA, Ellrott K, Shmulevich I, Sander C, and Stuart JM: The Cancer Genome Atlas Pan-Cancer analysis project. **Nature Genetics**, 2013. 45: 1113-20.
25. Wang L, Miao YL, Zheng X, Lackford B, Zhou B, Han L, Yao C, Ward JM, Burkholder A, Lipchina I, Fargo DC, Hochedlinger K, Shi Y, Williams CJ, and Hu G: The THO complex regulates pluripotency gene mRNA export and controls

- embryonic stem cell self-renewal and somatic cell reprogramming. **Cell Stem Cell**, 2013. 13: 676-90.
26. Yuan Y, VanAllen EM, Omberg L, Wagle N, Amin-Mansour A, Sokolov A, Byers LA, Xu Y, Hess KR, Diao L, Han L, Huang X, Lawrence MS, Weinstein JN, Stuart JM, Mills GB, Garraway LA, Margolin AA, Getz G, and Liang, H: Assessing the clinical utility of cancer genomic and proteomic data across tumor types. **Nature Biotechnology**, 2014. 32: 644-52.
27. Yang Y, Han L, Yuan Y, Li J, Hei N, and Liang H: Gene co-expression network analysis reveals common system-level properties of prognostic genes across cancer types. **Nature Communications**, 2014. 5: 3231.
28. Wang L, Du Y, Ward JM, Shimbo T, Lackford B, Zheng X, Miao YL, Zhou B, Han L, Fargo DC, Jothi R, Williams CJ, Wade PA, and Hu G: INO80 facilitates pluripotency gene activation in embryonic stem cell self-renewal, reprogramming, and blastocyst development. **Cell Stem Cell**, 2014. 14: 575-91.
29. Luo X\*, Huang L\*, Han L\*, Luo Z, Hu F, Tieu R, and Gan L: Systematic prioritization and integrative analysis of copy number variations in schizophrenia reveal key schizophrenia susceptibility genes. **Schizophrenia Bulletin**, 2014. 40: 1285-99.
30. Hoadley KA, Yau C, Wolf DM, Cherniack AD, Tamborero D, Ng S, Leiserson MD, Niu B, McLellan MD, Uzunangelov V, Zhang J, Kandoth C, Akbani R, Shen H, Omberg L, Chu A, Margolin AA, Van't Veer LJ, Lopez-Bigas N, Laird PW, Raphael BJ, Ding L, Robertson AG, Byers LA, Mills GB, Weinstein JN, Van Waes C, Chen Z, Collisson EA, Cancer Genome Atlas Research Network (Including Han L), Benz CC, Perou CM, and Stuart JM: Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. **Cell**, 2014. 158: 929-44.
31. Han L\*, Yuan Y\*, Zheng S, Yang Y, Li J, Edgerton ME, Diao L, Xu Y, Verhaak RG, and Liang H: The Pan-Cancer analysis of pseudogene expression reveals biologically and clinically relevant tumour subtypes. **Nature Communications**, 2014. 5: 3963.
32. Costello JC, Heiser LM, Georgii E, Gonen M, Menden MP, Wang NJ, Bansal M, Ammad-ud-din M, Hintsanen P, Khan SA, Mpindi JP, Kallioniemi O, Honkela A, Aittokallio T, Wennerberg K, NCI DREAM Community (Including Han L), Collins JJ, Gallahan D, Singer D, Saez-Rodriguez J, Kaski S, Gray JW, and Stolovitzky G: A community effort to assess and improve drug sensitivity prediction algorithms. **Nature Biotechnology**, 2014. 32: 1202-12.
33. Han L\*, Diao L\*, Yu S\*, Xu X\*, Li J, Zhang R, Yang Y, Werner HM, Eterovic KA, Yuan Y, Li J, Nair N, Minelli R, Tsang Y, Cheung LW, Jeong KJ, Roszik J, Ju Z, Woodman S, Lu Y, Scott KL, Li JB, Mills GB, Liang H: The genomic landscape and clinical relevance of A-to-I RNA editing in human cancers. **Cancer Cell**, 2015, 28: 515-528.

