

## CURRICULUM VITAE

### Akinyemi Ojesina MD, PhD

Assistant Professor  
Department of Obstetrics and Gynecology  
Division of Research and Advanced Education

#### OFFICE ADDRESS:

Translational and Biomedical Research Center  
8701 Watertown Plank Rd  
Milwaukee, WI 53226

#### EDUCATION:

11/1990 - 03/1998 M.D. with Distinction in Biochemistry, College of Medicine, University of Ibadan, Ibadan, Nigeria  
09/2001 - 11/2007 Ph.D. (Biological Sciences in Public Health), Harvard University, Cambridge, MA

#### POSTGRADUATE TRAINING AND FELLOWSHIP APPOINTMENTS:

03/1998 - 02/1999 House Officer, Clinical Rotations in Surgery, Internal Medicine, Pediatrics and Obstetrics/Gynecology, University College Hospital, Ibadan, Nigeria  
03/2001 UICC ICRET Fellow, University of Chicago, Chicago, IL  
08/2001 - 12/2007 APIN and Fogarty Fellow in Immunology and Infectious Diseases, Harvard School of Public Health (HSPH), Boston, MA  
01/2008 - 02/2015 Research Fellow in Medical Oncology, Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA  
01/2008 - 02/2015 Postdoctoral Scholar, Cancer Program, Broad Institute of MIT and Harvard, Cambridge, MA

#### FACULTY APPOINTMENTS:

03/2000 - 01/2008 Research Fellow, Medical Genetics Research Unit, Institute for Advanced Medical Research and Training, College of Medicine, University of Ibadan, Ibadan, Nigeria  
11/2014 - 07/2022 Adjunct Faculty Investigator, HudsonAlpha Institute for Biotechnology, Huntsville, AL  
03/2015 - 07/2022 Associate Scientist, O'Neal Comprehensive Cancer Center at UAB, Birmingham, AL  
03/2015 - 07/2022 Assistant Professor, Department of Epidemiology, University of Alabama at Birmingham (UAB), Birmingham, AL  
03/2015 - 07/2022 Research Scientist, UAB Center for AIDS Research (CFAR), Birmingham, AL  
03/2015 - 07/2022 Member, Microbiome Center, UAB Heersink School of Medicine, Birmingham, MA  
03/2015 - 07/2022 Associate Scientist, UAB Comprehensive Arthritis, Musculoskeletal, Bone and Autoimmunity Center (CAMBAC), Birmingham, AL  
08/2022 - Present Assistant Professor, Obstetrics and Gynecology, Medical College of Wisconsin, Milwaukee, WI 53226  
08/2022 - Present Assistant Professor, Microbiology and Immunology, Medical College of Wisconsin, Milwaukee, WI 53226  
10/2022 - Present Member, Cancer Control Program, Medical College of Wisconsin (MCW) Cancer Center, Milwaukee, WI

#### AWARDS AND HONORS:

1984 - 1989 Merit Scholarship, Federal Ministry of Education, Nigeria  
1988 - 1989 Kwara State Champion, National Junior Engineers, Technicians and Scientists (JETS) Competition, Nigeria  
1993 Distinction in Biochemistry, University of Ibadan

2000 Molecular Immunology Training Scholarship, International Centre for Genetic Engineering and Biotechnology (ICGEB)  
 2001 International Cancer Technology Transfer (ICRETT) Fellowship, Union for International Cancer Control (UICC)  
 2001 - 2006 APIN Doctoral Fellowship, AIDS Prevention Initiative in Nigeria (funded by the Bill and Melinda Gates Foundation)  
 2003 - 2004 James Souverine Gallo '27 Scholarship, Harvard University Graduate School of Arts and Sciences  
 2006 - 2007 Fogarty Fellowship, NIH Fogarty AIDS International Research Program  
 2008 - 2011 Rebecca Ridley Kry Fellowship, Damon Runyon Cancer Research Foundation  
 2010 Winning Submission (Team Member), Harvard Catalyst InnoCentive Ideation Challenge  
 2011 AACR-GlaxoSmithKline Outstanding Clinical Scholar Award  
 2013 AACR-GlaxoSmithKline Outstanding Clinical Scholar Award  
 2014 AACR-GlaxoSmithKline Outstanding Clinical Scholar Award  
 2015 - 2016 Career Development Award, NCI JHU/UAB Cervical Cancer SPORE  
 2015 - 2017 Stuart Scott Memorial V Scholar Award, V Foundation for Cancer Research  
 2015 - 2016 Angus Cooper Award in Transplant Investigation, UAB Transplant Center  
 2018 - 2019 V Scholar Plus Award, V Foundation for Cancer Research  
 2020 1000 Inspiring Black Scientists in America

#### **EDITORSHIPS/EDITORIAL BOARDS/JOURNAL REVIEWS:**

##### Editorship

12/1996 - 12/1997 Editor-in-Chief, DOKITA (equivalent to Student JAMA)

##### Editorial Board

04/2019 - Present Cancer

08/2020 - Present Journal of Global Medicine

##### Journal Review

01/2004 - Present African Journal for Medicine and Medical Sciences

01/2006 - Present Archives of Ibadan Medicine

02/2014 - Present Acta Obstetrica et Gynecologica Scandinavica

07/2014 - Present International Journal of Cancer

12/2014 - Present British Journal of Cancer

06/2015 - Present Molecular Carcinogenesis

07/2015 - Present Gynecologic Oncology

09/2015 - Present Oncogene

09/2015 - Present npj Genomic Medicine

05/2016 - Present Modern Pathology

06/2016 - Present PLoS Pathogens

09/2016 - Present Genome Research

02/2017 - Present Bioinformatics

09/2017 - Present Oncotarget

04/2019 - Present Cancer

05/2020 - Present Journal of Clinical Sciences

08/2020 - Present Journal of Global Medicine

##### Ad-Hoc Reviewer

01/2003 - 12/2007 AIDS

01/2003 - 12/2007 AIDS Research and Retroviruses

#### **COMMUNITY SERVICE ACTIVITIES:**

2019 - Present Member, Board of Directors, TamBo Foundation

## **BIBLIOGRAPHY**

### **Refereed Journal Publications/Original Papers**

1. **Ojesina AI**, Akang EE, Ojemakinde KO. Decline in the frequency of Burkitt's lymphoma relative to other childhood malignancies in Ibadan, Nigeria. *Ann Trop Paediatr.* 2002 Jun;22(2):159-63.

2. **Ojesina AI**. The role of beta-catenin in regulating angiogenesis in Wilms tumor. *J Pediatr Surg*. 2004 Sep;39(9):1446-7; author reply 1447.
3. **Ojesina AI**. Launching into the Deep: The Musings of a Budding Physician-Scientist. *Archives of Ibadan Medicine* 2005 Apr/Oct; 6(1): 31-33.
4. **Ojesina AI**, Sankalé JL, Odaibo G, Langevin S, Meloni ST, Sarr AD, Olaleye D, Kanki PJ. Subtype-specific patterns in HIV Type 1 reverse transcriptase and protease in Oyo State, Nigeria: implications for drug resistance and host response. *AIDS Res Hum Retroviruses*. 2006 Aug;22(8):770-9.
5. **Ojesina AI**, Kanki PJ. HIV-1 subtype and reverse transcriptase genotype: role for geographical location and founder effects. *PLoS Med*. 2006 Dec;3(12):e540. PMID: PMC1762043
6. Sankalé JL, Langevin S, Odaibo G, Meloni ST, **Ojesina AI**, Olaleye D, Kanki P. The complexity of circulating HIV type 1 strains in Oyo state, Nigeria. *AIDS Res Hum Retroviruses*. 2007 Aug;23(8):1020-5.
7. **Ojesina AI**, Mullins C, Imade G, Samuels J, Sankalé JL, Pam S, Sagay S, Idoko J, Kanki PJ. Characterization of HIV type 1 reverse transcriptase mutations in infants infected by mothers who received peripartum nevirapine prophylaxis in Jos, Nigeria. *AIDS Res Hum Retroviruses*. 2007 Dec;23(12):1587-92.
8. **Ojesina AI**, Chaplin B, Sankalé JL, Murphy R, Idigbe E, Adewole I, Ekong E, Idoko J, Kanki PJ. Interplay of reverse transcriptase inhibitor therapy and gag p6 diversity in HIV type 1 subtype G and CRF02\_AG. *AIDS Res Hum Retroviruses*. 2008 Sep;24(9):1167-74. PMID: PMC2928033
9. Kostic AD, **Ojesina AI**, Pdamallu CS, Jung J, Verhaak RG, Getz G, Meyerson M. PathSeq: software to identify or discover microbes by deep sequencing of human tissue. *Nat Biotechnol*. 2011 May;29(5):393-6. PMID: PMC3523678
10. Kostic AD, Gevers D, Pdamallu CS, Michaud M, Duke F, Earl AM, **Ojesina AI**, Jung J, Bass AJ, Taberner J, Baselga J, Liu C, Shivdasani RA, Ogino S, Birren BW, Huttenhower C, Garrett WS, Meyerson M. Genomic analysis identifies association of *Fusobacterium* with colorectal carcinoma. *Genome Res*. 2012 Feb;22(2):292-8. PMID: PMC3266036
11. Lohr JG, Stojanov P, Lawrence MS, Auclair D, Chapuy B, Sougnez C, Cruz-Gordillo P, Knoechel B, Asmann YW, Slager SL, Novak AJ, Dogan A, Ansell SM, Link BK, Zou L, Gould J, Saksena G, Stransky N, Rangel-Escareño C, Fernandez-Lopez JC, Hidalgo-Miranda A, Melendez-Zajgla J, Hernández-Lemus E, Schwarz-Cruz y Celis A, Imaz-Rosshandler I, **Ojesina AI**, Jung J, Pdamallu CS, Lander ES, Habermann TM, Cerhan JR, Shipp MA, Getz G, Golub TR. Discovery and prioritization of somatic mutations in diffuse large B-cell lymphoma (DLBCL) by whole-exome sequencing. *Proc Natl Acad Sci U S A*. 2012 Mar 06;109(10):3879-84. PMID: PMC3309757
12. Bhatt AS, Freeman SS, Herrera AF, Pdamallu CS, Gevers D, Duke F, Jung J, Michaud M, Walker BJ, Young S, Earl AM, Kostic AD, **Ojesina AI**, Hasserjian R, Ballen KK, Chen YB, Hobbs G, Antin JH, Soiffer RJ, Baden LR, Garrett WS, Hornick JL, Marty FM, Meyerson M. Sequence-based discovery of *Bradyrhizobium enterica* in cord colitis syndrome. *N Engl J Med*. 2013 Aug 08;369(6):517-28. PMID: PMC3889161
13. Cancer Genome Atlas Research Network, Weinstein JN, Collisson EA, Mills GB, Shaw KR, Ozenberger BA, Ellrott K, Shmulevich I, Sander C, Stuart JM. The Cancer Genome Atlas Pan-Cancer analysis project. *Nat Genet*. 2013 Oct;45(10):1113-20. PMID: PMC3919969
14. Francis JM, Kiezun A, Ramos AH, Serra S, Pdamallu CS, Qian ZR, Banck MS, Kanwar R, Kulkarni AA, Karpathakis A, Manzo V, Contractor T, Philips J, Nickerson E, Pho N, Hooshmand SM, Brais LK, Lawrence MS, Pugh T, McKenna A, Sivachenko A, Cibulskis K, Carter SL, **Ojesina AI**, Freeman S, Jones RT, Voet D, Saksena G, Auclair D, Onofrio R, Shefler E, Sougnez C, Grimsby J, Green L, Lennon N, Meyer T, Caplin M, Chung DC, Beutler AS, Ogino S, Thirlwell C, Shivdasani R, Asa SL, Harris CR, Getz G, Kulke M, Meyerson M. Somatic mutation of *CDKN1B* in small intestine neuroendocrine tumors. *Nat Genet*. 2013 Dec;45(12):1483-6. PMID: PMC4239432
15. **Ojesina AI**, Lichtenstein L, Freeman SS, Pdamallu CS, Imaz-Rosshandler I, Pugh TJ, Cherniack AD, Ambrogio L, Cibulskis K, Bertelsen B, Romero-Cordoba S, Treviño V, Vazquez-Santillan K, Guadarrama AS, Wright AA, Rosenberg MW, Duke F, Kaplan B, Wang R, Nickerson E, Walline HM, Lawrence MS, Stewart C, Carter SL, McKenna A, Rodriguez-Sanchez IP, Espinosa-Castilla M, Woie K, Bjorge L, Wik E, Halle MK, Hoivik EA, Krakstad C, Gabiño NB, Gómez-Macías GS, Valdez-Chapa LD, Garza-Rodríguez ML, Maytorena G, Vazquez J, Rodea C, Cravioto A, Cortes ML, Greulich H, Crum CP, Neuberg DS, Hidalgo-Miranda A, Escareno CR, Akslen LA, Carey TE, Vintermyr OK, Gabriel SB, Barrera-Saldaña HA, Melendez-Zajgla J, Getz G, Salvesen HB, Meyerson M. Landscape of genomic alterations in cervical carcinomas. *Nature*. 2014 Feb 20;506(7488):371-5. PMID: PMC4161954

16. Cancer Genome Atlas Research Network. Comprehensive molecular characterization of gastric adenocarcinoma. *Nature*. 2014 Sep 11;513(7517):202-9. PMID: PMC4170219
17. Cancer Genome Atlas Research Network. Integrated genomic characterization of papillary thyroid carcinoma. *Cell*. 2014 Oct 23;159(3):676-90. PMID: PMC4243044
18. Parfenov M, Peadamallu CS, Gehlenborg N, Freeman SS, Danilova L, Bristow CA, Lee S, Hadjipanayis AG, Ivanova EV, Wilkerson MD, Protopopov A, Yang L, Seth S, Song X, Tang J, Ren X, Zhang J, Pantazi A, Santoso N, Xu AW, Mahadeshwar H, Wheeler DA, Haddad RI, Jung J, **Ojesina AI**, Issaeva N, Yarbrough WG, Hayes DN, Grandis JR, El-Naggar AK, Meyerson M, Park PJ, Chin L, Seidman JG, Hammerman PS, Kucherlapati R, Cancer Genome Atlas Network. Characterization of HPV and host genome interactions in primary head and neck cancers. *Proc Natl Acad Sci U S A*. 2014 Oct 28;111(43):15544-9. PMID: PMC4217452
19. Cancer Genome Atlas Network. Comprehensive genomic characterization of head and neck squamous cell carcinomas. *Nature*. 2015 Jan 29;517(7536):576-82. PMID: PMC4311405
20. Arvey A, **Ojesina AI**, Peadamallu CS, Ballon G, Jung J, Duke F, Leoncini L, De Falco G, Bressman E, Tam W, Chadburn A, Meyerson M, Cesarman E. The tumor virus landscape of AIDS-related lymphomas. *Blood*. 2015 May 14;125(20):e14-22. PMID: PMC4432014
21. Chung TK, Van Hummelen P, Chan PK, Cheung TH, Yim SF, Yu MY, Ducar MD, Thorner AR, MacConaill LE, Doran G, Peadamallu CS, **Ojesina AI**, Wong RR, Wang VW, Freeman SS, Lau TS, Kwong J, Chan LK, