JUN ZHONG, Ph. D.

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RESEARCH INTERESTS:

Computational oncology (especially pancreatic cancer), genetic epidemiology, GWAS/TWAS in cross-ancestry populations, polygenic risk scores (PRS), AI-powered risk prediction models, cancer drivers, cancer multi-omics.

PROFESSIONAL EXPERIENCE:

Research Fellow (Full-time employee)……………………………………………......2022 - present
National Cancer Institute, National Institute of Health, US

Research experience including:

- Building a trans-ancestry polygenic risk score (PRS) model for pancreatic cancer.
- Identifying noncoding somatic driver mutations for cancer.

Postdoctoral Fellow……………………………..…………….................................2017 - 2022
National Cancer Institute, National Institute of Health, US
Advisor: Laufey Amundadottir, Senior Investigator

Research experience including:

- Data mining of large multi-omic datasets (International Cancer Genome Consortium (ICGC), UK Biobank, GTEx, ENCODE, 1KG Genomes Project, gnomAD, et al.)
- Transcriptome-wide association study (TWAS) identifies novel candidate susceptibility genes for pancreatic cancer.
- Fine-mapping of chr16q23.1, splicing quantitative trait locus (sQTL) analysis.
- Genome-wide association study (GWAS) for pancreatic cancer, meta-analysis.
- Building a PRS model for pancreatic cancer, absolute risk (AR) model.
- Identifying noncoding somatic driver mutations in regulatory elements for pancreatic cancer.
- High-resolution promoter capture C and HiChIP analyses.

Research Fellow (Full-time employee)…………...……………………………………2014 - 2017
University of Chinese Academy of Sciences, CN

Research experience including:

- Whole genome sequencing (WGS) analysis by PacBio single-molecule real-time (SMRT) technology.
- Precision methylome characterization by PacBio SMRT technology.
- Identification of ^{m6}A sequence motifs and corresponding methyltransferase (MTase) genes.
- Pan-genome and single nucleotide polymorphism (SNP) deserts analyses.
- Building a high-performance bioinformatic server.

EDUCATION:

Ph. D Bioinformatics………………………………………………………….………...2014
University of Chinese Academy of Sciences, CN
Dissertation: Genome sequencing, assembly, and comparative analysis of *Penicillium chrysogenum* and miniature *Sus scrofa.*

Research experience including:

- Whole genome sequencing analysis by and next generation sequencing (NGS) (Roche 454 and Illumina Hiseq 2000) and Sanger (ABI 3730).
- Building a first high-quality genome sequence of industrial high-penicillin strain of *P. chrysogenum*

- Discovery of a 53.7 Kb "new shift fragment" in a seven copies of determinative penicillin biosynthesis cluster in *P. chrysogenum* NCPC10086.
- Building a genome reference and identification of genome-wide genetic diversity for miniature *Sus scrofa.*

B. S Biotechnology…………………………………...………………………………….…………2009
South-Central University for Nationalities, CN
General molecular biology and bioinformatic training.

PROFESSIONAL SERVICE FOR JOURNALS:

Editorial Service:

- Editorial Board Member in *BMC Medicine* 2024 - present
- Youth Editor in *The Innovation* 2022 - present
- Associate Editor in *Frontiers in Oncology* 2021 - 2023

Journal Reviewer Service (select):

Gastroenterology, Med, Nature Communications, The Innovation, Journal of Hematology & Oncology, Genome Biology, BMC Medicine, eLife, Genomics Proteomics & Bioinformatics, Molecular Oncology, Cancer Letters.
All peer-review and editorial records have already been or being certified by Web of Science.