34. Li J\*, Han L\*, Roebuck P, Diao L, Liu L, Yuan Y, Weinstein J, Liang H: TANRIC: An Interactive Open Platform to Explore the Function of LncRNAs in Cancer. **Cancer Research**, 2015, 75: 3728-3733.
35. Vickers KC, Roteta LA, Hucheson-Dilks H, Han L, and Guo Y: Mining diverse small RNA species in the deep transcriptome. **Trends Biochemical Sciences**, 2015. 40: 4-7.
36. Lee WH, Nguyen P, Hu S, Liang G, Ong SG, Han L, Sanchez-Freire V, Lee AS, Vasanaawala M, Segall G, and Wu JC: Variable activation of the DNA damage response pathways in patients undergoing single-photon emission computed tomography myocardial perfusion imaging. **Circulation Cardiovascular Imaging**, 2015. 8: e002851.
37. Han L\*, Vickers KC\*, Samuels DC, and Guo Y: Alternative applications for distinct RNA sequencing strategies. **Briefings in Bioinformatics**, 2015. 16: 629-639.
38. Zhou B, Wang L, Zhang S, Bennett BD, He F, Zhang Y, Xiong C, Han L, Diao L, Li P, Fargo DC, Cox AD, Hu G: INO80 governs superenhancer-mediated oncogenic transcription and tumor growth in melanoma. **Genes & Development**. 2016, 30:1440-53
39. Liu X, Xiao ZD, Han L, Zhang J, Lee SW, Wang W, Lee H, Zhuang L, Chen J, Lin HK, Wang J, Liang H, Gan B: LncRNA NBR2 engages a metabolic checkpoint by regulating AMPK under energy stress. **Nature Cell Biology**, 2016, 18: 431-442
40. Redis RS, Vela LE, Lu W, Ferreira de Oliveira J, Ivan C, Rodriguez-Aguayo C, Adamoski D, Pasculli B, Taguchi A, Chen Y, Fernandez AF, Valledor L, Van Roosbroeck K, Chang S, Shah M, Kinnebrew G, Han L, Atlasi Y, Cheung LH, Huang GY, Monroig P, Ramirez MS, Catela Ivkovic T, Van L, Ling H, Gafà R, Kapitanovic S, Lanza G, Bankson JA, Huang P, Lai SY, Bast RC, Rosenblum MG, Radovich M, Ivan M, Bartholomeusz G, Liang H, Fraga MF, Widger WR, Hanash S, Berindan-Neagoe I, Lopez-Berestein G, Ambrosio AL, Gomes Dias SM, Calin GA: Allele-Specific Reprogramming of Cancer Metabolism by the Long Non-coding RNA CCAT2. **Molecular Cell**, 2016, 18: 520-534.
41. Lin A, Li C, Xing Z, Ma G, Hu Q, Liang K, Han L, Wang C, Hawke DH, Wang S, Zhang Y, Wei Y, Park P, Zhou J, Zhou Y, Marks J, Hu Z, Hung MC, Liang H, Zou Y, Lin C, Yang L: The LINK-A lncRNA Activates Normoxic HIF1 $\alpha$  Signaling in Triple-negative Breast Cancer. **Nature Cell Biology**, 2016, 18: 213-224.
42. Jiang HJ, Lee HS, Burt BM, Lee GK, Yoon KA, Park YY, Sohn BH, Kim SB, Kim MS, Lee JM, Joo J, Kim SC, Yoo JS, Na KJ, Choi YL, Oark JL, Kim SY, Lee YS, Han L, Liang H, Mak D, Burks JK, Zo J, Sugarbaker DJ, Shim YM, Lee JS: Integrated Genomic Analysis of Recurrence-Associated Small Non-coding RNAs in

Oesophageal Cancer. **Gut**. 2016 (In press)

43. Marini A, Lena AM, Panatta E, Ivan C, Han L, Liang H, Annicchiarico-Petruzzelli M, Di Daniele N, Calin GA, Candi E, Melino G: Ultraconserved long non-coding RNA uc.63 in breast cancer. **Oncotarget**. 2016 (In press)
44. Xia S, Feng J, Lei L, Hu J, Xia L, Wang J, Xiang Y, Liu L, Zhong S, Han L<sup>#</sup>, He C<sup>#</sup>: Comprehensive characterization of tissue-specific circular RNAs in the human and mouse genomes. **Briefings in Bioinformatics**. 2016, bbw081.
45. Gong J, Liu C, Liu W, Xiang Y, Diao L, Guo AY<sup>#</sup>, Han L<sup>#</sup>: LNCediting: a database for functional effects of RNA editing in lncRNAs. **Nucleic Acid Research**, 2017: D79-D84
46. Wang Y, Xu X, Yu S, Kang KJ, Zhou Z, Han L, Tsang YH, Li J, Chen H, Mangala LS, Yuan Y, Eterovic AK, Lu Y, Sood AK, Scott KL, Mills GB, Liang H: Systematic characterization of A-to-I RNA editing hotspots in microRNAs across human cancers. **Genome Research**, 2017
47. The Cancer Genome Atlas Research Network (Including Han L): Integrated genomic and molecular characterization of cervical cancer. **Nature**, 2017, 10.1038/nature21386
48. Lei L, Xia S, Liu D, Li X, Feng J, Zhu Y, Hu J, Xia L, Guo L, Chen F, Cheng H, Chen K, Hu H, Chen X, Li F, Zhong S, Mittal N, Yang G, Qian Z, Han L<sup>#</sup>, He C<sup>#</sup>: Genome-wide characterization of lncRNAs in acute myeloid leukemia. **Briefings in Bioinformatics**, 2017, bbx007
49. Lin A, Hu Q, Li C, Xing Z, Ma G, Wang C, Li J, Yao J, Liang K, Wang S, Park P, Marks J, Zhou Y, Zhou J, Hung MC, Liang H, Hu Z, Shen H, Hawke DH, Han L, Zhou Y, Lin C, Yang L: PtdIns (3,4,5)P3-lncRNA interaction exaggerates AKT activation and confers resistance to AKT inhibitors. **Nature Cell Biology**, 2017, 19: 238-251
50. Li C, Wang S, Xing Z, Lin A, Liang K, Song J, Hu Q, Yao J, Chen Z, Park P, Hawke DH, Zhou J, Zhou Y, Zhang S, Liang H, Hung MC, Gallick G, Han L, Lin C, and Yang L: A ROR1-HER3-lncRNA signaling axis modulates the Hippo-YAP pathway to regulate bone metastasis. **Nature Cell Biology**, 2017, 19: 106-119
51. Song A, Zhang Y, Han L, Yegutkin G, Liu H, Sun K, D'Alessandro A, Li J, Karmouty-Quintana H, Iriyama T, Weng T, Zhao S, Wang W, Wu H, Nemkov T, Subudhi A, Jameson-Van Houten S, Julian CG, Lovering AT, Hansen KC, Zhang H, Bogdanov M, Dowhan W, Jin J, Kellems RE, Eltzhig HK, Blackburn M, Roach RC, Xia Y: Erythrocytes retain hypoxic adenosine response for faster acclimatization upon re-ascension. **Nature Communications**, 2017, 8: 14108
52. Xiao Z, Han L, Lee H, Zhuang L, Zhang Y, Baddour J, Nagrath D, Wood C, Gu J, Wu

