Gary Hon, Ph.D.

Assistant Professor
University of Texas Southwestern Medical Center
Address: 5323 Harry Hines Boulevard / Dallas, TX 75390
E-mail: Gary.Hon@utsouthwestern.edu

EDUCATION

BA (Computer Science)   University of California, Berkeley, 2003
BA (Molecular and Cell Biology)   University of California, Berkeley, 2003
Ph.D. (Bioinformatics)   University of California, San Diego, 2009

RESEARCH EXPERIENCE

2015-current <u>Assistant professor</u>. Cecil H. and Ida Green Center for Reproductive Biology Sciences, University of Texas Southwestern Medical Center, Dallas, Texas.

2009-2014 <u>Postdoctoral researcher</u>. Laboratory of Gene Regulation, Ludwig Institute for Cancer Research, San Diego, California. Supervision by Bing Ren.

2006-2009 <u>Graduate student</u>. Laboratory of Gene Regulation, Ludwig Institute for Cancer Research, San Diego, California. Supervision by Bing Ren.
Thesis: Understanding the global architecture of gene regulation in human cells through analysis of chromatin signatures

2001-2003 <u>Undergraduate researcher</u>. Computational Genomics Research Group. University of California, Berkeley. Supervision by Steven Brenner.

1999-2006 <u>Summer intern</u>. Informatics. Lawrence Livermore National Laboratory, Livermore, California. Supervision by David Clague and Thomas Slezak.

AWARDS

2019   Addgene Blue Flame Award
2017   NIH New Innovator Award
2015   CPRIT Scholar Award
2013   AACR-Aflac, Incorporated Scholar-in-Training Award
2011   Sanofi-Aventis Outstanding Research Article Award at Cell Research
2011   William Guy Forbeck Scholar Award
2009   ISMB/EECB 2009 Travel Fellowship
2007   ISMB/EECB 2007 Travel Fellowship
2006-2007   Ruth L. Kirschstein National Research Service Award
1999   Co-Winner, Tri-Valley Science and Engineering Fair

TEACHING EXPERIENCE

2018-2020   Lecturer and organizer: Gene Expression Nanocourse (UTSW, Summer)
2017-2021   Lecturer: Advanced Genetics (UTSW, Spring)
2017-2021   Lecturer: Gene Expression (UTSW, Fall)
2017   Lecturer and organizer: Bioinformatics Survival Skills (UTSW, Spring)
2015   Lecturer and organizer: Introduction to Omics (UTSW, Fall)
2010   Seminar series on basic bioinformatics for bench scientists
2008   Teaching assistant – Applied Genomic Technologies
2007   Teaching assistant – Computational Molecular Biology

PUBLICATIONS

(See Google Scholar: https://scholar.google.com/citations?user=Ti5vXmUAAAAJ&hl=en)

1. Yu L†, Wei Y†, Duan J†, Schmitz DA, Sakurai M, Wang L, Wang K, Zhao S, **Hon GC***, Wu J*. Blastocyst-like structures generated from human pluripotent stem cells. Nature. 2021.

2. Duan J, **Hon GC**. FBA: feature barcoding analysis for single cell RNA-Seq. Bioinformatics. 2021. PMID: 33999185.

3. England AR, Chaney CP, Das A, Patel M, Malewska A, Armendariz D, **Hon GC**, Strand DW, Drake KA, Carroll TJ. Identification and characterization of cellular heterogeneity within the developing renal interstitium. Development. 2020. PMID: 32586976.

4. Xie S, Armendariz D, Zhou P, Duan J, **Hon GC**. Global Analysis of Enhancer Targets Reveals Convergent Enhancer-Driven Regulatory Modules. Cell Rep. 2019. PMID: 31775028

5. Zhang Z, Luo D, Zhong X, Choi JH, Ma Y, Wang S, Mahrt E, Guo W, Stawiski EW, Modrusan Z, Seshagiri S, Kapur P, **Hon GC**, Brugarolas J, and Wang T. SCINA: A Semi-Supervised Subtyping Algorithm of Single Cells and Bulk Samples. Genes. 2019. PMID: 31336988.

6. Duan J, Li B, Bhakta M, Xie S, Zhou P, Munshi NV, **Hon GC**. Rational reprogramming of cellular states by combinatorial perturbation. Cell Rep. 2019. PMID: 31216470.

7. Bhattacharyya S, Duan J, Wang L, Li B, Bhakta M, Fernandez-Perez A, **Hon GC**, Munshi NV. Using Gjd3-CreEGFP mice to examine atrioventricular node morphology and composition. Sci Rep. 2019. PMID: 30765799.

8. Xie S, **Hon GC**. Experimental and Computational Approaches for Single-Cell Enhancer Perturbation Assays.Methods Mol Biol. 2019. PMID: 30758829.

9. Henry GH, Malewska A, Joseph DB, Malladi VS, Lee J, Torrealba J, Mauck RJ, Gahan JC, Raj GV, Roehrborn CG, **Hon GC**, MacConmara MP, Reese JC, Hutchinson RC, Vezina CM, Strand DW. A Cellular Anatomy of the Normal Adult Human Prostate and Prostatic Urethra. Cell Rep. 2018. PMID: 30566875.

10. Hepler C, Shan B, Zhang Q, Henry GH, Shao M, Vishvanath L, Ghaben AL, Mobley AB, Strand D, **Hon GC**, Gupta RK. Identification of functionally distinct fibro-inflammatory and adipogenic stromal subpopulations in visceral adipose tissue of adult mice. Elife. 2018. PMID: 30265241.

11. Xie S, Cooley A, Armendariz D, Zhou P, **Hon GC**. Frequent sgRNA-barcode recombination in single-cell perturbation assays. PLoS One 2018. PMID: 29874289.

12. Yu M, Han D, **Hon GC**, He C. Tet-Assisted Bisulfite Sequencing (TAB-seq). Methods Mol Biol. 2018. PMID: 29224168.

13. Qi Z, Xie S, Chen R, Aisa HA, **Hon GC**, Guan Y. Tissue-specific Gene Expression Prediction Associates Vitiligo with SUOX through an Active Enhancer. https://www.biorxiv.org/content/10.1101/337196v2 .

14. Liu X, Zhang Y, Chen Y, Li M, Zhou F, Li K, Cao H, Ni M, Liu Y, Gu Z, Dickerson KE, Xie S, **Hon GC**, Xuan Z, Zhang MQ, Shao Z, Xu J. In Situ Capture of Chromatin Interactions by Biotinylated dCas9. Cell. 2017. PMID: 28841410.

15. Partin AC, Ngo TD, Herrell E, Jeong BC, **Hon G**, Nam Y. Heme enables proper positioning of Drosha and DGCR8 on primary microRNAs. Nat Commun 2017. PMID: 29170488

16. Xie S, Duan J, Li B, Zhou P, **Hon GC**. Multiplexed Engineering and Analysis of Combinatorial Enhancer Activity in Single Cells. Mol Cell 2017. PMID: 28416141.

17. Villa GR, Hulce JJ, Zanca C, Bi J, Ikegami S, Cahill GL, Gu Y, Lum KM, Masui K, Yang H, Rong X, Hong C, Turner KM, Liu F, **Hon GC**, Jenkins D, Martini M, Armando AM, Quehenberger O, Cloughesy TF, Furnari FB, Cavenee WK, Tontonoz P, Gahman TC, Shiau AK, Cravatt BF, Mischel PS. An LXR-Cholesterol Axis Creates a Metabolic Co-Dependency for Brain Cancers. Cancer Cell. 2016. PMID: 27746144.

18. Liu F, **Hon GC***, Villa GR, Turner KM, Ikegami S, Yang H, Ye Z, Li B, Kuan S, Lee AY, Zanca C, Wei B, Lucey G, Jenkins D, Zhang W, Barr CL, Furnari FB, Cloughesy TF, Yong WH, Gahman TC, Shiau AK, Cavenee WK, Ren B, Mischel PS. EGFR Mutation Promotes Glioblastoma through Epigenome and Transcription Factor Network Remodeling. Mol Cell 2015. PMID: 26455392.

19. **Hon GC**, Song CX, Du T, Jin F, Selvaraj S, Lee AY, Yen CA, Ye Z, Mao SQ, Wang BA, Kuan S, Edsall LE, Zhao BS, Xu GL, He C, Ren B. 5mC Oxidation by Tet2 Modulates Enhancer Activity and Timing of Transcriptome Reprogramming during Differentiation. Mol Cell 2014. PMID: 25263596.

20. Wang X, Lu Z, Gomez A, **Hon GC**, Yue Y, Han D, Fu Y, Parisien M, Dai Q, Jia G, Ren B, Pan T, He C. N6-methyladenosine-dependent regulation of messenger RNA stability. Nature 2014. PMID: 24284625

21. **Hon GC**, Rajagopal N, Shen Y, McCleary D, Yue F, Dang MD, Ren B. Epigenetic memory at embryonic enhancers identified in DNA methylation maps from adult mouse tissues. Nature Genetics 2013. PMID: 23995138.

