

# Adam W. Hansen

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## Education

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<b>Baylor College of Medicine – PhD, Molecular &amp; Human Genetics</b>	July 2020
Bioinformatics, Genomics and Systems Biology track; GPA 3.80	Houston, TX
<ul style="list-style-type: none"><li>Human Genome Sequencing Center</li><li>Advisor: Richard A. Gibbs, AC PhD</li></ul>	
<b>Brigham Young University (BYU) – BS, Bioinformatics</b>	June 2016
Minors in Computer Science, Chinese, and Global Business & Literacy; GPA 3.68	Provo, UT
<b>Nanjing University – Semester Abroad</b>	Dec 2013
Advanced Chinese Language and Literature; GPA 4.0	Nanjing, China

## Research Interests

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Identifying novel genetic causes of human disease through next-generation sequencing (NGS), data integration, Mendelian and population genetics, and high-performance computing. Leveraging technology to accelerate the pace of discovery.

## Research Experience

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<b>Baylor College of Medicine</b>	May 2017 – Present
Human Genome Sequencing Center	Houston, TX
Advisor: Richard A. Gibbs, AC PhD	
<ul style="list-style-type: none"><li>Discovered 154 candidate Mendelian disease genes via a genocentric, query-optimization strategy for exome sequencing data 18,000+ individuals</li><li>Expanded known phenotypic spectrum of <i>POLR2A</i>, <i>KIF1A</i>, and <i>DDX3X</i>-related disorders</li><li>Trained two postdoctoral associates and five graduate students on Hadoop</li><li>Led informatic strategy for 5-year consortium U01 grant application</li><li>Represented BCM Centers of Mendelian Genomics consortium group at annual meeting</li></ul>	
<b>Baylor College of Medicine</b>	Aug 2016 – May 2017
Other Research Rotations	Houston, TX
<ul style="list-style-type: none"><li><b>Huda Zoghbi Lab:</b> identified candidate suppressor alleles of Rett Syndrome; integrated patient WES with data from RNAi and CRISPR cell-based screen for modifiers of MECP2</li><li><b>Sharon Plon Lab:</b> investigated the role of germline mutation in PTPN12 in breast and colorectal cancers; identified novel candidate germline risk alleles for pediatric cancers</li><li><b>Rui Chen Lab:</b> identified novel candidate coloboma disease genes; optimized pipeline for variant calling and annotation of NGS data; trained lab on git version control</li></ul>	

## Research Experience (Continued)

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**Brigham Young University** Dec 2014 – Apr 2016  
Stephen R. Piccolo Computational Biology Research Lab Provo, UT

- Achieved proficiency in data science technologies in order to profile machine learning algorithms based on performance when input data exhibits extreme class imbalance
- Developed novel applications of machine learning to investigate how genetic variants impact mRNA expression levels

**Brigham Young University** Jan 2015 – Apr 2015  
Genetics of Human Disease Course Provo, UT  
Advisor: John “Keoni” Kauwe, PhD

- Designed and performed a genome-wide association study (GWAS) to look for genetic variants associated with CSF prolactin levels

**Brigham Young University** Sept 2009 – Apr 2010  
Phage Hunters Integrating Research and Education (PHIRE) Provo, UT  
Advisors: Sandra Burnett, PhD, Don Breakwell, PhD (assistant Dean, College of Life Sciences)

- Isolated novel bacteriophage PhrostyMug, sequenced and annotated genome
- Characterized variant distance between Shine-Dalgarno sequences and start codons across distinct Mycobacterium smegmatus bacteriophage
- Assessed efficacy of alternate DNA isolation protocols for M. smegmatis bacteriophage research – purification columns vs. phenol-chloroform extraction

## Industry Experience

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**Enventure** Feb 2019 – Mar 2020  
ENRICH Program Director – Biomedical Innovation Consulting Houston, TX

- Direct student-run consulting program contracted to provide services related to market research, IP & technology, business development and strategy, and grant support for 15 clients ranging in size from pre-seed to fortune 500
- Define and execute program strategy, business development, human resources, marketing, and operations
- Manage 30 student consultants assigned to client-facing projects and 20 volunteers assisting with internal efforts

**Tute Genomics** Nov 2014 – Apr 2015  
Bioinformatics and Project Management Intern Provo, UT

- Led team of five interns in designing and developing pharmacogenomics annotation and report-generation platform; led curation of pharmacogenomics literature

## **Publications: Journal Articles**

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Pathogenic *AHDC1* Missense Mutations Leading to Xia-Gibbs. Jiang Y, Hu J, Khayat MM, Li H, Chander V, **Hansen AW**, Li S, Herman GE, Cross L, Friedman J, Bijlsma E, Sansbury F, Hurst J, Omark J, Meng Q, Traynelis J, Rosenfeld JA, McWalter K, Wangler MF, Lupski JR, Murdock D, Gibbs RA. *In preparation*.

Phenotypic Expansion in *KIF1A*-related Disorders: A Novel In-frame Deletion in a Peruvian Family and Review of Published Cases. Montenegro-Garreud X\*, **Hansen AW\***, Khayat MM, Chander V, Grochowski CM, Jiang Y, Li H, Mitani T, Kessler K, Jayaseelan J, Shen H, Gezdirici A, Pehlivan DP, Meng Q, Rosenfeld JA, Jhangiani SN, Madan-Khetarpal S, Scott DA, Abarca-Barriga H, Trubnykova M, Gingras M, Muzny DM, Posey JE, Liu P, Lupski JR, Gibbs RA. (2020). *Human Mutation*.

Germline Mutation in *POLR2A*—A Heterogeneous, Multi-systemic Developmental Disorder Characterized by Transcriptional Dysregulation. **Hansen AW**, Arora P, Khayat MM, Smith LJ, Lewis AM, Rossetti LZ, Jayaseelan J, Cristian I, Haynes D, DiTroia S, Meeks M, Delgado M, Rosenfeld JA, Pais L, White SM, Meng Q, Pehlivan D, Liu P, Gingras M, Wangler MF, Muzny DM, Lupski JR, Kaplan CD, Gibbs RA. (2020). *Human Genetics and Genomics Advances*.

*RCL1* copy number variants are associated with a range of neuropsychiatric phenotypes. Brownstein CA, Smith R, Rodan LH, Gorman MP, Hojlo M, Garvey E, Li J, Cabral K, Bowen J, Rao A, Genetti CA, Carroll D, Deaso E, Agrawal PB, Rosenfeld JA, Bi W, Howe J, Stavropoulos DJ, **Hansen AW**, Hamoda HM, Pinard F, Caracansi A, Walsh CA, D'Angelo E, Beggs AH, Zarrei M, Gibbs RA, Scherer SW, Glahn DC, Gonzalez-Heydrich J. *Submitted*.

A Genocentric Approach to Discovery of Mendelian Disease Genes. **Hansen AW**, Murugan M, Li H, Khayat MM, Wang L, Rosenfeld J, Andrews K, Jhangiani S, Sedlazeck F, Muzny M, Sabo A, Posey JE, Wangler MF, Eng C, Lupski JR, Gibbs RA. (2019). *American Journal of Human Genetics*.

Phenotypic expansion in *DDX3X* – a common cause of intellectual disability in females. Wang X, Posey JE, Rosenfeld JA, Bacino CA, Scaglia F, Imken L, Harris JM, Hickey SE, Mosher TM, Slavotinek A, Zhang J, Beuten J, Leduc MS, He W, Vetrini F, Walkiewicz MA, Bi W, Xiao R, Liu P, Shao Y, Gezdirici A, Gulec EY, Jiang Y, Darilek SA, **Hansen AW**, Khayat MM, Pehlivan D, Piard J, Muzny DM, Hanchard, Belmont JW, Van Maldergem L, Gibbs RA, Eldomery MK, Akdemir ZC, Adesina AM, Chen S, Lee Y, Undiagnosed Diseases Network, Lee B, Lupski JR, Eng CM, Xia F, Yang Y, Graham BH, Moretti P. (2018). *Annals of Clinical and Translational Neurology*.

## **Publications: Journal Articles (Continued)**

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Genome Sequences of Thirteen Mycobacterium smegmatis Bacteriophages. Sargent CJ, Sharma R, Maxfield EA, Bajgain P, Earley BJ, Engle JM, **Hansen AW**, Jackson KR, Kiser CD, Marlow S, Smith KC, Vance KS, Fisher JN, Gardner AV, Lunt BL, Brown MP, Merrill BD, Payne DE, Sheflo MA, Ward A, Woodward TJ, Hope S, Breakwell DP, Grose JH. *Submitted*.

Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. Pope WH, Bowman CA, Russell DA, Jacobs-Sera D, Asai DJ, Cresawn SG, Jacobs WR, Hendrix RW, Lawrence JG, Hatfull GF, Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science, Phage Hunters Integrating Research and Education (**PHIRE**), Mycobacterial Genetics Course. (2015). eLife.