X, Liang H, Gan B: Energy stress-induced lncRNA FILNC1 represses c-Myc-mediated energy metabolism and inhibits renal tumor development. **Nature Communications**, In press

53. Feng J\*, Xiang Y\*, Xia S\*, Liu H, Wang J, Ozguc FM, Lei L, Kong R, Diao L, He C, Han L<sup>#</sup>: CircView: A Visualization and Exploration Tool for Circular RNAs. **Briefings in Bioinformatics**, 2017, bbx070
54. Chen C-Y, Zhang Y, Xiang Y, Han L, Shyu A-B: Antagonistic actions of two human Pan3 isoforms on global mRNA turnover. **RNA**, In press
55. Xiang Y, Ye Y, Lou Y, Yang Y, Cai C, Zhang Z, Mills T, Chen NY, Kim Y, Ozguc FM, Diao L, Karmouty-Quintana H, Xia Y, Blackburn M, Kellems R, Chen Z, Yoo SH, Shyu AB, Mills G, Han L<sup>#</sup>: Comprehensive characterization of alternative polyadenylation in human cancer. **Journal of the National Cancer Institute** (Accept).
56. Gong J, Mei S, Liu C, Xiang Y, Ye Y, Zhang Z, Feng J, Liu R, Diao L, Guo AY, Miao X, Han L<sup>#</sup>: PancanQTL: systematic identification of cis-eQTLs and trans-eQTLs in 33 cancer types. **Nucleic Acids Research**, 2017, gkx861
57. Xia S, Feng J, Chen K, Ma Y, Gong J, Cai F, Jin Y, Gao Y, Xia L, Chang H, Wei L, Han L<sup>#</sup>, He C<sup>#</sup>: CSCD: A database for cancer-specific circular RNAs. **Nucleic Acids Research**, 2017, gkx863

### Invited Articles (Reviews, Editorials, etc.) in Journals

1. Han, L<sup>#</sup>, Guo, Y, Su, Z, Zheng, S, and Lu, Z, Advances in Computational Genomics. **BioMed Research International**, 2015: 187803. (Editorial)
2. Han L, Liang H: RNA Editing in Cancer: Mechanistic, Prognostic and Therapeutic Implications. **Molecular & Cellular Oncology**, 2016 (Invited author's view)
3. Guo Y, Han L, Sheng Q: Recent Advances in high throughput sequencing analysis. **International Journal of Genomics**, 2017 (Editorial)

### Chapters

1. Zhao Z, Han L: CpG Islands in the Human Genome: Identification, Features, Mutations and Diseases. In: Matsumoto A and Nakano M Eds. **Human Genome: Features, Variation and Genetic Disorders**, 2009. 1-27. Nova Science Publishers, Inc, New York (ISBN 978-1-60741-695-1).
2. Guo Y, Zhao S, Bjoring M, Han L: Data Mining of High Throughput Sequencing. In:

## **Presentations**

1. 8/2017, **Invited Talks**, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China  
Institute of Life Science, Chinese Academy of Sciences, Beijing, China  
School of Life Sciences, Fudan University, Shanghai, China  
School of Life Sciences and Technology, Tongji University, Shanghai, China
2. 2/2017, **Invited Talk**, Center for Precision Health, School of Biomedical Informatics, The University of Texas Health Science Center at Houston, Houston, TX, USA
3. 2/2017, **Invited Talk**, Distinguished Scientist Seminar Series in Department of Molecular Oncology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA
4. 1/2017, **Invited Talk**, Department of Molecular and Cellular Biology, Baylor College of Medicine, Houston, TX, USA
5. 1/2017, **Invited Talk**, SCBA-Texas Faculty Club, Houston, TX, USA
6. 9/2016, **Invited Talk**, Distinguished Lecture Series in Experimental Therapeutics, The University of Texas MD Anderson Cancer Center, Houston, TX, USA