22. Chang KN, Zhong S, Weirauch MT, **Hon G**, Pelizzola M, Li H, Huang SS, Schmitz RJ, Urich MA, Kuo D, Nery JR, Qiao H, Yang A, Jamali A, Chen H, Ideker T, Ren B, Bar-Joseph Z, Hughes TR, Ecker JR. Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. Elife 2013 Jun 11. PMID: 23795294.

23. Zhang L*, Szulwach KE*, **Hon GC***, Song CX, Park B, Yu M, Lu X, Dai Q, Wang X, Street CR, Tan H, Min JH, Ren B, Jin P, He C. Tet-mediated covalent labelling of 5-methylcytosine for its genome-wide detection and sequencing. Nat Commun. 2013. PMID: 23443545.

24. Yu M, **Hon GC**, Szulwach KE, Song CX, Jin P, Ren B, He C. Tet-assisted bisulfite sequencing of 5-hydroxymethylcytosine. Nature Protocols 2012 Nov 29. PMID: 23196972.

25. Smallwood A, **Hon GC**, Jin F, Henry RE, Espinosa JM, Ren B. CBX3 regulates efficient RNA processing genome-wide. Genome Research 2012 Aug 22. PMID: 22684280.

26. Yu M*, **Hon GC***, Szulwach KE*, Song CX, Zhang L, Kim A, Li X, Dai Q, Shen Y, Park B, Min JH, Jin P, Ren B, He C. Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. Cell 2012 May 17. PMID: 22608086.

27. **Hon GC**, Hawkins RD, Caballero OL, Lo C, Lister R, Pelizzola M, Valsesia A, Ye Z, Kuan S, Edsall LE, Camargo AA, Stevenson BJ, Ecker JR, Bafna V, Strausberg RL, Simpson AJ, Ren B. Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. Genome Research 2011 Dec 7. PMID: 22156296.

28. Hawkins RD*, **Hon GC***, Yang C, Antosiewicz-Bourget JE, Lee LK, Ngo QM, Klugman S, Ching KA, Edsall LE, Ye Z, Kuan S, Yu P, Liu H, Zhang X, Green RD, Lobanenkov VV, Stewart R, Thomson JA, Ren B. Dynamic chromatin states in human ES cells reveal potential regulatory sequences and genes involved in pluripotency. Cell Res. 2011 Oct 21.

29. Lister R, Pelizzola M, Kida YS, Hawkins RD, Nery JR, **Hon GC**, Antosiewicz-Bourget J, O'Malley R, Castanon R, Klugman S, Downes M, Yu R, Stewart R, Ren B, Thomson JA, Evans RM, Ecker JR. Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. Nature 2011 Feb 2. PMID: 21289626.

30. Hawkins RD*, **Hon GC***, Ren B. Next-generation genomics: an integrative approach. Nat Rev Genet. 2010 Jun 8. PMID: 20531367.

31. Hawkins RD*, **Hon GC***, Lee LK, Ngo Q, Lister R, Pelizzola M, Edsall LE, Kuan S, Luu Y, Klugman S, Antosiewicz-Bourget J, Ye Z, Espinoza C, Agarwahl S, Shen L, Ruotti V, Wang W, Stewart R, Thomson JA, Ecker JR, Ren B. Distinct epigenomic landscapes of pluripotent and lineage-committed human cells. Cell Stem Cell. 2010 May 7;6(5):479-91.PMID: 20452322.

32. **Hon GC**, Hawkins RD, Ren B. Predictive chromatin signatures in the mammalian genome. Hum Mol Genet. 2009 Oct 15;18(R2):R195-201. Review.

33. **Hon G**, Wang W, Ren B. Discovery and annotation of functional chromatin signatures in the human genome. PLoS Comput Biol. 2009 Nov;5(11):e1000566. Epub 2009 Nov 13.

34. Lister R, Pelizzola M, Dowen RH, Hawkins RD, **Hon G**, Tonti-Filippini J, Nery JR, Lee L, Ye Z, Ngo QM, Edsall L, Antosiewicz-Bourget J, Stewart R, Ruotti V, Millar AH, Thomson JA, Ren B, Ecker JR. Human DNA methylomes at base resolution show widespread epigenomic differences. Nature. 2009 Nov 19;462(7271):315-22. Epub 2009 Oct 14.

35. Heintzman ND*, **Hon GC***, Hawkins RD*, Kheradpour P, Stark A, Harp LF, Ye Z, Lee LK, Stuart RK, Ching CW, Ching KA, Antosiewicz-Bourget JE, Liu H, Zhang X, Green RD, Lobanenkov VV, Stewart R, Thomson JA, Crawford GE, Kellis M, Ren B. Histone modifications at human enhancers reflect global cell-type-specific gene expression. Nature, 2009.