## **Publications: Genomes**

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Mycobacteriophage phage PhrostyMug, complete genome. **Hansen AW**, Irons DL, Sargent CJ, Fisher JN, Gardner AV, Lunt BL, Merrill BD, Payne ID, Breakwell DP, Grose JH, Burnett SH. (2013). National Center for Biotechnology Information, U.S. National Library of Medicine, GenBank: KF279415.1.

Mycobacteriophage phage KLucky39, complete sequence. Haskell KJ, Giri I, Issac TF, Liechty ZS, Daetwyler ME, Bull LA, Payne DE, Lunt BL, Argueta LB, Bajgain P, Benedict AB, Earley BJ, Engle JM, Fisher JN, Greenhalgh E, **Hansen AW**, Ladle KC, Petersen SK, Sabin DS, Sargent CJ, Severson MC, Smith KC, Taylor MA, Woodward TJ, Wright BA, Burnett SH, Breakwell DP, Zhang X, Meincke LJ, Goodwin LA, Detter JC, Han S, Green LD, Bradley KW, Khaja R, Lewis MF, Barker LP, Jordan TC, Russell DA, Leuba KD, Fritz MJ, Bowman CA, Pope WH, Jacobs-Sera D, Hendrix RW and Hatfull GF. (2012). National Center for Biotechnology Information, U.S. National Library of Medicine, GenBank: JF704099.1.

## **Talks**

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Accelerating Mendelian Discovery: A Genocentric Approach. **Hansen AW**, Wang L, Palazzo BG, Panchel P, Easton-Marks JR, Coban-Akdemir Z, Rosenfeld JA, Eng C, Yang Y, Posey JE, Lupski JR, Murugan M, Gibbs RA. (2020). NIH National Human Genome Research Institute [NHGRI] Genome Sequencing Program annual meeting, Bethesda, MD.

A Genocentric, Optimization-based Approach to Discovery of Mendelian Disease Genes. **Hansen AW**, Wang L, Palazzo BG, Panchel P, Easton-Marks JR, Coban-Akdemir Z, Rosenfeld JA, Eng C, Yang Y, Posey JE, Lupski JR, Murugan M, Gibbs RA. (2019). NIH National Human Genome Research Institute [NHGRI] Genome Sequencing Program annual meeting, Bethesda, MD.

## Poster Presentations

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Accelerating Mendelian Discovery: A Genocentric Approach. **Hansen AW**, Wang L, Palazzo BG, Panchel P, Easton-Marks JR, Coban-Akdemir Z, Rosenfeld JA, Eng C, Yang Y, Posey JE, Lupski JR, Murugan M, Gibbs RA. (2019). American Society of Human Genetics [ASHG], Houston, TX.

A Genocentric, Optimization-based Approach to Discovery of Mendelian Disease Genes. **Hansen AW**, Wang L, Palazzo BG, Panchel P, Easton-Marks JR, Coban-Akdemir Z, Rosenfeld JA, Eng C, Yang Y, Posey JE, Lupski JR, Murugan M, Gibbs RA. (2019). Cold Spring Harbor Biology of Genomes annual conference, Cold Spring Harbor, NY.

A Hadoop Data Lake Enables Genocentric Mining of Genetic Variation Associated with Mendelian Disease. **Hansen AW**, Wang L, Palazzo BG, Panchel P, Easton-Marks JR, Coban-Akdemir Z, Rosenfeld JA, Eng C, Yang Y, Posey JE, Lupski JR, Murugan M, Gibbs RA. (2018). American Society of Human Genetics [ASHG], San Diego, CA.

Smartphone-recorded audio clips for predicting sleep apnea through snore classification. **Hansen AW**, Soderquist P, Young JT. (2015). Biotechnology and Bioinformatics Symposium, Provo, UT.

Mycobacteriophage exhibit discrepancies in Shine-Dalgarno Sequence Distance from Start Codon. **Hansen AW**, Benedict AB, Ladle KC, Breakwell DP, Burnett SH. (2010). American Society of Microbiology, Intermountain Branch Meeting, Provo, UT.

