**Cassandra N. Spracklen, PhD**

Department of Biostatistics and Epidemiology Email: cspracklen@umass.edu

University of Massachusetts Amherst Cell: (319) 621-8965

715 N. Pleasant St., 429 Arnold House Office: (413) 545-2379

Amherst, MA 01003 Website: <https://thespracklenlab.com>

**EDUCATION**

**University of Iowa** 2011-2014  
Ph.D. Epidemiology,

Thesis: *Dyslipidemia and the risk of preeclampsia: genetic causes and related modifiers*

**University of Iowa** 2012-2014

Certificate in Graduate Teaching

**University of Iowa** 2009-2011  
M.S. Epidemiology

**Anderson University** 2005-2009

B.A. Biology

**RESEARCH AND PROFESSIONAL EXPERIENCE**

**Assistant Professor, University of Massachusetts, Amherst** 2019-Present

Department of Biostatistics and Epidemiology

**Postdoctoral Research Fellow, University of North Carolina, Chapel Hill** 2014-2019

Department of Genetics

Advisor: Karen Mohlke

**Graduate Research Assistant, University of Iowa, Iowa City** 2010-2014

Department of Epidemiology

Advisors: Kelli Ryckman, Audrey Saftlas, Elizabeth Chrischilles

**HONORS AND AWARDS**

**Elected Member**, Delta Omega Honorary Society of Public Health, Rho Chapter, University 2023  
 of Massachusetts Amherst