36. **Hon GC**, Ren B, Wang W. ChromaSig: A Probabilistic Approach to Finding Common Chromatin Signatures in the Human Genome. PLoS Comput Biol 4(10): e1000201.

37. The ENCODE Project Consortium. Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature. 2007 Jun 14;447(7146):799-816.

38. Heintzman ND, Stuart RK, **Hon GC**, Fu Y, Ching CW, Hawkins RD, Barrera LO, Van Calcar S, Qu C, Ching KA, Wang W, Weng Z, Green RD, Crawford GE, Ren B.. Distinct and predictive chromatin signatures of transcriptional promoters and enhancers in the human genome. <u>Nature Genetics</u> 2007 Mar; 39(3):311-8.

39. Reguly T, Breitkreutz A, Boucher L, Breitkreutz BJ, **Hon GC**, Myers CL, Parsons A, Friesen H, Oughtred R, Tong A, Stark C, Ho Y, Botstein D, Andrews B, Boone C, Troyanskya OG, Ideker T, Dolinski K, Batada NN, Tyers M. Comprehensive curation and analysis of global interaction networks in Saccharomyces cerevisiae. <u>J Biol</u>. 2006 Jun; 5(4):11.

40. Crooks GE, **Hon G**, Chandonia JM, Brenner SE. WebLogo: a sequence logo generator. <u>Genome Res</u>. 2004 Jun;14(6):1188-90.

41. Chandonia JM, **Hon G**, Walker NS, Lo Conte L, Koehl P, Levitt M, Brenner SE. The ASTRAL Compendium in 2004. <u>Nucleic Acids Res</u>. 2004 Jan; 1;32(Database issue):D189-92.

PRESENTATIONS

1. UCSF, 2021 (invited).
2. Genentech, 2020. (invited)
3. Hong Kong University of Science and Technology, 2019. (invited)
4. Duke University, 2019. (invited)
5. Memorial Sloan Kettering Cancer Center, 2019. (invited)
6. University of Kentucky, 2019. (invited)
7. University of South Carolina, 2019. (invited)
8. University at Albany - SUNY, 2019. (invited)
9. Albany Medical College, 2019. (invited)
10. NorthShore University HealthSystem (Chicago, IL), 2019. (invited)
11. Keystone Symposium for Single-Cell Biology 2019, Breckenridge, CO. (platform presentation)
12. Society for Basic Urologic Research 2018, Palm Springs, CA. (invited)
13. University of Massachusetts Medical School, 2018. (invited)
14. Single Cell Genomics 2017, Weizmann Institute for Science, Rehovot, Israel. (invited)
15. William Guy Forbeck Scholar Retreat 2014, Lake Geneva, WI. (invited)
16. Experimental Biology 2014, San Diego, CA. (invited)
17. Systems Biology: Global Regulation of Gene Expression 2014, CSHL. (platform presentation)
18. William Guy Forbeck Scholar Retreat 2013, Lake Geneva, WI. (invited)
19. TCGC: The Clinical Genome Conference 2013, San Francisco, CA. (invited)
20. AACR 2013, Washington, DC. (platform presentation)
21. Keystone: Epigenetic Marks and Cancer Drugs 2013, Santa Fe, NM. (platform presentation)
22. William Guy Forbeck Scholar Retreat 2012, Lake Geneva, WI. (platform presentation)
23. HitSeq / ISMB 2012, Long Beach, CA. (platform presentation)
24. La Jolla Institute of Immunology Seminar Series 2011, La Jolla, CA. (platform presentation)
25. William Guy Forbeck Research Forum 2011, Hilton Head Island, SC. (platform presentation)
26. Mechanisms and Models of Cancer 2011, Salk Institute, San Diego, CA. (platform presentation)
27. Illumina User Group Meeting 2011, San Diego, CA. (platform presentation)
28. X-Gen Congress and Expo 2011, San Diego, CA. (platform presentation)
29. Ludwig Institute Melanoma Initiative Meeting 2010, Lausanne, Switzerland. (invited)
30. Fifth Barbados Workshop on Gene Regulation: The Role of Chromatin 3D structure. 2010. (invited)
31. ISMB 2009, Stockholm, Sweden. (platform presentation)
32. Bioinformatics Program EXPO 2009, UC San Diego. (invited)
33. Cracking the Code with the Bear Research Symposium 2008. (invited)
34. Genome Informatics 2008, Wellcome Trust. (invited)
35. Systems Biology: Global Regulation of Gene Expression 2008, CSHL. (platform presentation)
36. ISMB/EECB 2007, PLoS Track. (selected)