## Honors and Awards

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<b>Baylor College of Medicine President's Circle Grant (x4)</b>	2020
Team lead, awarded \$15,000 as part of BCM Precision Medicine / Population Health Strategic Initiative, project aims to pilot a BCM data lake to power a learning healthcare system	
<b>ASHG Reviewer's Choice Abstract</b>	2019
Abstract for ASHG 2019 annual meeting ranked in top 10%	
<b>Baylor College of Medicine President's Circle Grant (x3)</b>	2019
Team contributing member, awarded \$30,000 as part of BCM Precision Medicine / Population Health Strategic Initiative, project aims to develop a sensitive assay for detecting clonal hematopoiesis	
<b>Baylor College of Medicine President's Circle Grant (x2)</b>	2018
Team contributing member, awarded additional \$30,000 as part of BCM Precision Medicine / Population Health Strategic Initiative, project aims to develop a high-throughput protein assay to assess the pathogenicity of genomic variants	
<b>Baylor College of Medicine President's Circle Grant (x1)</b>	2018
Team lead, awarded \$30,000 as part of BCM Precision Medicine / Population Health Strategic Initiative, project aims to discover novel Mendelian disease genes through a big data mining approach coupled with functional modeling in drosophila	

## Honors and Awards (continued)

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<b>Baylor College of Medicine Cullen Foundation award</b>	2018
Full graduate tuition and stipend covered by the Cullen Foundation	
<b>NIH NIGMS Program in Human and Molecular Genetics (T32GM008307)</b>	2016-2017
Full graduate tuition and stipend covered by T32 training grant	
<b>BYU Dean's List</b>	2013-2015
Qualified for Dean's List three times by holding a 4.0 GPA for each semester	
<b>BYU Crocker Innovation Fellow</b>	2015
Recruited an interdisciplinary team of five fellows to apply lean startup methodology in commercializing a digital signaling technology; awarded \$10,000 in seed funding	
<b>2<sup>nd</sup> Place, BYU Chinese Speech Competition (Advanced Level)</b>	2015
Advanced to qualifying round of international competition, placed in top five	
<b>Cheri de Bonneville Scholarship</b>	2012-2013
Awarded full-tuition scholarship based on combination of academic merit and financial need	

## Technical Skills

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Python, R, Java, SQL, JavaScript, C++, Reproducible Computing, Machine Learning, Version Control, Unix, Web Development, Regular Expressions, Hadoop, Impala, Hive  
Algorithms, Statistics, Bootstrapping, Discrete Mathematics, Data Structures  
Genomics, Exome Sequencing, Targeted Capture Sequencing, Genome Sequencing, Microarrays, Copy Number Variation, Pedigree Analysis, GWAS

## Selected Graduate Coursework

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Genetics A	Molecular Methods
Genetics B	Method and Logic in Molecular Biology
Human Genetics	Translational Cancer Biology
Gene Regulation	Explorative Data Analysis

## Languages

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Chinese (**Mandarin**) – Advanced-mid | Chinese (**Cantonese**) – Elementary | **Spanish** – Intermediate-low

## Teaching Experience

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<b>Brigham Young University</b>	May 2014 – Aug 2014
Teaching Assistant, Chinese 102 (Mandarin)	Provo, UT
<ul style="list-style-type: none"><li>Created lesson plans for and taught 3 hours of classroom instruction weekly</li></ul>	
<b>LDS Missionary Training Center</b>	Sept 2012 – Jul 2013
Mandarin Chinese Instructor	Provo, UT
<ul style="list-style-type: none"><li>Helped classes of 4-12 students with no prior language experience gain intermediate-level conversational Mandarin ability over 8-week program</li></ul>	

## **Extracurricular/Volunteer**

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**BYU Entrepreneurship Club – Life Sciences Chapter** Jan 2015 – Apr 2015

Founding Member – Event Coordinator Provo, UT

- Spearheaded first event – brought successful biotech entrepreneurs to BYU to speak
- High attendance and quality of speakers established positive brand for club

**Utah Valley Chinese LDS Congregation** Sept 2014 – Jul 2016

Young Men Program Vice President Provo, UT

- Served first- and second-generation Chinese immigrant youth ages 12-18 through teaching, coaching, training, and planning and executing activities
- Bridged cultural gaps by performing simultaneous interpretation of key meetings

**The Church of Jesus Christ of Latter-day Saints (LDS)** Jun 2010 – Jul 2012

Voluntary Representative and Regional Supervisor (Chinese-speaking) Calgary, AB

- Led diverse workforce of nine full-time Chinese-speaking volunteers for 14 months, with complete responsibility over strategy, training, and operations
- Increased team critical performance measures by 500%

**BYU Jazz Ensembles; BYU Symphony Orchestra** Sept 2009 – Apr 2010

Drum Set; Percussion Provo, UT

- Only non-music major or freshman selected to perform with BYU jazz groups