Conference Reviewer Service:

American Society of Human Genetics (ASHG) annual meeting (2024)

AWARDS AND HONORS:

- DCEG Intramural Research Award, National Cancer Institute 2021
- Fellows Award for Research Excellence (FARE), NIH (Top 25%) 2021
- Reviewers’ Choice Abstract Award at American Society of Human Genetics (ASHG) annual meeting (Top 10%) 2020
- Fellows Award for Research Excellence (FARE), NIH (Top 25%) 2020
- 2021 NCI Directors Innovation Award (Participant) 2020
- Summer Research Mentor Award, NIH 2019
- Cancer Research Training Award (CRTA) from National Cancer Institute, NIH 2017
- Best Paper Award in the Twelfth Asia Pacific Bioinformatics Conference 2014
- Merit Student, University of Chinese Academy of Sciences (Top 15%) 2011
- Merit Student, University of Chinese Academy of Sciences (Top 15%) 2010

PUBLICATIONS IN JOURNALS:

($^{\#}$ for co-first author, § for co-corresponding author)

I. first/co-first/co-corresponding author papers

1. **Zhong J**$^{(\S)}$, Amundadottir LT$^{(\S)}$. Uncovering dark matter in cancer by identifying epigenetic drivers. ***Trends in Genetics.*** 2024, 40(3): 211-212.
2. **Zhong J**$^{(\S)}$, Shi J$^{(\S)}$, Amundadottir LT$^{(\S)}$. Artificial intelligence and improved early detection for pancreatic cancer. ***The Innovation***. 2023, 4(4):100457. (**Highlighted** in the cover legend of Volume 4, Issue 4: New Cool, AI for pancreatic cancer).
3. Jermusyk A$^{(\#)}$, **Zhong J**$^{(\#)}$, Connelly KE$^{(\#)}$, Gordon N$^{(\#)}$, Perera S, Abdolalizadeh E, Zhang T, O'Brien A, Hoskins JW, Collins I, Eiser D, Yuan C; PanScan Consortium; PanC4 Consortium, Risch HA, Jacobs EJ,

Li D, Du M, Stolzenberg-Solomon RZ, Klein AP, Smith JP, Wolpin BM, Chanock SJ, Shi J, Petersen GM, Westlake CJ, Amundadottir LT. A 584 bp deletion in CTRB2 inhibits chymotrypsin B2 activity and secretion and confers risk of pancreatic cancer. ***The American Journal of Human Genetics,*** 2021, 108(10):1852-1865.

4. **Zhong J,** Jermusyk A, Wu L, Hoskins JW, Collins I, Mocci E, Zhang M, Song L, Chung CC, Zhang T, Xiao W, Albanes D, Andreotti G, Arslan AA, Babic A, Bamlet WR, Beane-Freeman L, Berndt S, Borgida A, Bracci PM, Brais L, Brennan P, Bueno-de-Mesquita B, Buring J, Canzian F, Childs EJ, Cotterchio M, Du M, Duell EJ, Fuchs C, Gallinger S, Gaziano JM, Giles GG, Giovannucci E, Goggins M, Goodman GE, Goodman PJ, Haiman C, Hartge P, Hasan M, Helzlsouer KJ, Holly EA, Klein EA, Kogevinas M, Kurtz RJ, LeMarchand L, Malats N, Männistö S, Milne R, Neale RE, Ng K, Obazee O, Oberg AL, Orlow I, Patel AV, Peters U, Porta M, Rothman N, Scelo G, Sesso HD, Severi G, Sieri S, Silverman D, Sund M, Tjønneland A, Thornquist MD, Tobias GS, Trichopoulou A, Van Den Eeden SK, Visvanathan K, Wactawski-Wende J, Wentzensen N, White E, Yu H, Yuan C, Zeleniuch-Jacquotte A, Hoover R, Brown K, Kooperberg C, Risch HA, Jacobs EJ, Li D, Yu K, Shu XO, Chanock SJ, Wolpin BM, Stolzenberg-Solomon RZ, Chatterjee N, Klein AP, Smith JP, Kraft P, Shi J, Petersen GM, Zheng W, Amundadottir LT. A Transcriptome-Wide Association Study (TWAS) Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. ***JNCI: Journal of the National Cancer Institute***, 2020, 112(10):1003-1012. (**Highlighted** by an editorial in *JNCI*: Identifying Novel Genetic Markers Through a Transcription-Wide Association Study: Can This Be a Path to Reducing the Burden of Pancreatic Cancer?)
5. Yang T(#), **Zhong J(#)**, Zhang J(#), Li C(#), Yu X(#), Xiao J, Jia X, Ding N, Ma G, Wang G, Yue L, Liang Q, Sheng Y, Sun Y, Huang H, Chen F. Pan-genomic study of *Mycobacterium tuberculosis* reflecting the primary/secondary genes, generality/individuality, and the interconversion through copy number variations. ***Frontiers in Microbiology***, 2018, 9:1886.
6. Zhang L(#), **Zhong J(#)**, Liu H, Xin K, Chen C, Li Q, Wei Y, Wang Y, Chen F(*), Shen X(*). Complete genome sequence of the drought resistance-promoting endophyte *Klebsiella* sp. LTGPAF-6F. ***Journal of Biotechnology,*** 2017, 246: 36-39.
7. Zhu L(#), **Zhong J(#)**, Jia X(#), Liu G(#), Kang Y(#), Dong M, Zhang X, Li Q, Yue L, Li C, Fu J, Xiao J, Yan J, Zhang B, Lei M, Chen S, Lv L, Zhu B, Huang H(*), Chen F(*). Precision methylome characterization of *Mycobacterium tuberculosis* complex (MTBC) using PacBio single-molecule real-time (SMRT) technology. ***Nucleic Acids Research,*** 2016, 44, 730-743.
8. Wang FQ(#), **Zhong J(#)**, Zhao Y, Xiao J, Liu J, Dai M, Zheng G, Zhang L, Yu J, Wu J(*), Duan B(*). Genome sequencing of high-penicillin producing industrial strain of *Penicillium chrysogenum*. ***BMC Genomics*** 2014, 15 S1:S11.

II. Co-author papers

1. Lindström S, Wang L, Feng H, Majumdar A, Huo S, Macdonald J, Harrison T, Turman C, Chen H, Mancuso N, Bammler T; Breast Cancer Association Consortium (BCAC); Gallinger S, Gruber SB, Gunter MJ, Le Marchand L, Moreno V, Offit K; Colorectal Transdisciplinary Study (CORECT), Colon Cancer Family Registry Study (CCFR), Genetics And Epidemiology Of Colorectal Cancer Consortium (GECCO); De Vivo I, O'Mara TA, Spurdle AB, Tomlinson I; Endometrial Cancer Association Consortium (ECAC); Fitzgerald R, Gharahkhani P, Gockel I, Jankowski J, Macgregor S, Schumacher J, Barnholtz-Sloan J, Bondy ML, Houlston RS, Jenkins RB, Melin B, Wrensch M, Brennan P, Christiani DC, Johansson M, Mckay J, Aldrich MC, Amos CI, Landi MT, Tardon A; International Lung Cancer Consortium (ILCCO); Bishop DT, Demenais F, Goldstein AM, Iles MM, Kanetsky PA, Law MH; Ovarian Cancer Association Consortium (OCAC); Amundadottir LT, Stolzenberg-Solomon R, Wolpin BM; Pancreatic Cancer Cohort Consortium (PanScan, including **Zhong J**); Klein A, Petersen G, Risch H; Pancreatic Cancer Case-Control

Consortium (PanC4), The PRACTICAL Consortium; Chanock SJ, Purdue MP, Scelo G, Pharoah P, Kar S, Hung RJ, Pasaniuc B, Kraft P. Genome-wide analyses characterize shared heritability among cancers and identify novel cancer susceptibility regions. ***JNCI: Journal of the National Cancer Institute***. 2023, 115(6):712-732.

2. King SD, Veliginti S, Brouwers MCGJ, Ren Z, Zheng W, Setiawan VW, Wilkens LR, Shu XO, Arslan AA, Beane Freeman LE, Bracci PM, Canzian F, Du M, Gallinger SJ, Giles GG, Goodman PJ, Haiman CA, Kogevinas M, Kooperberg C, LeMarchand L, Neale RE, Visvanathan K, White E, Albanes D, Andreotti G, Babic A, Berndt SI, Brais LK, Brennan P, Buring JE, Rabe KG, Bamlet WR, Chanock SJ, Fuchs CS, Gaziano JM, Giovannucci EL, Hackert T, Hassan MM, Katzke V, Kurtz RC, Lee IM, Malats N, Murphy N, Oberg AL, Orlow I, Porta M, Real FX, Rothman N, Sesso HD, Silverman DT, Thompson IM, Wactawski-Wende J, Wang X, Wentzensen N, Yu H, Zeleniuch-Jacquotte A, Yu K, Wolpin BM, Duell EJ, Li D, Hung RJ, Perdomo S, McCullough ML, Freedman ND, Patel AV, Peters U, Riboli E, Sund M, Tjønneland A, **Zhong J**, Van Den Eeden SK, Kraft P, Risch HA, Amundadottir LT, Klein AP, Stolzenberg-Solomon RZ, Antwi SO. Genetic Susceptibility to Nonalcoholic Fatty Liver Disease and Risk for Pancreatic Cancer: Mendelian Randomization. ***Cancer Epidemiol Biomarkers Prev***. 2023, 32(9):1265-1269.
3. Hoskins JW, Chung CC, O'Brien A, **Zhong J**, Connelly K, Collins I, Shi J, Amundadottir LT. Inferred expression regulator activities suggest genes mediating cardiometabolic genetic signals. ***PLoS Computational Biololgy***, 2021, 17(11):e1009563.
4. Julián-Serrano S, Yuan F, Wheeler W, Benyamin B, Machiela MJ, Arslan AA, Beane-Freeman LE, Bracci PM, Duell EJ, Du M, Gallinger S, Giles GG, Goodman PJ, Kooperberg C, Marchand LL, Neale RE, Shu XO, Van Den Eeden SK, Visvanathan K, Zheng W, Albanes D, Andreotti G, Ardanaz E, Babic A, Berndt SI, Brais LK, Brennan P, Bueno-de-Mesquita B, Buring JE, Chanock SJ, Childs EJ, Chung CC, Fabiánová E, Foretová L, Fuchs CS, Gaziano JM, Gentiluomo M, Giovannucci EL, Goggins MG, Hackert T, Hartge P, Hassan MM, Holcátová I, Holly EA, Hung RI, Janout V, Kurtz RC, Lee IM, Malats N, McKean D, Milne RL, Newton CC, Oberg AL, Perdomo S, Peters U, Porta M, Rothman N, Schulze MB, Sesso HD, Silverman DT, Thompson IM, Wactawski-Wende J, Weiderpass E, Wenstzensen N, White E, Wilkens LR, Yu H, Zeleniuch-Jacquotte A, **Zhong J**, Kraft P, Li D, Campbell PT, Petersen GM, Wolpin BM, Risch HA, Amundadottir LT, Klein AP, Yu K, Stolzenberg-Solomon RZ. Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. ***The American Journal of Clinical Nutrition***, 2021, 114(4), 1408–1417.
5. Zhang YD, Hurson AN, Zhang H, Choudhury PP, Easton DF, Milne RL, Simard J, Hall P, Michailidou K, Dennis J, Schmidt MK, Chang-Claude J, Gharahkhani P, Whiteman D, Campbell PT, Hoffmeister M, Jenkins M, Peters U, Hsu L, Gruber SB, Casey G, Schmit SL, O'Mara TA, Spurdle AB, Thompson DJ, Tomlinson I, De Vivo I, Landi MT, Law MH, Iles MM, Demenais F, Kumar R, MacGregor S, Bishop DT, Ward SV, Bondy ML, Houlston R, Wiencke JK, Melin B, Barnholtz-Sloan J, Kinnersley B, Wrensch MR, Amos CI, Hung RJ, Brennan P, McKay J, Caporaso NE, Berndt SI, Birmann BM, Camp NJ, Kraft P, Rothman N, Slager SL, Berchuck A, Pharoah PDP, Sellers TA, Gayther SA, Pearce CL, Goode EL, Schildkraut JM, Moysich KB, Amundadottir LT, Jacobs EJ, Klein AP, Petersen GM, Risch HA, Stolzenberg-Solomon RZ, Wolpin BM, Li D, Eeles RA, Haiman CA, Kote-Jarai Z, Schumacher FR, Al Olama AA, Purdue MP, Scelo G, Dalgaard MD, Greene MH, Grotmol T, Kanetsky PA, McGlynn KA, Nathanson KL, Turnbull C, Wiklund F; Breast Cancer Association Consortium (BCAC); Barrett's and Esophageal Adenocarcinoma Consortium (BEACON); Colon Cancer Family Registry (CCFR); Transdisciplinary Studies of Genetic Variation in Colorectal Cancer (CORECT); Endometrial Cancer Association Consortium (ECAC); Genetics and Epidemiology of Colorectal Cancer Consortium

(GECCO); Melanoma Genetics Consortium (GenoMEL); Glioma International Case-Control Study (GICC); International Lung Cancer Consortium (ILCCO); Integrative Analysis of Lung Cancer Etiology and Risk (INTEGRAL) Consortium; International Consortium of Investigators Working on Non-Hodgkin's Lymphoma Epidemiologic Studies (InterLymph); Ovarian Cancer Association Consortium (OCAC); Oral Cancer GWAS; Pancreatic Cancer Case-Control Consortium (PanC4); Pancreatic Cancer Cohort Consortium (PanScan) (including **Zhong J**); Prostate Cancer Association Group to Investigate Cancer Associated Alterations in the Genome (PRACTICAL); Renal Cancer GWAS; Testicular Cancer Consortium (TECAC), Chanock SJ, Chatterjee N, Garcia-Closas M. Assessment of Polygenic Architecture and Risk Prediction based on Common Variants Across Fourteen Cancers. ***Nature Communications,*** 2020, 11:3353.

6. Lin Y, Nakatochi M, Hosono Y, Ito H, Kamatani Y, Inoko A, Sakamoto H, Kinoshita F, Kobayashi Y, Ishii H, Ozaka M, Sasaki T, Matsuyama M, Sasahira N, Morimoto M, Kobayashi S, Fukushima T, Ueno M, Ohkawa S, Egawa N, Kuruma S, Mori M, Nakao H, Adachi Y, Okuda M, Osaki T, Kamiya S, Wang C, Hara K, Shimizu Y, Miyamoto T, Hayashi Y, Ebi H, Kohmoto T, Imoto I, Kasugai Y, Murakami Y, Akiyama M, Ishigaki K, Matsuda K, Hirata M, Shimada K, Okusaka T, Kawaguchi T, Takahashi M, Watanabe Y, Kuriki K, Kadota A, Okada R, Mikami H, Takezaki T, Suzuki S, Yamaji T, Iwasaki M, Sawada N, Goto A, Kinoshita K, Fuse N, Katsuoka F, Shimizu A, Nishizuka SS, Tanno K, Suzuki K, Okada Y, Horikoshi M, Yamauchi T, Kadowaki T, Yu H, **Zhong J**, Amundadottir LT, Doki Y, Ishii H, Eguchi H, Bogumil D, Haiman CA, Le Marchand L, Mori M, Risch H, Setiawan VW, Tsugane S, Wakai K, Yoshida T, Matsuda F, Kubo M, Kikuchi S, Matsuo K. Genome-wide association meta-analysis identifies *GP2* gene risk variants for pancreatic cancer. ***Nature Communications,*** 2020, 11:3175.
7. Huang H(#), Ding N(#), Yang T(#), Li C(#), Jia X(#), Wang G(#), **Zhong J**, Zhang J, Jiang G, Wang S, Zong Z, Jing W, Zhao Y, Xu S, Chen F. Cross-sectional Whole-genome Sequencing and Epidemiological Study of Multidrug-resistant *Mycobacterium tuberculosis* in China. ***Clinical Infectious Diseases***, 2019, 69(3):405-413.