**Nominee, Outstanding Teaching Award**, School of Public Health and Health Sciences, 2023

University of Massachusetts Amherst

**Research Scholar**, Center for Research on Families, University of Massachusetts Amherst 2022-2023

**Nominee, Outstanding Teaching Award**, School of Public Health and Health Sciences 2022

University of Massachusetts Amherst

**Reviewer’s Choice Abstract**, American Society for Human Genetics 2019

**Distinguished Young Alumni Award**, Anderson University 2019

**Travel Award**, Quantitative Genetics and Genomics Gordon Research Conference 2019

**Postdoctoral Award for Research Excellence**, University of North Carolina at Chapel Hill 2018

**Finalist, Charles J. Epstein Trainee Award for Excellence in Human Genetics Research**, 2018

American Society for Human Genetics

**David Liu Prize Paper**, Royal College of Obstetrics and Gynaecology 2018

**Trainee Spotlight Paper**, American Society for Human Genetics 2017

**Reviewer’s Choice Abstract**, American Society for Human Genetics 2017

**Travel Grant**, Executive Council of Graduate and Professional Students, University of Iowa 2014

**Outstanding Teaching Assistant of the Year**, University of Iowa 2014

**Milford E. Barnes Award for Academic Excellence**, University of Iowa 2014

**Dean’s List**, Anderson University 2005-2009

**Dean’s Scholarship**, Anderson University 2005-2009

**PUBLICATIONS**

*\* denotes co-first and/or co-last authors*

*Tr denotes trainee supervised by Cassandra Spracklen*

Published in peer-review journals

1. Daniele CTr, Farland LV, Garcia L, Park K, Schnatz PF, Shadyab AH, Stefanick ML, Wactawski-Wende J, Wild RA, **Spracklen CN.** Association of maternal birth weight and maternal preterm birth with subsequent adverse reproductive outcomes: the Women’s Health Initiative. In press at *Early Human Development.*
2. Holman-Vittone ATr, Monahan BTr, LeBlanc ES, Liu S, Nassir R, Saquib N, Schnatz PF, Shadyab AH, Sinkey R, Wactawski-Wende J, Wild RA, Chasan-Taber L, **Spracklen CN**. Associations of maternal preterm birth with subsequent risk for self-reported type 2 diabetes in women. In press at *J Develop Origins Health Disease;* doi: 10.1017/S204017442300089*.*
3. Kanoni S\*, Graham SE\*, Wang Y\*, Surakka I\*, Ramdas S\*, Zhu X\*, Clarke SL, Bhatti KF, Vedantam S, Winkler TW, Locke AE, Marouli E, Zajac GJM, Wu KHH, Ntalla I, Hui Q, Klarin D, Hilliard A, Wang Z, Xue C, Thorleifsson G, Helgadottir A, Gudbjartsson DF, Holm H, Olafsson I, Hwang MY, Han S, Akiyama M, Sakaue S, Terao C, Kanai M, Zhou W, Brumpton BM, Rasheed H, Havulinna AS, Veturi Y, Pacheco JA, Rosenthal EA, Lingren T, Feng Q, Kullo IJ, Narita A, Takayama J, Martin HC, Hunt KA, Trivedi B, Haessler J, Giulianini F, Bradford Y, Miller JE, Campbell A, Lin K, Millwood IY, Rasheed A, Hindy G, Faul JD, Zhao W, Weir DR, Turman C, Huang H, Graff M, Choudhury A, Sengupta D, Mahajan A, Brown MR, Zhang W, Yu K, Schmidt EM, Pandit A, Gustafsson S, Yin X, Luan J, Zhao JH, Matsuda F, Jang HM, Yoon K, Medina-Gomez C, Pitsillides A, Hottenga JJ, Wood AR, Ji Y, Gao Z, Haworth S, Mitchell RE, Chai JF, Aadahl M, Bjerregaard AA, Yao J, Manichaikul A, Hwu CM, Hung YJ, Warren HR, Ramirez J, Bork-Jensen J, Kårhus LL, Goel A, Sabater-Lleal M, Noordam R, Mauro P, Matteo F, McDaid AF, Marques-Vidal P, Wielscher M, Trompet S, Sattar N, Møllehave LT, Munz M, Zeng L, Huang J, Yang B, Poveda A, Kurbasic A, Lamina C, Forer L, Scholz M, Galesloot TE, Bradfield JP, Ruotsalainen SE, Daw EW, Zmuda JM, Vazquez-Moreno M, Feitosa MF, Wojczynski MK, Wang Z, Preuss M, Mangino M, Christofidou P, Verweij N, Benjamins JW, Engmann J, Tsao NL, Verma A, Slieker RC, Lo KS, Zilhao NR, Le P, Kleber ME, Delgado GE, Huo S, Ikeda DD, Iha H, Yang J, Liu J, Leonard HL, Marten J, Frank M, Schmidt B, Smyth LJ, Cañadas-Garre M, Wang C, Nakatochi M, Wong A, Hutri-Kähönen N, Sim X, Xia R, Huerta-Chagoya A, Fernandez-Lopez JC, Lyssenko V, Nongmaithem SS, Bayyana S, Stringham HM, Irvin MR, Oldmeadow C, Kim HN, Ryu S, Timmers PRHJ, Arbeeva L, Dorajoo R, Lange LA, Prasad G, Lorés-Motta L, Pauper M, Long J, Li X, Theusch E, Takeuchi F, **Spracklen CN**, Loukola A, Bollepalli S, Warner SC, Wang YX, Wei WB, Nutile T, Ruggiero D, Sung YJ, Chen S, Liu F, Yang J, Kentistou KA, Banas B, Brumat M, Meidtner K, Bielak LF, Smith JA, Hebbar P, Farmaki AE, Hofer E, Lin M, Concas MP, Vaccargiu S, van der Most PJ, Pitkänen N, Cade BE, van der Laan SW, Chitrala KN, Weiss S, Bentley AR, Ekoru K, Doumatey AP, Adeyemo AA, Lee JY, Petersen ERB, Nielsen AA, Choi HS, Nethander M, Freitag-Wolf S, Southam L, Rayner NW, Wang CA, Lin SY, Wang JS, Couture C, Lyytikäinen LP, Nikus K, Cuellar-Partida G, Vestergaard H, Hildago B, Giannakopoulou O, Cai Q, Obura MO, van Setten J, Liang J, Tang H, Terzikhan N, Shin JH, Jackson RD, Reiner AP, Martin LW, Chen Z, Li L, Kawaguchi T, Thiery J, Bis JC, Launer LJ, Li H, Nalls MA, Raitakari OT, Ichihara S, Wild SH, Nelson CP, Campbell H, Jäger S, Nabika T, Al-Mulla F, Niinikoski H, Braund PS, Kolcic I, Kovacs P, Giardoglou T, Katsuya T, de Kleijn D, de Borst GJ, Kim EK, Adams HHH, Ikrani MA, Zhu X, Asselbergs FW, Kraaijeveld AO, Beulens JWJ, Shu XO, Rallidis LS, Pedersen O, Hansen R, Mitchell P, Hewitt AW, Kähönen M, Pérusse L, Bouchard C, Tönjes A, Chen YDI, Pennell CE, Mori TA, Lieb W, Franke A, Ohlsson C, Mellström D, Cho YS, Lee H, Yuan JM, Koh WP, Rhee SY, Woo JT, Heid IM, Stark KJ, Zimmerman ME, Völzke H, Homuth G, Evans MK, Zonderman AB, Polasek O, Pasterkamp G, Hoefer IE, Redline S, Pahkala K, Oldehinkel AJ, Snieder H, Biino G, Schmidt R, Schmidt H, Bandinelli S, Dedoussis G, Thanaraj TA, Kardia SLR, Kato N, Schulze MB, Girotto G, Böger CA, Jung B, Joshi PK, Bennett DA, De Jager PL, Lu X, Mamakou V, Brown M, Caulfield MJ, Munroe PB, Guo X, Ciullo M, Jonas JB, Samani NJ, Chasman DI, Kaprio J, Pajukanta P, Tusié-Luna T, Aguilar-Salinas CA, Adair LS, Bechayda SA, de Silva HJ, Wickremasinghe AR, Krauss RM, Wu JY, Zheng W, den Hollander AI, Bharadwaj D, Correa A, Wilson JG, Lind L, Heng CK, Nelson AE, Golightly YM, Wilson JF, Penninx B, Kim HL, Attia J, Scott RJ, Rao DC, Arnett DK, Walker M, Koistinen HA, Chandak GR, Mercader JM, Tusie-Luna T, Aguilar-Salinas C, Villalpando CG, Orozco L, Fornage M, Tai ES, van Dam RM, Lehtimäki T, Chaturvedi N, Yokota M, Liu J, Reilly DF, McKnight AJ, Kee F, Jöckel KH, McCarthy MI, Palmer CAN, Vitart V, Hayward C, Simonsick E, van Duijn CM, Jin ZB, Qu J, Hishigaki H, Lin X, März W, Gudnason V, Tardif JC, Lettre G, Hart LM, Elders PJM, Rader DJ, Damrauer SM, Kumari M, Kivimaki M, van der Harst P, Spector TD, Loos RJF, Province MA, Parra EJ, Cruz M, Psaty BM, Brandslund I, Pramstaller PP, Rotimi CN, Christensen K, Ripatti S, Widén E, Hakonarson H, Grant SFA, Kiemeney LALM, de Graaf J, Loeffler M, Kronenberg F, Gu D, Erdmann J, Schunkert H, Franks PW, Linneberg A, Jukema JW, Khera AV, Männikkö M, Jarvelin MR, Kutalik Z, Francesco C, Mook-Kanamori DO, van Dijk KW, Watkins H, Strachan DP, Grarup N, Sever P, Poulter N, Chuang LM, Rotter JI, Dantoft TM, Karpe F, Neville MJ, Timpson NJ, Cheng CY, Wong TY, Khor CC, Li H, Sabanayagam C, Peters A, Gieger C, Hattersley AT, Pedersen NL, Magnusson PKE, Boomsma DI, Willemsen AHM, Cupples LA, van Meurs JBJ, Ikram A, Ghanbari M, Gordon-Larsen P, Huang W, Kim YJ, Tabara Y, Wareham NJ, Langenberg C, Zeggini E, Kuusisto J, Laakso M, Ingelsson E, Abecasis G, Chambers JC, Kooner JS, de Vries P, Morrison AC, Hazelhurst S, Ramsay M, North KE, Daviglus M, Kraft P, Martin NG, Whitfield JB, Abbas S, Saleheen D, Walters RG, Holmes MV, Black C, Smith BH, Baras A, Justice AE, Buring JE, Ridker PM, Chasman DI, Kooperberg C, Tamiya G, Yamamoto M, van Heel DA, Trembath RC, Qei WQ, Jarvik GP, Namjou B, Hayes MG, Ritchie MD, Jousilahati P, Salomaa V, Hveem K, Åsvold BO, Kubo M, Kamatani Y, Okada Y, Murakami Y, Kim BJ, Thorsteinsdottir U, Stefansson K, Zhang J, Chen YE, Ho YL, Lynch JA, Dader D, Tsao PS, Chang KM, Cho K, O’Donnell CJ, Gaziano JM, Wilson P, Frayling TM, Hirschhirn JN, Kathiresan S, Mohlke KL, Million Veteran Program, Global Lipids Genetics Consortium, Sun YV, Morris AP, Boehnke M, Brown CD\*, Natarajan P\*, Deloukas P\*, Willer CJ\*, Assimes TL\*, Peloso G\*. Implicating genes, pleiotropy, and sexual dimorphism at blood lipid loci through multi-ancestry meta-analysis. *Genome Biol* 2022;23(1):268.
4. Yengo L\*, Vedantam S\*, Marouli E\*, Sidorenko J, Bartell E, Sakaue S, Graff M, Eliasen AU, Jiang Y, Raghavan S, Miao J, Arias JD, Mukamel RE, **Spracklen CN**, Yin X, Chen SH, Ferreira T, Ji Y, Karedera T, Lüll K, Malden DE, Medina-Gomez C, Moara M, Moore A, Rueger S, Ahluwalia TS, Akiyama M, Allison MA, Alvarez M, Andersen MF, Ani A, Appadurai V, Arbeeva L, Arzumanyan Z, Bhaskar S, Bielak LF, Bollepalli S, Bonnycastle LL, Bork-Jensen J, Bradfield JP, Bradford Y, Braund PS, Brody JA, Burgdorf KS, Cade BE, Cai H, Cai Q, Campbell A, Cañadas-Garre M, Catamo E, Chai JF, Chai X, Chang LC, Chang YC, Chen CH, Chesi A, Choi SH, Chung RH, Cocca M, Concas MP, Couture C, Cuellar- Partida G, Danning R, Daw EW, Degenhard F, Delgado GE, Delitala A, Deng X, Devineni P, Dietl A, Dimitriou M, Dimitrov, Dorajoo R, Ekici AB, Engmann JE, Fairhurst- Hunter Z, Farmaki AE, Faul JD, Fernandez-Lopez JC, Forer L, Francescatto M, Freitag-Wolf S, Fuchsberger F, Galesloot TE, Gao Y, Gao Z, Geller F, Giannakopoulou O, Giulianini F, Gjessing AP, Goel A, Gordon SD, Gorski M, Graham SE, Grove J, Guo X, Gustafsson S, Haessler J, Hansen TF, Havulinna A, Haworth SJ, He J, Heard-Costa N, Hebbar P, Hindy G, Ho YLA, Hofer E, Holliday E, Horn K, Hornsby WE, Hottenga JJ, Huang H, Huang J, Huerta-Chagoya A, Huffman JE, Hung YJ, Huo S, Hwang MY, Iha H, Ikeda DD, Isono M, Jackson AU, Jäger S, Jansen IE, Johansson I, Jonas JB, Jonsson A, Jørgensen T, Kalafati IP, Kanai M, Kanoni S, Kårhus LL, Kasturiratne A, Katsuya T, Kawaguchi T, Kember RL, Kentistou KA, Kim HN, Kim YJ, Kleber ME, Knol MJ, Kurbasic A, Lauzon M, Le P, Lea R, Lee JY, Leonard HL, Li SA, Li X, Li X, Liang J, Lin H, Lin K, Lin SY, Liu J, Liu X, Lo KS, Long J, Lores-Motta L, Luan J, Lyssenko V, Lyytikäinen LP, Mahajan A, Mamakou V, Mangino M, Manichaikul A, Marten J, Mattheisen M, Mavarani L, McDaid AF, Meidtner K, Melendez T, Mercader JM, Milaneschi Y, Miller JE, Millwood IY, Mishra PP, Mitchell RE, Møllehave LT, Morgan A, Mucha S, Munz M, Nakatochi M, Nelson CP, Nethander M, Nho CW, Nielsen AA, Nolte IM, Nongmaithem SS, Noordam R, Ntalla I, Nutile T, Oldmeadow C, Pandit A, Paraskevi C, Pärna K, Pauper M, Petersen ERB, Petersen LV, Pitkänen L, Polasek O, Poveda A, Preuss MH, Pyarajan S, Raffield LM, Rakugi H, Ramirez J, Rasheed A, Raven D, Rayner NW, Rohde R, Roll K, Ruggiero D, Ruotsalainen SE, Ryan KA, Sabater-Lleal M, Saxena R, Scholz M, Sendamarai A, Shen B, Shi J, Shin JH, Sidore C, Sim X, Sitlani CM, Slieker RC, Smith AV, Smith JA, Smyth LJ, Southam L, Steinthorsdottir V, Sun L, Takeuchi F, Tallapragada DSP, Tan J, Taylor KD, Tayo BO, Tcheandjieu C, Terzikhan N, Tesolin P, Teumer A, Theusch E, Thompson D, Thorleifsson G, Timmers PRHJ, Trompet S, Turman C, Vaccargiu S, van der Laan SW, van der Most PJ, van Klinken JB, van Setten J, Verma SS, Verweij N, Veturi Y, Wang CA, Wang C, Wang L, Wang Z, Warren HR, Wei WB, Wickremasinghe AR, Wielscher M, Wiggins KL, Winsvold BS, Wong A, Wu Y, Wuttke M, Xia R, Xiang AH, Xie T, Yamamoto K, Yang J, Yao J, Young H, Yousri NA, Yu L, Zeng L, Zhang W, Zhang X, Zhao JH, Zhao W, Zhou W, Zimmermann ME, Zoledziewska M, Adair LS, Adams HHH, Aguilar-Salinas CA, Al-Mulla F, Arnett DK, Asselbergs FW, Asvold BO, Attia J, Banas B, Bandinelli S, Bergler T, Bharadwaj D, Biino G, Bisgaard H, Boerwinkle E, Böger CA, Bønnelykk K, Boomsma DI, Børglum AD, Borja JB, Bouchard C, Bowden DW, Brandslund I, Brumpton B, Buchanan T, Buring JE, Caulfield MJ, Chambers JC, Chandak GR, Chanock SJ, Chaturvedi N, Chen YDI, Chen Z, Cheng CY, Christophersen IE, Ciullo M, Cole JW, Collins FS, Cooper RS, Cruz M, Cucca F, Cupples LA, . Cutler MJ, Damrauer SM, Dantoft TM, de Borst GJ, de Groot LCPGM, De Jager PL, de Kleijn DPV, de Silva HJ, Dedoussis GV, den Hollander AI, Du S, Easton DF, Elders PJM, Eliassen AH, Ellinor PT, Elmståhl S, Erdmann J, Evans MK, Fatkin D, Feenstra B, Feitosa MF, Ferrucci L, Ford I, Fornage M, Franke A, Franks PW, Freedman BI, Gasparini P, Gieger C, Girotto G, Goddard ME, Golightly YM, Gonzalez-Villalpando C, Goodarzi MO, Gordon-Larsen P, Grallert H, Grant SFA, Grarup N, Griffiths L, Groop L, Gudnason V, Haiman C, Hakonarson H, Hansen T, Hartman CA, Hattersley AT, Hayward C, Heckbert SR, Heng CK, Hengstenberg C, Hewitt AW, Hishigaki H, Hoyng CB, Hsueh WA, Huang PL, Huang W, Hunt SC, Hveem K, Hypponen E, Iacono WG, Ichihara S, Ikram MA, Isasi C, Jackson RD, Jarvelin MR, Jin ZB, Jöckel KH, Joshi PK, Jousilahti P, Jukema JW, Kähönen M, Kamatani Y, Kang KD, Kaprio J, Kardia SLR, Karpe F, Kato N, Kee F, Kessler T, Khera AV, Khor CC, Kiemeney LALM, Kim BJ, Kim EK, Kim HL, Kirchhof P, Kivimaki M, Koh WP, Koistinen HA, Kolovou GD, Kooner JS, Kooperberg C, Köttgen A, Kovacs P, Kraaijeveld A, Kraft P, Krauss RM, Kumari M, Kutalik Z, Laakso M, Lange LA, Langenberg C, Launer LJ, Marchand LL, Lee H, Lee NR, Lehtimäki T, Li H, Li L, Lieb W, Lin X, Lind L, Linneberg A, Liu CT, Liu J, Loeffler M, London B, Lubitz SA, Lye SJ, Mackey DA, Mägi R, Magnusson PKE, Marcus GM, Vidal PM, Martin NG, März W, Matsuda F, McGarrah RW, McGue M, McKnight AJ, Medland SE, Mellström D, Metspalu A, Mitchell BD, Mitchell P, Mook-Kanamori DO, Morris AD, Mucci LA, Munroe PB, Nalls MA, Nazarian S, Nelson AE, Neville MJ, Newton-Cheh C, Nielsen CS, Nöthen MM, Ohlsson C, Oldehinkel AJ, Orozco L, Pahkala K, Pajukanta P, Palmer CNA, Parra EJ, Pattaro C, Pedersen O, Pennell CE, Penninx BWJH, Perusse L, Peters A, Peyser PA, Porteous DJ, Posthuma D, Power C, Pramstaller PP, Province MA, Qi Q, Qu J, Rader DJ, Raffel LJ, Raitakari OT, Ralhan S, Rallidis LS, Rao DC, Redline S, Reilly DF, Reiner AP, Rhee SY, Ridker PM, Rienstra M, Ripatti S, Ritchie M, Roden DM, Rosendaal FR, Rotter JI, Rudan I, Rutters F, Sabanayagam C, Saleheen D, Salomaa V, Samani NJ, Sanghera DK, Sattar N, Schmidt B, Schmidt H, Schmidt R, Schulze MB, Schunkert H, Scott LJ, Scott R, Sever P, Shiroma EJ, Shoemaker MB, Shu XOP, Simonsick EM, Sims M, Singh J, Singleton AB, Sinner MF, Smith JG, Snieder H, Spector TD, Stampfer MJ, Stark KJ, Strachan DP, Hart LM, Tabara Y, Tang H, Tardif JC, Thanaraj TA, Timpson NJ, Tönjes A, Tremblay A, Tuomi T, Tuomilehto J, Tusié-Luna MT, Uitterlinden AG, van Dam RM, van der Harst P, Van der Velde N, van Duijn CM, van Schoor N, Vitart V, Völker U, Vollenweider P, Völzke H, Vrieze S, Wacher-Rodarte NH, Walker M, Wang YX, Wareham NJ, Watanabe R, Watkins H, Weir DR, Werge TM, Widen E, Wilkens LR, Willemsen G, Willett WC, Wilson JF, Wong TY, Woo JT, Wright AF, Wu JY, Xu H, Yajnik CS, Yokota M, Yuan JM, Zeggini E, Zemel BS, Zheng W, Zhu X, Zmuda JM, Zonderman AB, Zwart JA, 23andMe Research Team, DiscovEHR (DiscovEHR and MyCode Community Health Initiative), eMERGE (Electronic Medical Records and Genomics Network), Lifelines Cohort Study, Regeneron Genetics Center, The PRACTICAL Consortium, Understanding Society Scientific Group, Chasman DI, Cho YS, Heid IM, McCarthy MI, Ng MCY, O'Donnell CJ, Rivadeneira F, Stefansson K, Sun YV, Tai ES, Boehnke M, Deloukas P, Justice AE, Lindgren CM, Loos RJF, Mohlke KL, North KE, Thorsteinsdottir U, Walters RG, Winkler TW, Young K, Loh PR, Yang J, Esko T, Assimes TL, Auton A, Abecasis GR, Willer CJ, Locke AE, Berndt SI, Lettre G, Frayling TM, Okada Y\*, Wood AR\*, Visscher PM\*, Hirschhorn JN\*. A saturated map of common genetic variants associated with human height from 5.4 million individuals of diverse ancestries. Nature, 2022;610(7933):704-712.
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Ramdas S\*, Judd J\*, Graham SE\*, Kanoni S\*, Wang Y\*, Surakka I, Wenz B, Clarke SL, Chesi A, Wells A, Bhatti KF, Vedantam S, Winkler TW, Locke AE, Marouli E, Zajac GJM, Wi KHH, Ntalla I, Hui Q, Klarin D, Hilliard A, Wang Z, Xue C, Thorleifsson G, Helgadottir A, Gudbjartsson DF, Holm H, Olafsson I, Hwang MY, Han S, Akiyama M, Sakaue S, Terao Ch, Kanai M, Zhou W, Brumpton BM, Rasheed H, Havulinna AS, Veturi Y, acheco JA, Rosenthal EA, Lingren T, Feng QP, Kullo IJ, Narita A, Takayama J, Martin HC, Hunt KA, Trivedi B, Haessler J, Giulianini F, Bradford Y, Miller JE, Campbell A, Lin K, Millwood IY, Rashee A, Hindy G, Faul JD, Zhao W, Weir DR, Turman C, Huang H, Graff M, Choudhury A, Sengupta D, Mahajan A, Brown MR, Zhang W, Yu K, Schmidt EM, Pandit A, Gustafsson S, Yin X, Luan J, Zhao JH, Matsuda F, Jang HM, Yoon K, Medina-Gomez C, Pitsillides A, Hottenga JJ, Wood AR, Ji Y, Gao Z, Haworthh S, Mitchell RE, Chai JF, Aadahl M, Bjerregaard AA, Yao J, Manichaikul A, Lee WJ, Chao A, Warren HR, Ramirez J, Bork-Jensen J, Kårhus LL, Goel A, Sabatre-Lleal M, Noordam R, Mauro P, Matteo F, Trompet AF, Sattar N, Møllehave LT, Munz M, Zeng L, Huang J, Yang B, Poveda A, Kurbasic A, Schönherr S, Forer L, Scholz M, Galesloot TE, Bradfield JP, Ruotsalainen SE, Daw EW, Zmuda JM, Mitchell JS, Fuchsberger C, Christensen H, Brody JA, Le P, Feitosa MF, Wojczynski MK, Hemerich D, Preuss M, Mangino M, Christofidou P, Verweij N, Benjamins JW, Engmann J, Noah TL, Verma A, Slieker RC, Lo KS, Zilhao NR, Kleber ME, Delgado GE, Huo S, Ikeda DD, Iha H, Yang J, Liu J, Leonard HL, Marten J, Emmel C, Schmidt B, Smyth LJ, Cañadas-Garre M, Wang C, Nakatochi M, Wong A, Hutri-Kähönen N, Sim X, Xia R, Huerta-Chagoya A, Fernandez-Lopez JC, Lyssenko V, Nongmaithem SS, Sankareswaran A, Irvin MR, Oldmeadow C, Kim HN, Ryu S, Timmers PRHJ, Arbeeva L, Dorajoo R, Lange LA, Prasad G, Lorés-Motta L, Pauper M, Long J, Li X, Theusch E, Takeuchi F, **Spracklen CN**, Loukola A, Bollepalli S, Warner SC, Wang YX, Wei WB, 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Collaborative manuscripts and banner authorship

1. Wainschtein P, Jain D, Zheng Z, **TOPMed Anthropometry Working Group**, **National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Consortium**,Cupples LA, Shadyab AH, McKnight B,Shoemaker BM, Mitchell BD, Psaty BM, Kooperberg C, Liu CT, Albert CM, Roden D, Chasman DI, Darbar D, Lloyd-Jones DM, Arnett DK, Regan EA, Boerwinkle E, Rotter JI, O’Connell JR, Yanek LR, de Andrade M, Allison MA, McDonald MN, Chung MK, Fornage M, Chami N, Smith NL, Ellinor PT, Vasan RS, Mathias RA, Loos RJF, Rich SS, Lubitz SA, Heckbert SR, Redline S, Guo X, Chen Y-I, Laurie CA, Hernandez RD, McGarvey ST, Goddard ME, Laurie CC, North KE, Lange LA, Weir BS, Yengo L, Yang J, Visscher PM.Assessing the contribution of rare variants to complex trait heritability from whole-genome sequencing data. Nat Genet 2022;54(3):263-273.
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Letter to the Editor

1. **Spracklen CN,** Harland KK, Stegmann BJ, Saftlas AF. Response to Letter to the Editor Re: Cervical surgery for cervical intraepithelial neoplasia and prolonged time to conception of a live birth: a case-control study. *Br J Obstet Gynaec,* 2013;120(13):1697-8.

Submitted manuscripts

1. Saftlas AF, Rigterink E, Rubenstein LM, Triche EW, **Spracklen CN**. Smoking patterns in pregnancy effect risks for preeclampsia and gestational hypertension. Under review *Women’s Health Issues*.
2. Petty LE, Chen HH, Zhu W, Downie CG, Graff M, Boehnke M, Bowden DW, Chambers JC, Mahajan A, McCarthy MI, Ng MCY, Sim X, **Spracklen CN**, Zhang W, Preuss M, Bottinger EP, Nadkarni GN, Loos RJF, Chen YDI, Tan J, Ipp E, Genter P, Emery L, Louie T, Sofer T, North KE, Stilp AM, Gao C, Palmer ND, Norris JM, Wagenknecht LE, Nousome D, Varma R, McKean-Cowdin R, Guo X, Hai Y, Hsueh W, Sandow K, Parra EJ, Cruz M, Valladares-Salgado A, Wacher-Rodarte N, Rotter JI, Goodarzi MO, Rich SS, Bertoni A, Raffel LJ, Nadler JL, Kandeel FR, Duggirala R, Blangero J, Lehman DM, DeFronzo RA, Thameem F, Huerta A, Florez JC, Tusie-Luna T, González-Villalpando C, Orozoco L, Haiman CA, Hanis CL, Rohde R, Whitsel EA, Reiner AP, Kooperberg C, Li Y, Duan Q, Lee M, McCormick JB, Fisher-Hoch SP, Morris AP, Mercader JM, Highland HM, Below JE, on behalf of the DIAMANTE Hispanic/Latino and Global Hispanic Lipids Consortia. Large scale study of cardiometabolic trait genetics in Hispanic/Latino populations identifies novel loci for type 2 diabetes and lipid traits. In revision at *Circulation*.
3. Fairhurst-Hunter Z, Lin K, Millwood I, Pozarickij A, Chen TT, Torres JM, Luan K, Kartsonaki C, Gan W, Mahajan A, Du H, Sohoni R, Guo Y, Sansome S, Yang L, Yu C, Chen Y, Lv J, Hemani G, Koido M, Kamatani Y, **Spracklen CN,** Gordon-Larsen P, Koprulu M, Meng X, Kuchenbaecker K, Fatumo S, Bhatta L, Brumpton B, Alegre-Diaz J, Kuri-Morales P, Tapia-Conter R, Graham S, Willer C, Neville M, Karpe F, Graf M, North K, Loos R, Haiman C, Peters U, Buyske S, Gignoux C, Wojcik G, Lin YF, Li L, McCarthy M, Chen Z, Holmes M, Walters RG. Trans-ancestry meta-analysis improves performance of genetic scores for multiple adiposity-related traits in East Asian populations. In revision at *Nat Genetics*.
4. Suzuki K\*, Hatzikotoulas K\*, Southam L\*, Taylor HJ\*, Yin X\*, Lorenz KM\*, Mandla R\*, Huerta-Chagoya A, Rayner NW, Bocher O, de S. V. Arruda AL, Sonehara K, Namba S, Lee SSK, Preuss MH, Petty LE, Schoeder P, Vanderwerff B, Kals M, Bragg F, Lin K, Guo X, Zhang W, Yao J, Kim YJ, Graff M, Takeuchi F, Nano J, Lamri A, Nakatochi M, Moon S, Scott RA, Cook JP, Lee JJ, Pan I, Talium D, Parra EJ, Chai JF, Bielak LF, Tabara Y, Hai Y, Thorleifsson G, Grarup N, Sofer T, Wuttke M, Sarnowski C, Gieger C, Nousome D, Trompet S, Kwak SH, Long J, Sun M, Tong L, Chen WM, Nongmaithem SS, Noordam R, Lim VJY, Tam CHT, Joo YY, Chen CH, Raffield ML, Prins BP, Nicholas A, Yanek LR, Chen G, Brody JA, Kabagambe E, An P, Xiang AH, Choi HS, Cade BE, Tan J, Broadaway KA, Williamson A, Kamali Z, Cui J, Adair LS, Adeyemo A, Aguilar-Salinas CA, Ahluwalia TS, Anand SS, Bertona A, Bork-Jensen J, Brandslund I, Buchanan TA, Burant CF, Butterworth AS, Canouil M, Chan JCN, Chang LC, Chee ML, Chen J, Chen SH, Chen YT, Chen Z, Chuang LM, Cushman M, Danesh H, Das SK, de Silva HJ, Dedoussis G, Dimitrov L, Doumatey AP, Du S, Duan Q, Eckardt KU, Emery LS, Evans DS, Evans MK, Fischer K, Floyd JS, Ford I, Franco OH, Frayling TM, Freedman BI, Genter P, Gerstein HC, Giedraitis V, Gonzalez-Villalpando C, Gonzalez-Villalpando ME, Gordon-Larsen P, Gross M, Guare LA, Hackinger S, Han S, Hattersley AT, Herder C, Horikoshi M, Howard AG, Hsueh W, Huang M, Huang W, Hung YJ, Hwang MY, Hwu CM, Ichihara S, Ikram MA, Ingelsson M, Islam MT, Isono M, Jang HM, Jasmine F, Jiang G, Jonas JB, Jorgensen T, Kandeel FR, Kasturiratne A,Katsuya T, Kaur V, Kawaguchi T, Keaton JM, Kho AN, Khor CC, Kibriya MG, Kim DH, Kronenberg F, Kuusisto J, Lall K, Lange LA, Lee KM, Lee MS, Lee NR, Leong A, Li L, Li Y, Li-Gao R, Lithgart S, Lindgren CM, Linneberg A, Liu CT, Liu J, Locke AE, Louie T, Luan J, Luk AO, Lou X, Lv J, Lynch JA, Lyssenko V, Maeda S, Mamakou V, Mansuri SR, Matsuda K, Meitinger T, Metspalu A, Mo H, Morris AD, Nadler JL, Nalls MA, Nayak U, Ntalla I, Okada Y, Orozco L, Patel SR, Patil S, Pei P, Pereira MA, Peters A, Pirie FJ, Polikowsky HG, Porneala B, Prasad G, Rasmussen-Torvik LJ, Reiner AP, Roden M, Rohde R, Roll K, Sabanayagam C, Sandow K, Sankareswaran A, Sattar N, Schonherr S, Shahriar M, Shen B, Shi J, Shin DM, Shojima N, Smith JA, So WY, Stancakova A, Steinthorsdottir V, Stilp AM, Strauch K, Taylor KD, Thorand B, Thorsteinsdottir U, Tomlinson B, Tran TC, Tsai FJ, Tuomilehto J, Tusie-Luna T, Udler MS, Valladares-Salgado A, van Dam RM, van Klinken JB, Varma R, Wacher-Rodarte N, Wheeler E, Wickremasinghe AR, van Dijk KW, Witte DR, Yajik CS, Yamamoto K, Yamamoto K, Yoon K, Yu C, Yuan JM, Yusuf S, Zawistowski M, Zhang L, Zheng W, VA Million Veterans Progam, AMED GRIFIN Diabetes Initative Japan, Biobank Japan Project, Penn Medicine Biobank, Regeneron Genetics Center, eMERGE Consortium, International Consortium for Blood Pressure (ICBP), Meta-analysis of Glucose and Insulin-Related Traits Consortium (MAGIC), RaffelLD, Igase M, Ipp E, Redline S, Cho YS, Lind L, Province MA, Fornage M, Hanis CL, Ingelsson E, Zonderman AB, Psaty BM, Wang YX, Rotimi CN, Becker DM, Matsuda F, Liu Y, Yokota M, Kardia SLR, Peyser PA, Pankow JS, Engert JC, Bonnefond A, Froguel P, Wilson JG, Sheu WHH, Wu JY, Hayes MG, Ma RCW, Wong TY, Mook-Kanamori DO, Tuomi T, Chandak GR, Collins FS, Bharadwaj D, Pare G, Sale MM, Ahsan H, Motala AA, Shu XO, Park KS, Jukema JW, Cruz M, Chen YDI, Rich SS, McKean-Cowdin R, Grallert H, Cheng CY, Ghanbari M, Tai ES, Dupuis J, Kato N, Laakso M, Kottgen A, Koh WP, Bowden DW, Palmer CAN, ooner JS, Kooperberg C, Liu S, North KE, Saleheen D, Hansen T, Pedersen O, Wareham NJ, Lee J, Kim BJ, Millwood IY, Walter RG, Stefansson K, Goodarzi MO, Mohlke KL, Langenberg C, Haiman CA, Loos RJF, Florez JC, Rader DJ, Ritchie MD, Zollner S, Magi R, Denny JC, Yamauchi T, Kadowaki T, Chambers JC, Ng MCY, Sim X, Below JE, Tsao PS, Change KM, McCarthy MI\*, Meigs JB\*, Mahajan A\*, **Spracklen CN\***, Mercader JM\*, Boehnke M\*, Rotter JI\*, Vujkovic M\*, Voight BF\*, Morris AP\*, Zeggini E\*. Multi-ancestry genome-wide study in >2.5 million individuals reveals heterogeneity in mechanistic pathways of type 2 diabetes and complications. Under review at *Nature*.
5. Sarsani VTr, Brotman S, Xianyong Y, Fernandes Silva L, Laakso M, **Spracklen CN**. A multi-ancestry genome-wide meta-analysis, fine-mapping, and target gene prioritization to characterize the genetic architecture of adiponectin. Under review at *HGG Advances*. Available on medRxiv: <https://www.medrxiv.org/content/10.1101/2023.05.02.23289402v1>
6. Daniele CTr, Farland LV, Manson J, Qi L, Shadyab AH, Smoller S, **Spracklen CN**. Associations between birthweight and preterm birth and the ages of menarche and menopause. Under review at *International Journal Epidemiology.*

Manuscripts in preparation

1. Zhao CTr, Wagner KTr, Darst B, Highland H, Balasubramanian R, Garcia DO, Garcia L, Lamonte M, LeBlanc ES, Liu S, Ma Y, Nassir R, Phillips LS, Saquib N, Shadyab AH, Tabung FK, Manson J, **Spracklen CN**. Associations of combined genetic and lifestyle risks with incident diabetes in the Women’s Health Initiative.
2. Zhao CTr, Jackson K, Wu Y, Shi J, Huang W, Yuan W, Wang Y, Luo J, Popkin BM, Du S, Gordon-Larsen P, Mohlke KL, **Spracklen CN**. Genome-wide and conditional analyses reveal novel lipid signals.
3. Eroglu A, Kursawe R, Bhuiyan R, Thibodeau A, Zhang L, **Spracklen CN**, Ucar D\*, Stitzel ML\*. Integrated single cell genomics define T2D variant effects on shared and cell type-specific human islet *cis*-regulatory element use.
4. Rahalkar NTr, Holman-Vittone ATr, Daniele CTr, Wacks RTr, Gagnon ATr, D’Agata A, Saquib N, Schnatz PF, Sullivan M, Wallace R, **Spracklen CN**. Preterm birth, maternal birthweight, and subsequent risk for depression.
5. Bhuiyan RMTr, Kursawe R, Zhao CTr, Selvam V, Tamtam H, Krishnan S, Ucar D, **Spracklen CN\***, Stitzel ML\*. Multiomic profiling of steady state and inflammatory stress-responsive human islet *cis*-regulatory networks reveal context-specific diabetes risk variant effects.
6. Daniele C Tr, Garcia L, LeBlanc ES, Rillamas-Sun E, Robinson JG, Sarto GE, Sturgeon S, Tindle H, Tylavsky F, Van Horn L, Wallace R, Waring M, White M, Ryckman KK, **Spracklen CN**. Association between birthweight and preterm birth and subsequent risk of hypertension in postmenopausal women from the Women’s Health Initiative.

**PRESENTATIONS**

*Tr denotes trainee supervised by Cassandra Spracklen*

*\* first author listed is the presenter*

Invited oral presentations

1. American Diabetes Association Annual Meeting, June 2023
2. Gordon Research Conference, Quantitative Genetics and Genomics, February 15, 2023.
3. Jackson Laboratories for Genomic Medicine Seminar Series, March 11, 2020
4. University of Massachusetts Medical School, Endocrine Grand Rounds, November 2019
5. University of Delaware, Department of Epidemiology Seminar, January 2019
6. University of Colorado-Denver, Division of Bioinformatics and Personalized Medicine Seminar, December 2018
7. University of Massachusetts Amherst, Department of Biostatistics and Epidemiology Seminar, November 2018
8. University of Michigan, Institute for Social Research Seminar, May 2018
9. University of North Carolina, Department of Epidemiology Cardiovascular Epidemiology  
   Seminar, September 2017
10. University of North Carolina, Department of Genetics Research Colloquium, May 2017
11. University of Iowa, Department of Epidemiology Seminar, March 2017
12. University of Iowa, Department of Epidemiology Seminar, May 2014
13. Case Western Reserve University, Department of Epidemiology and Biostatistics  
    Seminar, April 2014

Abstract oral presentations

1. Mandla R, Lorenz K, Yin X, Southam L, Suzuki K, Hatzikotoulas K, Taylor H, Huerta A, Rayner N, DIAMANTE Consortium, VA Million Veterans’ Program, Meigs J, McCarthy M, Mahajan A, **Spracklen CN**, Boehnke M, Vujkovic M, Rotter J, Voight B, Zeggini E, Morris A, Mercader J, T2DGGI. Identification of 489 type 2 diabetes shared and tissue specific effector genes by integrating eQTL data with a multi-ancestry GWAS of 2.5 million individuals. *American Diabetes Association Annual Meeting,* San Diego, CA, June 2023 (Upcoming).
2. Suzuki K, Hatzikotoulas K, Southam L, Yin X, Lorenz K, Mandla R, Taylor H, Huerta A, Rayner N, DIAMANTE Consortium, VA Million Veterans’ Program, Meigs J, McCarthy M, Mahajan A, **Spracklen CN**, Boehnke M, Vujkovic M, Rotter J, Voight B, Zeggini E, Morris A, Mercader J, T2DGGI. Multi-ancestry genome-wide association study reveals distinct biological pathways and cell types driving type 2 diabetes risk with heterogeneous effects across diverse populations. *American Diabetes Association Annual Meeting,* San Diego, CA, June 2023.
3. Mandla R, Lorenz K, Yin X, Southam L, Suzuki K, Hatzikotoulas K, Taylor H, Huerta A, Rayner N, DIAMANTE Consortium, VA Million Veterans’ Program, Meigs J, McCarthy M, Mahajan A, **Spracklen CN**, Boehnke M, Vujkovic M, Rotter J, Voight B, Zeggini E, Morris A, Mercader J, T2DGGI. Identification of 489 type 2 diabetes shared and tissue specific effector genes by integrating eQTL data with a multi-ancestry GWAS of 2.5 million individuals. *CHARGE Consortium Annual Meeting,* Boston, MA, May 2023.
4. Bhuiyan RMTr, Kursawe R, **Spracklen CN,** Ucar D, Stitzel ML. Integrated ca/eQTL analyses uncover diabetes GWAS variants modulating human islet proinflammatory cytokine responses. *American Society for Human Genetics Annual Meeting*, Los Angeles, CA, October 2022.
5. Sarsani VTr, Brotman S, **Spracklen CN**. Multi-ancestry meta-analysis, fine-mapping, and target gene prioritization to characterize the genetic architecture of adiponectin. *American Society for Human Genetics Annual Meeting*, Los Angeles, CA, October 2022.
6. Hatzikotoulas K, Southam L, Suzuki K, Yin X, **Spracklen CN**, Rayner NW, DIAMANTE Consortium, Million Veterans’ Program, Vujkovic M, Mahajan A, Rotter JI, Voight BF, Zeggini E, Morris AP. Multi-ancestry genome-wide association study in >2.5 million individuals reveals distinct biological pathways driving type 2 diabetes susceptibility with heterogeneous effects across diverse population groups. *American Society for Human Genetics Annual Meeting*, Los Angeles, CA, October 2022.
7. Tai ES, **Spracklen CN,** Horikoshi M, Kim YJ, Sim X, on behalf of the AGEN and DIAMANTE consortia. Ethnically determined diabetes variants (Asian Diabetes). Keystone Symposium, March 2019.
8. **Spracklen CN,** Horikoshi M, Kim YJ, Iyengar A, Lim VJY, AGEN consortium, DIAMANTE consortium, Mohlke KL, Sim X. Genetic architecture of type 2 diabetes in non-European populations: genome-wide meta-analysis in 283,422 East Asians identifies 32 new loci associated with type 2 diabetes. *Quantitative Genetics and Genomics Gordon Research Seminar,* Lucca, Italy, February 2019. [**Travel award winner]**
9. **Spracklen CN,** Sim X, Kim YJ, Horikoshi M, on behalf of the AGEN and DIAMANTE consortia. Meta-analysis in 283,579 East Asians identifies 28 new loci associated with type 2 diabetes. *American Society for Human Genetics Annual Meeting*, San Diego, CA, October 2018. [**ASHG Charles J. Epstein Trainee Award for Excellence in Human Genetics Award, Finalist]**
10. **Spracklen CN**, Jackson AU, Stringham HM, Wu Y, Civelek M, Fuchsburger C, Locke AE, Welch R, Chines PS, Narisu N, Lusis AJ, Kuusisto JK, Collins FS, Boehnke M, Laakso M, Mohlke KL. Fine-mapping GWAS loci containing extensive allelic heterogeneity reveals complex patterns of association. *American Society for Human Genetics Annual Meeting*, Baltimore, MD, 2015.
11. **Spracklen CN**, Harland KK, Stegmann BJ, Saftlas AF. Cervical surgery for cervical intraepithelial neoplasia and prolonged time to conception of a live birth: a case-control study. *Society for Epidemiological Research Annual Meeting*, Boston, MA, 2013.

Poster presentations

1. Zhao CTr, **Spracklen CN**. Genome-wide association study of lipids in the China Health and Nutrition Survey. *American Society for Human Genetics Annual Meeting,* Washington DC, Nov 2023 (Upcoming).
2. Walters RG, Siderenko J, Lin K, Pozarickij A, Young K, Berndt S, Lu Y, Vedantam S, Yengo L, **Spracklen CN**, on behalf of the GIANT Consortium. Comparative analysis of fine-mapping methods at loci with multiple association signals. *American Society for Human Genetics Annual Meeting,* Washington DC, Nov 2023 (Upcoming).
3. Mandla R, Lorenz K, Yin X, Bocher O, Southam L, Suzuki K, Hatzikotoulas K, Taylor H, Huerta A, Arrua AL, Rayner N, DIAMANTE Consortium, VA Million Veterans’ Program, Meigs J, McCarthy M, Mahajan A, **Spracklen CN**, Boehnke M, Vujkovic M, Rotter J, Voight B, Zeggini E, Morris A, Mercader J, T2DGGI. Integrative analysis of multi-ancestry GWAS of 2.5 million individuals with multiple omics and quantitative trait datasets identifies effector transcripts, proteins, and metabolites for 528 type 2 diabetes loci. *American Society for Human Genetics Annual Meeting,* Washington DC, Nov 2023 (Upcoming).
4. Zhao CTr, **Spracklen CN**. Genome-wide association study of lipids in the China Health and Nutrition Survey. *University of Massachusetts Amherst School of Public Health and Health Sciences Research Day*, April 14, 2023.
5. Rahalkar NTr, Holman-Vittone ATr, Gagnon ATr, D’Agata A, Saquib N, Schnatz PF, Sullivan M, Wallace R, **Spracklen CN**. Preterm birth, maternal birthweight, and subsequent risk for depression. *University of Massachusetts Amherst School of Public Health and Health Sciences Research Day*, April 14, 2023.
6. Wacks RTr, Fieldman STr, **Spracklen CN**. Early age of menarche increases a woman’s risk for adverse pregnancy and reproductive outcomes in the Women’s Health Initiative. *University of Massachusetts Amherst School of Public Health and Health Sciences Research Day*, April 14, 2023.
7. Daniele CPTr, Ryckman KK, **Spracklen CN**. Association of maternal birthweight and preterm birth with subsequent risk for hypertension in women from the Women’s Health Initiative. *University of Massachusetts Amherst School of Public Health and Health Sciences Research Day*, April 14, 2023.
8. Suzuki K, Southam L, Hatzikotoulas K, Yin X, **Spracklen CN,** Rayner NW, DIAMANTE Consortium, Million Veterans’ Program, Vujkovic M, Mahajan A, Rotter JI, Voight BF, Zeggini E, Morris AP. Integrative analysis of large-scale multi-ancestry genome-wide association study and single-cell omics data provides high-resolution insight of cell-types in the pathogenesis of type 2 diabetes. *American Society for Human Genetics Annual Meeting*, Los Angeles, CA, October 2022.
9. Bhuiyan RMTr, Kursawe R, **Spracklen CN,** Ucar D, Stitzel ML. Integrated ca/eQTL analyses uncover diabetes GWAS variants modulating human islet proinflammatory cytokine responses. *MD PhD National Student Conference*, Copper Mountain, CO, July 2022.
10. Daniele CPTr, Smoller SW, **Spracklen CN**. Associations between maternal birthweight and preterm birth and subsequent reproductive and pregnancy outcomes. *Massachusetts Undergraduate Research Conference*, April 22, 2022.
11. Holman-Vittone ATr, LeBlanc ES, Liu S, Nassir R, Saquib N, Schnatz PF, Shadyab AH, Sinkey R, Wactawski-Wende J, Wild RA, Chasan-Taber L, **Spracklen CN**. Preterm birth and subsequent risk of type 2 diabetes among postmenopausal women in the Women’s Health Initiative. *University of Massachusetts Amherst School of Public Health and Health Sciences Research Day*, April 6, 2022.
12. Fields CTr and **Spracklen CN.** The effect of the microbiome on rheumatoid arthritis risk: literature review and steps for the future. *University of Massachusetts Amherst School of Public Health and Health Sciences Research Day*, April 6, 2022.
13. Daniele CPTr, Smoller SW, **Spracklen CN**. Associations between maternal birthweight and preterm birth and subsequent reproductive and pregnancy outcomes. *University of Massachusetts Amherst School of Public Health and Health Sciences Research Day*, April 6, 2022.
14. **Spracklen CN**, on behalf of the Meta-Analysis of Glucose and Insulin-related traits Consortium (MAGIC) Investigators. Trans-ancestral genomic architecture of glycemic traits. *CHARGE Consortium Annual Meeting,* Virtual, May 2021.
15. Salo NTr and **Spracklen CN**. An analysis of the relationship between maternal depression and preterm birth risk among racial and ethnic groups. University of Massachusetts Amherst School of Public Health and Health Sciences Research Day, Virtual, April 2021.
16. Monahan BTr, Farland LV, Shadyab AH, Manson JE, **Spracklen CN**. Birthweight and subsequent risk of autoimmune and thyroid conditions. University of Massachusetts Amherst School of Public Health and Health Sciences Research Day, Virtual, April 2021.
17. **Spracklen CN,** Horikoshi M, Kim YJ, Lin K, on behalf of the AGEN and DIAMANTE constorita. Meta-analysis in 433,530 East Asians identifies 49 new loci associated with type 2 diabetes. *American Society for Human Genetics Annual Meeting*, Houston, TX, October 2019. **[Reviewer’s Choice Abstract]**.
18. Wittemans LBL, Lu Y, Yaghootkar H, Preuss MH, Erzurumluoglu AM, Hemerich D, Ji Y, Karaderi T, Schurmann C, **Spracklen CN,** Huang LO, Day FR, Zilikens MC, Frayling T, Kutalik Z, Kilpelainen TO, Langenberg C, Mohlke KL, Lindgren CM, Loos RJF, on the Genetics of Body Composition Consortium. Integration of body fat and lean mass loci reveals genetic clusters with distinct cardiometabolic effects. *American Society for Human Genetics Annual Meeting*, Houston, TX, October 2019.
19. **Spracklen CN,** Horikoshi M, Kim YJ, Iyengar A, Lim VJY, AGEN consortium, DIAMANTE consortium, Mohlke KL, Sim X. Genetic architecture of type 2 diabetes in non-European populations: genome-wide meta-analysis in 283,422 East Asians identifies 32 new loci associated with type 2 diabetes. *Quantitative Genetics and Genomics Gordon Research Conference,* Lucca, Italy, February 2019.
20. **Spracklen CN**, Jackson AU, Iyengar A, Vadlamudi S, Stringham HM, Raulerson CK, Cannon ME, Currin K, Wu Y, Fuchsburger C, Welch R, Chines PS, Narisu N, Kuusisto JK, Pajukanta P, Collins FS, Boehnke M, Laakso M, Mohlke KL. Fine-mapping and characterization of adiponectin GWAS loci harboring extensive allelic heterogeneity. *American Heart Association Epi/Lifestyle Annual Meeting*, New Orleans, LA, March 2018 **[Moderated Poster Session]**.
21. **Spracklen CN**, Jackson AU, Iyengar A, Vadlamudi S, Stringham HM, Wu Y, Cannon ME, Civelek M, Currin K, Fuchsburger C, Locke AE, Welch R, Chines PS, Narisu N, Lusis AJ, Kuusisto JK, Collins FS, Boehnke M, Laakso M, Mohlke KL. Fine-mapping and characterization of GWAS loci harboring extensive allelic heterogeneity. *American Society for Human Genetics Annual Meeting*, Orlando, FL, October 2017 **[Reviewer’s Choice Abstract]**.
22. Sim X, Horikoshi M, **Spracklen CN**, Kim YJ, AGEN DIAMANTE Consortium. Meta-analysis in 93,701 East Asians identifies new loci associated with type 2 diabetes. *American Society for Human Genetics Annual Meeting*, Orlando, FL, October 2017. [**Reviewer’s Choice Abstract]**
23. **Spracklen CN**, Sim X, Chen P, Kim YJ, Wang X, Cai H, Li S, Long J, Wu Y, Wang YX, Takeuchi F, Wu JY, Jung KJ, Akiyama K, Zhang Y, Hou X, Hiu C, Moon S, Johnson TA, Li H, Dorajoo R, He M, Mohlke KL, AGEN Consortium. Association analyses of up to 72,043 East Asian individuals and trans-ancestry analyses with up to 186,265 European individuals reveal new loci associated with cholesterol and triglyceride levels. *American Society for Human Genetics Annual Meeting*, Vancouver, BC, October 2016.
24. **Spracklen CN,** Ryckman KK, Harland KK, Saftlas AF. Effects of smoking and preeclampsia on birth weight for gestational age. *Society for Pediatric and Perinatal Epidemiologic Research Annual Meeting*, Seattle, WA, June 2014.
25. **Spracklen CN,** Sealy-Jefferson S, Wallace RB, Robinson JG, Freudenheim JL, Wellons MF, Saftlas AF, Snetselaar LG, Manson JE, Hou L, Qi L, Chlebowski RT, Ryckman KK. Birth weight and subsequent risk of cancer in postmenopausal women. *University of Iowa Holden Comprehensive Cancer Center Scientific Retreat*, Coralville, IA, June 2014.
26. **Spracklen CN,** Sealy-Jefferson S, Wallace RB, Robinson JG, Freudenheim JL, Wellons MF, Saftlas AF, Snetselaar LG, Manson JE, Hou L, Qi L, Chlebowski RT, Ryckman KK. Birth weight and subsequent risk of cancer. *University of Iowa Epidemiology Departmental Poster Session*, Iowa City, IA, May 2014.

1. **Spracklen CN,** Sealy-Jefferson S, Wallace RB, Robinson JG, Freudenheim JL, Wellons MF, Saftlas AF, Snetselaar LG, Manson JE, Hou L, Qi L, Chlebowski RT, Ryckman KK. Birth weight and subsequent risk of cancer. *Pediatric Academic Societies Annual Research Meeting*, Vancouver, BC, May 2014.
2. **Spracklen CN,** Ryckman KK, Wallace RB, Garcia L, Tylavsky FA, Howard BV, Liu S, Song Y, Rillamas-Sun E, LeBlanc ES, White MV, Parikh NI, Robinson JG. Birth weight and the risk of type 2 diabetes mellitus in postmenopausal women. *University of Iowa Health Sciences Research Week*, Iowa City, IA, April 2014.
3. **Spracklen CN,** Ryckman KK, Wallace RB, Garcia L, Tylavsky FA, Howard BV, Liu S, Song Y, Rillamas-Sun E, LeBlanc ES, White MV, Parikh NI, , Robinson JG. Birth weight and the risk of type 2 diabetes mellitus in postmenopausal women. *University of Iowa International Cardiovascular Research Center Symposium*, Iowa City, IA, October 2013.
4. **Spracklen CN,** Gryzlak BM, Rubenstein LM, Chrischilles EA. Computer and Health IT Use Among Older Iowa Adults. *University of Iowa Epidemiology Departmental Poster Session*, May 2011.

Oral and poster presentations (banner authorship from ongoing consortia work)

1. Josyula NS, Chittoor G, Graff M, Wilson W, Wang Z, Lin M, Chin HH, Linchangco G, Justice AE, on behalf of the GIANT Waist Traits Working Group. Phenome-wide association study of polygenic risk for central adiposity. *International Genetic Epidemiology Society Annual Meeting*, Nashville, TN November 2023 (*Upcoming).*
2. Wilson EP, Kim D, Diez-Obrero V, Vedantam S, Bartell E, Pozarickij A, Fairhurst-Hunter Z, Marouli E, Young KL, Graff M, Arias JD, Chittoor G, Berndt SI, Winkler TW, Lingren CM, Loos R, North K, Walters RG, Mohlke KL, Justice AE, on behalf of the **GIANT Consortium**. Multi-population GWAS meta-analysis detects potential genes for central obesity. *American Society for Human Genetics Annual Meeting*, Washington DC, November 2023 (*Upcoming).*
3. Zeggini E, Hatzikotoulas K, Southam L, Suzuki K, Yin X, Lorenz KM, **DIAMANTE Consortium**, Million Veterans’ Program. Multi-ancestry genome-wide association study in 2.5 million individuals reveals distinct biological pathways driving type 2 diabetes susceptibility with heterogeneous effects across diverse population groups. *International Congress of Human Genetics Annual Meeting*, Cape Town, South Africa February 2023.
4. Suzuki K, Southam L, Hatzikotoulas K, Yin X, Vujkovic M, **DIAMANTE Consortium**, Million Veterans’ Program. Integrative analysis of genetic and single-cell omics data reveals cell-types in the pathogenesis of type 2 diabetes. *International Diabetes Federation Annual Meeting*, Lisbon, Portugal, December 2022.
5. Morris AP, Hatzikotoulas K, Southam L, Suzuki K, Yin X, Vujkovic M, **DIAMANTE Consortium**, Million Veterans’ Program. Multi-ancestry genome-wide association study reveals distinct biological pathways driving type 2 diabetes susceptibility. *International Diabetes Federation Annual Meeting*, Lisbon, Portugal, December 2022.
6. Li X, Li Z, Brody J, Ferrier K, Hirschhorn J, Liu CT Lange L, Lin X, on behalf of the **TOPMed Anthropometry-Adiposity Working Group.** Whole genome sequencing analyses of 87,652 individuals reveal rare variants in promoter of HMGA1 associated with height. *American Society for Human Genetics Annual Meeting*, Los Angeles, CA, October 2022.
7. Wilson EP, Vedantam S, Fairhurst-Hunter A, Marouli E, Arias JD, Chittoor G, Berndt SI, Winkler TW, Young KL, Graff M, Liu CT, Lindgren CM, Mohlke KL, Justice AE, on behalf of the **Gentic Investigation of Anthropometric Traits (GIANT) Consortium**. GWAS meta-analysis of WHRadjBMI identifies differences across sexes and populations. *American Society for Human Genetics Annual Meeting*, Los Angeles, CA, October 2022.
8. Josyula NS, Chittoor G, Graff M, Wilson E, North KE, eMERGE, GIANT consortium, Mohlke KL, Justice AE, on behalf of the **GIANT Waist Traits Working Group**. Phenome-wide association study of polygenic risk for central adiposity. *American Society for Human Genetics Annual Meeting*, Los Angeles, CA, October 2022.
9. Morris AP, Hatzikotoulas K, Southam L, Suzuki K, Yin X, Lorenz KM, **DIAMANTE Consortium**, VA Million Veteran Program. Multi-ancestry genome-wide association study in >2.5 million individuals reveals distinct biological pathways driving type 2 diabetes susceptibility with heterogeneous effects across diverse population groups. *CHARGE Consortium Annual Meeting, Seattle*, October 2022.
10. Li Z, Li X, Zhou H, Brody J, Graff M, Lange L, North K, Lin X, on behalf of the **TOPMed Anthropometry-Adiposity Working Group**. Whole genome sequence association analysis of body mass index in 45,159 individuals of the TOPMed program. *American Society for Human Genetics Annual Meeting*, Houston, TX, October 2019.
11. Raffield LM, Vuckovic D, Bao EL, Lareau CA, Jiang T, Chen MH, Akbari P, Mousas A, Reiner A, Johnson AD, Auer P, Lettre G, Sankaran VG, Soranzo N, on behalf of the **BCX consortium**. Large scale GWAS identifies clinically relevant rare variation for blood cell traits. *American Society for Human Genetics Annual Meeting*, Houston, TX, October 2019.
12. Chen J. on behalf of the **MAGIC consortium**. Leveraging ancestry differences for glycaemic trait locus discovery and fine-mapping. *EASD Study Group on the Genetics of Diabetes*, May 2019.
13. Vedantam S, Locke AE, Marouli E, Berndt S, Yengo L, Wood AR, Ferreira T, Graham S, on behalf of the **GIANT consortium**. Large scale meta-analysis of genome-wide association studies for height in multipke ancestries. *American Society for Human Genetics Annual Meeting*, San Diego, CA, October 2018.
14. Locke AE, Vedantam S, Marouli E, Berndt S, Yengo L, Wood AR, Ferreira T, Graham S, on behalf of the **GIANT consortium**. Global, multi-ethnic genome-wide association meta-analysis of body mass index. *American Society for Human Genetics Annual Meeting*, San Diego, CA, October 2018.
15. Chen J, on behalf of the **MAGIC Consortium** Investigators. Large trans-ethnic discovery identifies distinct genomic and expression signatures in glycemic traits. *American Society for Human Genetics Annual Meeting*, San Diego, CA, October 2018.
16. Mahajan A, Kitajima H, Sim X, Ng MCY, Zhang W, Below JE, Payne A, Gaulton KJ, and Morris AP on behalf of the **DIAMANTE Consortium**. Discovery and fine-mapping of type 2 diabetes susceptibility loci in diverse populations using more than a million individuals. *American Diabetes Association Annual Meeting*, Orlando, FL, June 2018.
17. Mahajan A on behalf of the **DIAMANTE Consortium**. Expandng the spectrum of type 2 diabetes predisposing alleles through genome-wide association study imputed up to Haplotype Reference Consortium reference panel*. European Society for Human Genetics Annual Meeting*, Milan, Italy, June 2018.
18. Morris AP on behalf of the **DIAMANTE Consortium**. Discovery and fine-mapping of type 2 diabetes susceptibility loci in diverse populations. *CHARGE Annual Meeting 2018*.
19. Marenne G on behalf of the **MAGIC Investigators.** Trans-ethnic analyses using densely imputed genetic data: novel loci discoveru for glycemic traits. *French Conference of Human and Medical Genetics Meeting*, Nantes, France, January 2018.
20. Langenberg C on behalf of the **MAGIC Investigators**. Trans-ethnic discovery analyses of the genetic architecture of glycaemic control. *American Society for Human Genetics Annual Meeting*, Orlando, FL, October 2017. [**Reviewer’s Choice Abstract]**
21. Mahajan A, Kitajima H, Sim X, Ng M, Zhang W, Below JE, Taliun D, Gaulton KJ, Morris AP, **DIAMANTE Consortium**. Discovery and fine-mapping of type 2 diabetes susceptibility loci across ethnically diverse populations. *American Society for Human Genetics Annual Meeting*, Orlando, FL, October 2017.
22. Chen J. on behalf of the **MAGIC Investigators**. Exploring the use of Fuzzy clustering approaches to classify HbA1c associated signals into glycaemic and/or erythrocyte pathways. *International Genetic Epidemiology Society Annual Meeting*, Cambridge, UK, September 2017.
23. Below, JE on behalf of the **DIAMANTE Consortium**. Discovery and fine mapping of type 2 diabetes susceptibility loci across diverse populations. *International Genetic Epidemiology Society Annual Meeting*, Cambridge, UK, September 2017.
24. Morris A, on behalf of the **DIAMANTE Consortium**. Discovery and fine-mapping of type 2 diabetes susceptibility loci in diverse populations. *Genomics of Complex Diseases Annual Meeting*, Cambridge, UK, September 2017.
25. Locke AE on behalf of **GIANT Consortium**. Global GWAS meta-analysis of anthropometric traits in >1 million individuals. *Genomics of Complex Diseases Annual Meeting*, Cambridge, UK, September 2017.
26. Kitajima H, Mahajan A, Sim X, Ng M, Zhang W, Below JE, Taliun D, Gaulton KJ, Morris AP, **DIAMANTE Consortium**. Discovery and fine-mapping of type 2 diabetes susceptibility loci across diverse populations. *American Diabetes Association Annual Meeting*, San Diego, CA, June 2017.
27. Sim X, Horikoshi M, **AGEN Consortium**. Meta-analysis of 93,838 East Asians identifies new loci associated with type 2 diabetes. *American Diabetes Association Annual Meeting*, San Diego, CA, June 2017.

**RESEARCH GRANTS AND FELLOWSHIPS**

Active grants

Jan 2023-Dec 2023 *2023 Quantitative Genetics and Genomics Gordon Research Conference and*Role: PI *Seminar*

R13HG012696 (Cassandra N. Spracklen, PI)

NIH/NHGRI R13 Scientific Meeting Grant

Project description: The major goal of this proposal is to seek partial support for the Gordon Research Conference and Gordon Research Seminar on Quantitative Genetics and Genomics: Leveraging High-Throughput Phenotyping Techniques to Study Complex Traits to be held in Ventura, California on February 11-17, 2023

Direct costs: $10,000 (total); $0 (UMass)

Impact score: 21 (no percentile provided)

July 2022-June 2024 *Trans-ethnic genetic architecture of obesity and glycemic traits*

Role: PI2L30DK126146-02 (Cassandra Spracklen, PI)

NIH/NIDDK Loan Repayment Program (LRP) Renewal

Project description: The major research goals during the LRP period are:1) to use trans-ancestry approaches to identify comprehensive sets of plausible candidate variants at established and novel loci for glycemic traits and obesity. From the list of candidate variants, 2) identify potentially causal metabolic disease variants and elements that exhibit functional regulatory elements.

Direct cost: $38,250 total; $0 (UMass)

Impact score: not provided

Mar 2022-Mar 2024 *Dissecting the Roles of Type 2 Diabetes-associated SNPs and Effector Genes in*Role: Co-mentor *Islet Endoplasmic Reticulum Stress Response*

F30DK130582-01A1 (Redwan Bhuiyan, PI, Jackson Labs)

NIH/NIDDK Predoctoral Fellowship for MD/PhD

Project description: The major goal of this proposal is to identify type 2 diabetes-associated variants that alter pancreatic islet and/or beta-cell stress-responsive *cis-*regulatory element activity and to assess the effects of the stress responsive effector genes on islet function and resilience.

Direct costs: $169,096 (total); $0 (UMass)

Impact score: 20 (no percentile provided)

Dec 2020-Nov 2024 *Genetic Programming on Human Islet Metabolic and Endoplasmic Reticulum (ER)*Role: Co-Inv *Stress Responses in Diabetes*

R01DK118011-01A1 (Michael Stitzel, PI, Jackson Labs)

NIH/NIDDK R01 Research Project Grant

Project description: The major goal of this proposal is to dissect the genetic regulation of human islet metabolic and ER stress responses and to determine how genetic variants associated with type 2 diabetes modulate the responses to contribute to islet dysfunction and type 2 diabetes pathogenesis.

Direct costs: $2,614,367 (total); $232,850 (UMass)

Impact score: 24 (8%)

Nov 2022-Nov 2025 *Using the genetic architecture of glycemic traits and obesity to elucidate the*Role: PI *mechanisms underlying type 2 diabetes development and predict personal  
 T2D risk*

11-22-JDFPM-06 (Cassandra N. Spracklen, PI)

ADA Precision Medicine and Diabetes Jr. Faculty Development Award

Project description: The major research goals of this project are: 1) to use trans-ancestry approaches to identify comprehensive sets of plausible candidate variants at established and novel loci for glycemic traits and obesity. From the list of candidate variants, 2) identify potentially causal metabolic disease variants and elements that exhibit functional regulatory elements, and 3) create and fine-tune polygenic/genetic risk scores for predicting T2D risk.

Direct costs: $414,000 (total; UMass)

Impact score: not provided

July 2023-June 2027 *Type 2 diabetes risk variant effects on mitochondrial (patho)physiology*Role: Co-InvR01DK136671-01 (Scott Soleimanpour and Michael Stitzel, MPIs)

NIH/NIDDK R01 Research Project Grant

Project description: The major goal of this proposal is to identify type 2 diabetes-associated variants that alter pancreatic islet and/or beta-cell stress-responsive *cis-*regulatory element activity and to assess the effects of the stress responsive effector genes on islet function and resilience.

Direct costs: $2,99,166 (total); $71,839 (UMass)

Impact score: 21 (5%)

Pending grants

Submitted Feb 2023 *Analysis, interpretation, and fine-mapping of genetic and genomic data from*Role: PI *single- and multi-ancestry populations* R01HG013324 (Cassandra N. Spracklen, PI)

NIH/NHGRI R01 Research Project Grant

Project description: The major goal of this project is to establish the most feasible and robust analytical pipelines for performing genetic analyses in ancestrally diverse populations through rigorous simulations, benchmarking, and methods optimization.

Direct costs: $2,297,566 (total); $1,768,903 (UMass)

Impact score: 40 (32%) – *Awaiting council decision*

Previous funding

July 2020-June 2022 *Single- and trans-ethnic genetic architecture of obesity and glycemic traits*

Role: PI1L30DK126146-01 (Cassandra Spracklen, PI)

NIH/NIDDK Loan Repayment Program (LRP)

Project description: The major research goals during the LRP period are:1) to use single- and trans-ethnic approaches to identify comprehensive sets of plausible candidate variants at established and novel loci for glycemic traits and obesity. From the list of candidate variants, 2) identify potentially causal metabolic disease variants and elements that exhibit functional regulatory elements.

Direct cost: $59,332.58 total; $0 (UMass)

Impact score: not provided

July 2017-June 2019 *Single- and trans-ethnic genetic architecture of obesity and glycemic traits*

Role: PI17POST33650016 (Cassandra N. Spracklen, PI)  
 American Heart Association Postdoctoral Fellowship

Project description: The major goal of this postdoctoral fellowship is to use trans-ancestry genotype and phenotype data from large consortia to identify and fine-map loci associated with cardiometabolic traits and guide laboratory assays to identify allelic effects on gene expression at prioritized loci.

Direct cost: $106,532 (total; UNC)

Impact score: not provided

July 2015-June 2017 *Trans-ancestry Genetic Architecture of Circulating Lipid and C-reactive Protein*Role: PI *Levels*

15POST24470131 (Cassandra N. Spracklen, PI)  
 American Heart Association Postdoctoral Fellowship

Project description: The major goal of this postdoctoral fellowship is to use trans-ancestry genotype and phenotype data from large consortia to identify and fine-map loci associated with cardiometabolic traits and guide laboratory assays to identify allelic effects on gene expression at prioritized loci.

Direct cost: $86,000 (total; UNC)

Impact score: not provided

Submitted grant proposals

Submitted June 2022 *Characterization of sarcomere variants of unknown significance in health and*Role: Collaborator *disease*

R01HL167727-01 (J. Travis Hinton, Hesham Sadek, Mark Mercola, MPI)

NIH/NHLBI R01 Research Project Grant

Project description: The major goal of this project is to use a combination of genomics and 3D microtissue models to both functionally interrogate sarcomere variants of unknown significance and study the role of sex-dependent genetic modifiers.

Direct costs: $2,477,238 (total); $42,215 (UMass)

Impact score: Not discussed

Submitted Mar 2022 *Analysis, interpretation, and fine-mapping of genetic and genomic data from* Role: PI *single- and trans-ancestry populations*

R01HG012879 (Cassandra N. Spracklen, PI)

NIH/NHGRI R01 Supporting Talented Early Career Researchers in Genomics

Project description: The major goal of this project is to establish the most feasible and robust analytical pipelines for performing genetic analyses in ancestrally diverse populations through rigorous simulations, benchmarking, and methods optimization.

Direct costs: $3,388,704 (total); $2,802,079 (UMass)

Impact score: 37

Submitted Mar 2022 *Genetic regulation of islet mitochondrial health and dysfunction in T2D*Role: Co-InvR01DK132534-01A1 (Scott Soleimanpour and Michael Stitzel, MPIs)

NIH/NIDDK R01 Research Project Grant

Project description: The major goal of this proposal is to identify type 2 diabetes-associated variants that alter pancreatic islet and/or beta-cell stress-responsive *cis-*regulatory element activity and to assess the effects of the stress responsive effector genes on islet function and resilience.

Direct costs: $2,499,428 (total); $42,215 (UMass)

Impact score: 35 (28%)

Submitted Jan 2022 *Gene expression in visceral adipose tissues and functional validation of T2D loci*Role: CollaboratorOFIRG21nov-0048 (Xueling Sim, PI, National Univ. of Singapore)

National Medical Research Council Individual Research Grant, Singapore

Project description: The major goal of this project is to generate visceral adipose eQTLs in East Asian individuals to identify target genes for downstream candidate gene regulation in the relevant cell type for T2D pathogenesis.

Direct costs: Singapore Dollars $1,000,000 (total); $0 (UMass)

Impact score: not provided

Submitted Dec 2021 *Trans-Ancestry Genetic Architecture of Adiponectin and Its Role in Coronary*Role: PI  *Heart Disease*

AHA ID: 931672 (Cassandra N. Spracklen, PI)

American Heart Association Career Development Award

Project description: The major goals of this project are: 1) to use single- and trans-ethnic approaches to identify comprehensive sets of plausible candidate variants at established and novel loci for adiponectin. From the list of candidate variants: 2) identify potentially causal metabolic disease variants and elements that exhibit functional regulatory elements, and 3) use genetic risk scores for prediction of CHD and Mendelian randomization to assess for causality between adiponectin and CHD

Direct costs: $231,000 (total; UMass)

Impact score: 32.96%

Submitted Dec 2021 *Using the genetic architecture of glycemic traits and obesity to elucidate the* Role: PI *mechanisms underlying type 2 diabetes development and predict personal  
 T2D risk*

ADA ID: 123357 (Cassandra N. Spracklen, PI)

American Diabetes Association Precision Medicine & Diabetes Jr. Faculty Award

Project description: The major research goals of this project are: 1) to use trans-ancestry approaches to identify comprehensive sets of plausible candidate variants at established and novel loci for glycemic traits and obesity. From the list of candidate variants, 2) identify potentially causal metabolic disease variants and elements that exhibit functional regulatory elements, and 3) create and fine-tune polygenic/genetic risk scores for predicting T2D risk.

Direct costs: $414,000 (total; UMass)

Impact score: not provided

Submitted Aug 2021 *Genetic mechanisms underlying type 2 diabetes and obesity risk*

Role: PI Application ID: 4954 (Cassandra Spracklen, PI)

Smith Family Awards Program for Excellence in Biomedical Research

Project description: The major goals of this project are: 1) to use single- and trans-ethnic approaches to identify comprehensive sets of plausible candidate variants at established and novel loci for glycemic traits and obesity. From the list of candidate variants: 2) identify potentially causal metabolic disease variants and elements that exhibit functional regulatory elements, and 3) assess the effects of the stress responsive effector genes on islet function and resilience.

Direct costs: $300,000 (total; UMass)

Impact score: not provided

Submitted June 2021 *Genetic regulation of islet mitochondrial health and dysfunction in type 2*Role: Consultant *diabetes*

R01DK132534-01 (Scott Soleimanpour and Michael Stitzel, co-PIs)

NIH/NIDDK R01 Research Project Grant

Project description: The major goal of this proposal is to identify type 2 diabetes-associated variants that alter pancreatic islet and/or beta-cell stress-responsive *cis-*regulatory element activity and to assess the effects of the stress responsive effector genes on islet function and resilience.

Direct costs: $2,439,198 (total); $0 (UMass)

Impact score: 30 (21%)

Submitted Mar 2021 *Advancing methodologies for genetic association studies in diverse populations* Role: Co-applicant *to unravel the architecture of aging*

PLM23023 (Dr. Karoline Kuchenbaeker, PI)

Wellcome Trust Collaborative Awards in Science

Project description: The major goal of this project is to develop the most feasible and robust analytical pipelines for performing genetic analyses in ancestrally diverse populations through rigorous simulations and empirical data analysis. Aging-related outcomes are used as model traits.

Direct costs: $3,256,788 (total); $ 622,355 (UMass)

Impact score: not provided

Submitted Dec 2020 *Dissecting the roles of type 2 diabetes-associated SNPs and effector genes in* *islet* Role: Co-mentor *endoplasmic reticulum stress response*

F30DK130582-01 (Redwan Bhuiyan, PI)

NIH/NIDDK Predoctoral Fellowship for MD/PhD

Project description: The major goal of this proposal is to identify type 2 diabetes-associated variants that alter pancreatic islet and/or beta-cell stress-responsive *cis-*regulatory element activity and to assess the effects of the stress responsive effector genes on islet function and resilience

Direct costs: $169,096 (total); $0 (UMass)

Impact score: Not discussed

Submitted Oct 2020 *Analysis, interpretation, and fine-mapping of genetic and genomic data from* Role: PI *single- and trans-ancestry populations*

R35HG011962-01 (Cassandra N. Spracklen, PI)

NIH/NHGRI R35 Genomic Innovator Award

Project description: The major goal of this project is to establish the most feasible and robust analytical pipelines for performing genetic analyses in ancestrally diverse populations through rigorous simulations, benchmarking, and methods optimization.

Direct costs: $1,489,218 (total; UMass)

Impact score: Not discussed

Submitted Sept 2020 *Gene expression in visceral adipose tissues and functional validation of T2D loci*Role: CollaboratorMOET2EP3-02-2020 (Xueling Sim, PI, National Univ. of Singapore)

Ministry of Education Academic Research Fund Tier 2, Singapore

Project description: The major goal of this project is to generate visceral adipose eQTLs in East Asian individuals to identify target genes for downstream candidate gene regulation in the relevant cell type for T2D pathogenesis.

Direct costs: Singapore Dollars $1,000,000 (total); $0 (UMass)

Impact score: not provided

Submitted Mar 2020 *2023 Quantitative Genetics and Genomics Gordon Research Conference and  
 Seminar*

R13HG011541-01 (Cassandra N. Spracklen, PI)

NIH/NHGRI R13 Scientific Meeting Grant

Project description: The major goal of this proposal is to seek partial support for the Gordon Research Conference and Gordon Research Seminar on Quantitative Genetics and Genomics: Leveraging High-Throughput Phenotyping Techniques to Study Complex Traits to be held in Ventura, California on February 13-19, 2021

Direct costs: $10,000 (total); $0 (UMass)

Impact score: 29 (no percentile provided)

\*\* WITHDRAWN \*\* (conference postponed due to COVID-19)

Submitted Mar 2015 *Trans-ancestry genetic architecture of circulating lipid and c-reactive protein* Role: PI *levels*

F32HL131224-01 (Cassandra N. Spracklen, PI)

NIH/NHLBI Postdoctoral Fellowship

Project description: The major goal of this postdoctoral fellowship is to combine genetic data from several existing cohorts of different ancestries to perform trans-ancestry fine-mapping of DNA variants that function to influence lipid and C-reactive protein levels

Direct costs: $10,000 (total; UNC)

Impact score: 46 (48%)

**TEACHING EXPERIENCE**

Instructor

**Epidemiology 737**: Intermediate Epidemiology Methods, Graduate Public Health Fall 2023  
Majors, University of Massachusetts Amherst

**Epidemiology 690G**: Genetic Epidemiology, Graduate Pubic Health Majors, Spring 2023  
University of Massachusetts Amherst,

**Epidemiology 737**: Intermediate Epidemiology Methods, Graduate Public Health Fall 2022  
Majors, University of Massachusetts Amherst

**Public Health 224**: Epidemiology in Public Health, Undergraduate Public Health Spring 2022  
Majors, University of Massachusetts Amherst

**Epidemiology 690G**: Genetic Epidemiology, Graduate Pubic Health Majors, Spring 2021  
University of Massachusetts Amherst

**Public Health 224** Section 1: Epidemiology in Public Health, Undergraduate Public Fall 2020  
Health Majors, University of Massachusetts Amherst

**Public Health 224** Section 2: Epidemiology in Public Health, Undergraduate Public Fall 2020   
Health Majors, University of Massachusetts Amherst

**Public Health 224**: Epidemiology in Public Health, Undergraduate Public Health Spring 2020  
Majors, University of Massachusetts Amherst

**Public Health 224**: Epidemiology in Public Health, Undergraduate Public Health Fall 2019  
Majors, University of Massachusetts Amherst

Independent studies

**Epidemiology 896**: Independent Study, Lichen Hao, Epidemiology PhD Student, Fall 2022  
University of Massachusetts Amherst

**Epidemiology 696**: Independent Study, Neha Rahalkar, Epidemiology MS Fall 2022  
Student, University of Massachusetts

**Epidemiology 696**: Independent Study, Christian Daniele, Epidemiology MS Fall 2022  
Student, University of Massachusetts

**Epidemiology 696**: Independent Study, Aaron Holman-Vittone, Epidemiology Spring 2022  
MS Student, University of Massachusetts

**Public Health 396**: Independent Study, Bella Triolo, Undergraduate Microbiology Spring 2021  
Major, University of Massachusetts Amherst

**Public Health 396**: Independent Study, Autumn Gagnon, Undergraduate Public Spring 2021  
Health Major, University of Massachusetts Amherst, Spring 2021

**Public Health HI224**: Epidemiology/Public Health Honors Independent Study, Kara Spring 2021  
Chuang, Undergraduate Public Health Major, University of Massachusetts Amherst

**Public Health HI224**: Epidemiology/Public Health Honors Independent Study, Suzanne Fall 2020  
Wilson, Undergraduate Public Health Major, University of Massachusetts Amherst

**Public Health HI224**: Epidemiology/Public Health Honors Independent Study, Jacob Spring 2020  
Bear and Vera Rodic, Undergraduate Public Health Majors, University of   
Massachusetts Amherst

**Epidemiology 896**: Independent Study, Kathryn Wagner, Epidemiology PhD Student, Spring 2020  
University of Massachusetts Amherst

**Public Health 396**: Independent Study, Christina Ziogas, Undergraduate Public Spring 2020  
Health Major, University of Massachusetts Amherst, Spring 2020

Guest lectures

**Microbiology 639**: Microbiology Honors Colloquium, *“Genetic Epidemiology*”, Spring 2022  
Undergraduate students, University of Massachusetts Amherst

**Epidemiology 639**: Cancer Epidemiology, *“Introduction to Genetic Epidemiology” Fall 2019*Graduate Public Health majors, University of Massachusetts Amherst

**Epidemiology 743**: Genetic Epidemiology: Methods and Applications, *“Post-GWAS:* Spring 2019 *Fine-mapping, annotation, and variant function*, Epidemiology Graduate   
students, University of North Carolina

**Epidemiology 743**: Genetic Epidemiology: Methods and Applications, *“Post-GWAS:* Spring 2018 *Fine-mapping, annotation, and variant function*, Epidemiology Graduate   
students, University of North Carolina

**Genetics 647**: Human Genetics and Genomics, *“Linkage Disequilibrium”*, Genetics Spring 2018  
and Bioinformatics Graduate students, University of North Carolina

**Genetics 647**: Human Genetics and Genomics, *“Linkage Disequilibrium”*, Genetics Spring 2017  
and Bioinformatics Graduate students, University of North Carolina

**Epidemiology 6400**: Epidemiology II: Advanced Methods *Ecological Studies*, Spring 2013  
Epidemiology Graduate students, University of Iowa

Teaching Assistant

**Epidemiology 6400**: Epidemiology II: Advanced Methods, Epidemiology Graduate Spring 2014  
students, University of Iowa

**Epidemiology 5241**: Statistical Methods in Epidemiology, Epidemiology Graduate Fall 2013  
students, University of Iowa

**Epidemiology 6400**: Epidemiology II: Advanced Methods, Epidemiology Graduate Spring 2013  
students, University of Iowa

**Biology 2210**: Foundations of Modern Biology, Undergraduate biology majors, Fall 2008  
Anderson University

**Biology 4050**: Genetics, Undergraduate biology majors, Anderson University Fall 2008

**Biology 1000**: Principles of Modern Biology, Undergraduate biology majors, Spring 2007  
Anderson University

**Biology 2210:** Foundations of Modern Biology, Undergraduate biology majors, Fall 2007  
Anderson University

**Biology 1000**: Principles of Modern Biology, Undergraduate biology majors, Spring 2007  
Anderson University

**Biology 2210**: Foundations of Modern Biology, Undergraduate biology majors, Fall 2006  
Anderson University

International Workshops

“*The Michigan Imputation Server: Data Preparation, Genotype Imputation, and Data* Fall 2020  
 *Analysis*” Workshop, American Society for Human Genetics, Annual Meeting

“*The Michigan Imputation Server: Data Preparation, Genotype Imputation, and Data* Fall 2019  
 *Analysis*” Workshop, American Society for Human Genetics, Annual Meeting

**MENTORING EXPERIENCE**

Ph.D. Dissertation Chair (University of Massachusetts Amherst)

Rachel Wacks, PhD Student, Epidemiology 2023-

Title: *To be determined*

Lichen Hao, PhD Student, Epidemiology 2021-

Title: *To be determined*

Chi Zhao, PhD Student, Epidemiology 2021-

Title: *To be determined*

Ph.D. Dissertation Committee Member (University of Massachusetts Amherst)

Teah Snyder, PhD student, Epidemiology 2022-2023

Title: *Epidemiologic analysis of infectious disease data*

*Current position*: Pennsylvania Department of Public Health

Ph.D. Dissertation Committee Member (Other Institutions)

Eric Bartell, PhD student, Bioinformatics and Integrated Genomics, Harvard University 2023

Title: *Polygenic architecture of human body size and proportion*

MS Thesis Chair (University of Massachusetts Amherst)

Godness Biney, MS student, Epidemiology 2023-

Title: *Earlier age of type 2 diabetes onset is associated with an increased risk for   
 depression*

Emily Nyhan, MS student, Epidemiology 2023-

Title: *Birth weight,* p*reterm birth and subsequent risk of dementia and Alzheimer’s   
 in postmenopausal women*

Christian Daniele, MS student, Epidemiology 2022-2023

Title: *Birth weight,* p*reterm birth and subsequent risk of hypertension in   
 postmenopausal women*

*Current position*: Research Scientist, Sanofi

Aaron Holman-Vittone, MS Student, Epidemiology 2021-2022

Title: *Preterm birth and subsequent risk of type 2 diabetes in   
 postmenopausal women*

*Current position*: Research Scientist, Sanofi

Brian Monahan, MS student, Epidemiology 2020-2021

Title: *Birth weight and subsequent risk of autoimmune and thyroid conditions*

*Current position*: Associate Researcher, Ichan School of Medicine at Mount Sinai

MS Thesis Committee Member (University of Massachusetts Amherst)

Ashely Moineau, MS student, Epidemiology 2019-2020

Title: *The association between dengue virus infection and liver and kidney  
 function among Cambodian children*

*Current position*: General Supervisor; QA/QC Manager, IALS Testing Center,

University of Massachusetts Amherst

MPH Project Advisor (University of Massachusetts Amherst)

Caitlin Fields, MPH student, Epidemiology 2021-2022

Title: *The effect of the microbiome on rheumatoid arthritis risk: a literature   
 review and steps for the future*

*Current position*: Epidemiologist, Massachusetts Department of Public Health

Savannah Kangas, MPH student, Epidemiology 2021-2022

Title: *Incidence of congenital heart defects in newborns born to   
 mothers with pregestational diabetes*

*Current position*: Research assistant, Baystate Health

Nora Salo, MPH student, Epidemiology 2020-2021

Title: *Racial and ethnic disparities in the association between maternal  
 depression and preterm birth risk among women in the US*

*Current position*: Pediatric Global Health Clinical Research Coordinator,

Massachusetts General Hospital

Isabella Gleckman, MPH student, Epidemiology 2019-2020

Title: *Patterns of smoking cessation and the risk of preterm birth*

*Current position*: Data Quality Control Biostatistician, Foundation Medicine

Undergraduate Honors Thesis Advisor (University of Massachusetts Amherst)

Jillian Hughes, BS student, Public Health 2022-2023

Title: *The portrayal and intersection of savior siblings and human clones in fiction  
 novels*

*Current position*: Genetic counselor assistant

Research Advisor (University of Massachusetts Amherst)

Spencer Friedman, BS student, Math/Computer Science 2022  
 Research project: Data Management in the UK Biobank

Christian Daniele, MS student, Epidemiology 2021-2023  
 Research project: Lifecourse etiologies of women’s health and reproductive  
 outcomes

*Current position*: Research Scientist, Sanofi

Vishal Sarsani, PhD student, Statistics 2021-2023

Research project: Multi-ancestry genome-wide association study meta-analysis

of circulating adiponectin levels

*Current position*: Postdoc, Liming Liang Lab, Harvard University

Christina Ziogas, Undergraduate, Public Health Sciences 2020-2021  
 Research project: Validation of birth characteristics from maternal self-report and  
 birth certificates with medical record data

*Current position*: Marketing Science Statistician, iMarketResearch

Academic Advisor (University of Massachusetts Amherst)

Emily Nyhan, MS student, Epidemiology 2023-

Godness Biney, MS student, Epidemiology 2023-

Anoushka Shrestha, MPH student, Epidemiology 2023-

Samual Danso, MPH student, Epidemiology 2023-

Rachel Wacks, PhD student, Epidemiology 2023-

Erin Daley, MPH 4+1 student, Epidemiology 2022-

Maira Lima, MPH 4+1 student, Epidemiology 2022-

Lichen Hao, PhD student, Epidemiology 2021-

Chi Zhao, PhD student, Epidemiology 2021-

Alivia Rinaldi, MPH student, Epidemiology 2021-

Sruthi Tanikella, MS 4+1 student, Epidemiology 2021-

Nicole Kim, MPH student, Epidemiology 2021-2023

Christian Daniele, MS 4+1 student, Epidemiology 2021-2023

Aaron Holman-Vittone, MS student, Epidemiology 2021-2022

Savannah Kangas, MPH student, Epidemiology 2020-2022

Caitlin Fields, MPH student, Epidemiology 2020-2022

Nora Salo, MPH student, Epidemiology 2020-2021

Brian Monahan, MS student, Epidemiology 2020-2021

Ramisa Rahman, MPH student, Epidemiology 2019-2021

Lucas Schildbach, MPH student, Epidemiology 2019-2020

Isabella Gleckman, MPH student, Epidemiology 2019-2020

Mentor

Redwan Bhuiyan, MD/Ph.D. student, Biostatistics and Bioinformatics, University of 2020-  
 Connecticut

Apoorva Iyengar, Ph.D. student, Biostatistics and Bioinformatics, Duke University 2019-

Victoria Parsons, Ph.D. student, Genetics and Molecular Biology, University of North 2019-  
 Carolina at Chapel Hill

K. Alaine Broadaway, Postdoctoral Research Associate University of North Carolina at 2018-2019  
 Chapel Hill

Apoorva Iyengar, Undergraduate and Postbaccalaureate scholar, University of North 2017-2019  
 Carolina at Chapel Hill

Chelsea K. Raulerson, Ph.D. student, Bioinformatics and Computational Biology, 2014-2019  
 University of North Carolina at Chapel Hill

Maren E. Cannon, Ph.D. student, Genetics and Molecular Biology, University of North 2014-2017  
 Carolina at Chapel Hill

Kayla Jackson, Undergraduate student, SOLAR program, University of North Carolina 2015-2016   
 at Chapel Hill

J. Caitlin Smith, Ph.D. student, Epidemiology, University of Iowa 2013-2014

**SERVICE AND OUTREACH**

**SERVICE TO DIVISION AND DEPARTMENT**

**Member**, Admissions Committee, Department of Biostatistics and Epidemiology, 2019-  
University of Massachusetts Amherst

**Member,** PhD Comprehensive Exam Committee, Department of Biostatistics and 2019-  
Epidemiology, University of Massachusetts Amherst

**Chair,** Non-Tenure Track Faculty Search Committee, Department of Biostatistics and 2023-2024  
Epidemiology, University of Massachusetts Amherst

**Member,** Tenure Track Faculty Search Committee, Department of Biostatistics and 2023-2024  
Epidemiology, University of Massachusetts Amherst

**Coordinator**, PhD Comprehensive Exam, Department of Biostatistics and Epidemiology, 2022-2023  
University of Massachusetts Amherst

**Member,** Faculty Search Committee, Department of Biostatistics and Epidemiology, 2021-2022  
University of Massachusetts Amherst

**Co-chair**, Epidemiology Seminar Series, Department of Biostatistics and Epidemiology, 2019-2021  
University of Massachusetts Amherst

**Coordinator**, Time Management Workshop, Department of Biostatistics and Epidemiology, 2020 University of Massachusetts Amherst

**Coordinator**, Epidemiology Masters Students “Speed Dating” for Thesis Advisors, 2020  
Department of Biostatistics and Epidemiology, University of Massachusetts Amherst

**Ambassador**, Ocracoke School, Ocracoke, NC, North Carolina DNA Day 2015

**Treasurer**, Epidemiology Student Association, University of Iowa 2010-2011

**SERVICE TO SCHOOL /COLLEGE**

**Member**, Faculty Assembly Organizing Committee, School of Public Health and Health, 2022-2023  
Sciences, University of Massachusetts Amherst

**Administrative Affairs/Communications Chair,** College of Public Health Student 2010-2011  
Association, University of Iowa, 2010-2011

**SERVICE TO UNIVERSITY**

**Member**, Academic Honesty Board, University of Massachusetts Amherst 2022-

**Panelist**, New Faculty Orientation “Navigating Your First Year: Advice from Colleagues”, 2022  
 University of Massachusetts Amherst

**Guest Speaker**, *Career Paths in Genetic Epidemiology*, BioTap Honors Program Seminar, 2020   
University of Massachusetts Amherst

**Judge**, Initiative for Maximizing Student Diversity Annual Research Symposium, 2016  
University of North Carolina

**Judge,** Undergraduate Summer Research Symposium, University of North Carolina 2015-2016

**Judge**, Fall Undergraduate Research Festival, University of Iowa 2013

**PROFESSIONAL SERVICE**

Service to national societies

**Conference Chair,** Gordon Research Conference, Quantitative Genetics and Genomics 2025-2027

**Conference Vice Chair,** Gordon Research Conference, Quantitative Genetics and 2023-2025  
Genomics

**Program Committee** Member, American Society for Human Genetics 2022-2024

**Judge,** American Society for Human Genetics DNA Day Essay Contest 2016-2023

**Session Moderator,** “Multi-ancestry and Longitudinal Type 2 Diabetes Genetic Risk”, 2023  
American Diabetes Association Annual Meeting

**Council on Genomic and Precision Medicine Membership Committee Member**, 2022-2024  
American Heart Association

**Genetics Subcommittee Member,** American Diabetes Association, Scientific Sessions 2022-2023

**Conference Co-Chair**, Gordon Research Seminar, Quantitative Genetics and Genomics 2019-2023

**Abstract Reviewer**, American Diabetes Association 2023

**Session Moderator**, “Applying Mendelian Randomization to Complex Traits”, 2022  
American Society for Human Genetics Annual Meeting

**Abstract Reviewer**, American Society for Human Genetics 2020-2022

**Council on Genomic and Precision Medicine Membership and Communications** 2020-2022  
**Committee Member,** American Heart Association

**Session Moderator,** “Genetics of Cardiac and Vascular Disorders”, American 2019  
Society for Human Genetics Annual Meeting

**Abstract Reviewer**, Society for Epidemiologic Research 2015-2019

**Abstract Reviewer**, Society for Pediatric and Perinatal Epidemiologic Research 2014-2016

Reviewer, grants

*Ad hoc,* Dutch Diabetes Research Foundation, Fellowship 2023

*Ad hoc,* Wellcome Trust, GW4 Clinical Academic Training Program 2023

*Ad hoc*, American Heart Association, Institutional Undergraduate Student Awards 2022

*Ad hoc,* Trans-Omics for Precision Medicine (TOPMed) Fellowship 2022

*Ad hoc,* Research Council of Norway 2022

*Ad hoc*, Kidney, Nutrition, Obesity, and Diabetes, National Institutes of Health 2022

*Ad hoc,* Infectious Diseases, Reproductive Health, and Asthma/Pulmonary Conditions 2021  
Study Section, National Institutes of Health

*Ad hoc,* Genetics of Health and Disease Study Section, National Institutes of Health 2021

*Ad hoc*, Executive Council of Graduate and Professional Students, University of Iowa 2011-2014

*Ad hoc*, Division of Tobacco Use, Prevention, and Control, Iowa Department of Public Health 2010

Editorial service, journals

**Academic Editor**, Public Library of Science (PLoS) One 2016-2022

Ad hoc reviewer, journals

American Journal of Epidemiology, American Journal of Human Genetics, American Journal of Reproductive Immunology, Biomedical and Environmental Sciences, BMC Medical Genomics, BMC Pregnancy and Childbirth, British Medical Journal, Communications Biology, Diabetes, Diabetes Care, Diabetes/Metabolism Research and Review, Diabetologia, Epidemiology, Environmental Health Perspectives, European Journal of Human Genetics, Frontiers in Cardiovascular Medicine, Human Molecular Genetics, International Journal of Epidemiology, International Journal of Obesity, Journal of Lipid Research, Journal of Women’s Health, Medicine and Science in Sports and Exercise, Molecular Genetics and Genomic Medicine, Nature Genetics, Nutrition and Metabolism, Public Library of Science (PLoS) Genetics, PLoS One, Women’s Health Issues

Ad hoc reviewer, book

Senie, RT*. Epidemiology of Women’s Health*. 1ed. Jones and Bartlett Learning. 2014

Other

**Session Chair**, Massachusetts Undergraduate Research Conference 2022

**MEMBERSHIP TO PROFESSIONAL SOCIETIES**

American Society for Human Genetics 2015-

American Heart Association 2014-

Society for Pediatric and Perinatal Epidemiologic Research 2014-2017

Society for Epidemiological Research 2013-2017; 2022

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