8. Klein AP, Wolpin BM, Risch HA, Stolzenberg-Solomon RZ, Mocci E, Zhang M, Canzian F, Childs EJ, Hoskins JW, Jermusyk A, **Zhong J**, Chen F, Albanes D, Andreotti G, Arslan AA, Babic A, Bamlet WR, Beane-Freeman L, Berndt SI, Blackford A, Borges M, Borgida A, Bracci PM, Brais L, Brennan P, Brenner H, Bueno-de-Mesquita B, Buring J, Campa D, Capurso G, Cavestro GM, Chaffee KG, Chung CC, Cleary S, Cotterchio M, Dijk F, Duell EJ, Foretova L, Fuchs C, Funel N, Gallinger S, M Gaziano JM, Gazouli M, Giles GG, Giovannucci E, Goggins M, Goodman GE, Goodman PJ, Hackert T, Haiman C, Hartge P, Hasan M, Hegyi P, Helzlsouer KJ, Herman J, Holcatova I, Holly EA, Hoover R, Hung RJ, Jacobs EJ, Jamroziak K, Janout V, Kaaks R, Khaw KT, Klein EA, Kogevinas M, Kooperberg C, Kulke MH, Kupcinskas J, Kurtz RJ, Laheru D, Landi S, Lawlor RT, Lee IM, LeMarchand L, Lu L, Malats N, Mambrini A, Mannisto S, Milne RL, Mohelníková-Duchoňová B, Neale RE, Neoptolemos JP, Oberg AL, Olson SH, Orlow I, Pasquali C, Patel AV, Peters U, Pezzilli R, Porta M, Real FX, Rothman N, Scelo G, Sesso HD, Severi G, Shu XO, Silverman D, Smith JP, Soucek P, Sund M, Talar-Wojnarowska R, Tavano F, Thornquist MD, Tobias GS, Van Den Eeden SK, Vashist Y, Visvanathan K, Vodicka P, Wactawski-Wende J, Wang Z, Wentzensen N, White E, Yu H, Yu K, Zeleniuch-Jacquotte A, Zheng W, Kraft P, Li D, Chanock S, Obazee O, Petersen GM, Amundadottir LT. Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. ***Nature Communications***, 2018, 9:556.
9. Hao L(#), Xia L(#), Huang D(#), Yang L(#), Xu X(#), Yan W(#), Zhang Y(#), Zou D(#), Liu S(#), Sang J, Deng W, Wang Y, Cheng H, Ma L, Yuan F, **Zhong J**, Li Q, Wu S, He Z, Luo Y, Wang X, Ji Z, Wang X, Xue Y, Chen L, Xiao J, Zhao W, Chen F, Zhang H(*), He H(*), Hu S(*), Zhang Z(*). Information Commons for Rice (IC4R). ***Nucleic Acids Research***, 2016, 44(D1):D1172-D1180.

10. Ling Y(#), Jin Z(#), Su M, **Zhong J**, Zhao Y, Yu J(*), Wu J(*), Xiao J(*). VCGDB: a dynamic genome database of the Chinese population. ***BMC Genomics*** 2014, 15:265.

11. Wu J, Xiao J, Wang L, **Zhong J**, Yin H, Wu S, Zhang Z, Yu J. Systematic analysis of intron size and abundance parameters in diverse lineages. ***Sci China Life Sci***, 2013, 56: 1–7.

PUBLICATIONS IN CONFERENCES:

1. O'Brien A, Hoskins JW, Eiser DR, Connelly KE, **Zhong J**, Andresson T, Collins I, Pancreatic Cancer Cohort Consortium, Pancreatic Cancer Case-Control Consortium, Chanock SJ, Klein AP, Arda HE, Amundadottir LT. Uncovering the functional variants and target genes of the 7q32 pancreatic cancer risk locus. Proceedings of the American Association for Cancer Research Virtual Special Conference on Pancreatic Cancer (AACR). ***Cancer Research***, 2022; 82(12_Suppl).

2. Jermusyk A, **Zhong J**, Gordon N, Connelly K, Perera S, Abdolalizadeh E, Zhang T, O'Brien A, Hoskins J, Collins I, Eiser D, Yuan C, Risch G, Jacobs EJ, Li D, Du M, Stolzenberg-Solomon R, Klein AP, Smith J, Wolpin BM, Chanock SJ, Shi J, Petersen GM, Westlake C, Amundadottir LT. An exception to the rule: A coding functional variant at a pancreatic cancer GWAS locus. Proceedings of the American Association for Cancer Research Virtual Special Conference on Pancreatic Cancer (AACR). ***Cancer Research***, 2020;80(22 Suppl).

3. **Zhong J** , Jermusyk A, Wu L, Hoskins JW, Collins I, Zhang M, Lei S, Chung CC, Zhang T, Xiao W, Stolzenberg-Solomon R, Klein AP, Wolpin BM, Shu XO, Chanock SJ, Olson S, Chatterjee N, Smith J, Shi J, Kraft P, Petersen GM, Zheng W, Amundadottir LT. Large-scale transcriptome-wide association study identifies novel candidate susceptibility genes for pancreatic cancer. Proceedings of the American Association for Cancer Research Annual Meeting (AACR). ***Cancer Research***, 2019; 79(13 Suppl).

MANUSCRIPTS IN PREPARATION:

1. **Zhong J**(#, §), O'Brien A(#), Eiser D, Collins I, Connelly K, Shen T, Zhao Y, Wang L, Guo K, TruongVo T, Wells A, Grant S, Arda E, Shi J, Hoskins J*, Amundadottir L(*, §). Identifying noncoding somatic driver mutations in regulatory elements for pancreatic cancer.

ACCEPTED MANUSCRIPT:

1. Ni Z, Kundu P, McKean D, Wheeler W, Albanes D, Andreotti G, Antwi SO, Arslan AA, Bamlet WR, Beane-Freeman L, Berndt SI, Bracci PM, Brennan P, Buring J, Chanock SJ, Gallinger S, Gaziano JM, Giles GG, Giovannucci E, Goggins M, Goodman PJ, Haiman C, Hassan M, Holly EA, Hung RJ, Katzke V, Kooperberg C, Kraft P, LeMarchand L, Li D, McCullough ML, Milne RL, Moore S, Neale RE, Oberg AL, Patel AV, Peters U, Rabe KG, Risch H, Shu X, Smith-Byrne K, Visvanathan K, Wactawski-Wende J, White E, Wolpin BM, Yu H, Zeleniuch-Jacquotte A, Zheng W, **Zhong J**, Amundadottir LT, Stolzenberg-Solomon RZ, Klein AP. Genome-wide analysis to assess if heavy alcohol consumption modifies the association between SNPs and pancreatic cancer risk. (***Cancer Epidemiol Biomarkers Prev***. 2024).

PRESENTATIONS:

Invited speaker:

1. **Identifying noncoding somatic driver mutations in pancreatic cancer**. Presented at NCI DCEG Early Career Scientist seminar, virtually, March 2023.

2. **Pancreatic Cancer Cohort Consortium (PanScan IV) Update**. Presented at Pancreatic Cancer Case-Control Consortium (PanC4) virtual annual meeting, virtually, December 2022.

3. **Identifying noncoding somatic driver mutations in regulatory elements for pancreatic cancer**. Presented (Platform) at American Society of Human Genetics (ASHG) annual meeting, Los Angeles, October 2022.
4. **Pancreatic Cancer Cohort Consortium (PanScan) IV GWAS update.** Presented in the FinnGen Scientific Committee/Analysis group meeting, virtually, January 2022.
5. **PanScan update and preliminary results for PANDoRA and Asian GWAS scans.** Presented in the PanScan cohort consortium annual meeting, virtually, October 2021.
6. **Uncovering the dark matter of pancreatic cancer: noncoding somatic driver mutations in regulatory elements.** Presented in the CRL (Consolidated Research Laboratory) seminar, Division of Cancer Epidemiology and Genetics (DCEG, NCI), virtually. September 2020.
7. **Large-scale Transcriptome-Wide Association Study (TWAS) Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer.** Presented in the 11th Annual Division of Cancer Epidemiology and Genetics (DCEG, NCI) Fellows' Training Symposium, Bethesda, MD. April 2019.
8. **A Transcriptome-Wide Association Study (TWAS) Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer**. Presented at the LTG (Laboratory of Translational Genomics) seminar, Division of Cancer Epidemiology and Genetics (DCEG, NCI), Gaithersburg, MD. February 2019.
9. **Genome sequencing of high-penicillin producing industrial strain of *Penicillium chrysogenum***. Presented at the twelfth Asia Pacific Bioinformatics Conference, Shanghai, China. January 2014. (**Best Paper Award** in the conference)

Posters (select):

1. **Zhong J**, Eiser D, Brien A, Connelly K, Hoskins J, Jermusyk A, Collins I, Shen T, Zhao Y, Li Wang3, Guo K, TruongVo T, Wildenthal J, McKinnon K, Wells A, Grant S, Arda E, Shi J, Amundadottir L. *Uncovering the dark matter of pancreatic cancer: identifying driver mutations in noncoding gene regulatory elements.* Presented at American Society of Human Genetics virtual meeting (ASHG), October 2020. **[Reviewers' Choice award, top 10%]**
2. **Zhong J**, Jermusyk A, Wu L, Hoskins J, Collins I, Zhang M, Lei S, Chung C, Zhang T, Xiao W, Stolzenberg-Solomon R, Klein A, Wolpin B, Shu X, Chanock S, Olson S, Chatterjee N, Smith J, Jianxin Shi, Kraft P, Petersen G, Zheng W, Amundadottir L. *Large-scale transcriptome-wide association study (TWAS) identifies novel candidate susceptibility genes for pancreatic cancer*. Presented at American Association for Cancer Research Annual Meeting (AACR), Atlanta, GA. March 2019.
3. **Zhong J**, Wu L, Jermusyk A, Hoskins J, Collins I, Zhang M, Lei S, Chung C, Zhang T, Xiao W, PanScan, PanC4, Stolzenberg-Solomon R, Klein A, Wolpin B, Brown K, Shu X, Chanock S, Olson S, Chatterjee N, Petersen G, Smith J, Shi J, Kraft P, Zheng W, Amundadottir L. A *Transcriptome-wide association study for pancreatic cancer.* Presented at American Society of Human Genetics annual meeting (ASHG), San Diego, CA. October 2018.

PROFESSIONAL MEMBERSHIP/ROLE:

Gold member in American Association for the Advancement of Science (AAAS)	2023 - 2024
Member in American Society of Human Genetics (ASHG)	2021 - 2024
Review Committee Member in NIH DCEG Fellows Award for Research Excellence competition (DFARE)	2019
Associate Member in American Association for Cancer Research (AACR)	2018 - 2020
Member in Tumor Microenvironment Group of the AACR	2018 - 2019
Planning Committee Member in 10th Annual NCI DCEG Fellows' Training Symposium	2017 - 2018

MENTORSHIP:

- A Ph. D candidate, Morehouse School of Medicine, summer intern
  Project: *Uncovering the dark matter of pancreatic cancer by assessing noncoding regulatory variations.*
  2019
- A M.S candidate, Georgia Institute of Technology, summer intern
  Project: *Genome-wide association study to identify risk loci for pancreatic cancer in Asian.*
  2018
- 2 Ph. D candidates, Beijing Institute of Genomics, University of Chinese Academy of Sciences
  Projects: *The methylome and pan-genome analysis of Mycobacterium tuberculosis complex*
  2014-2016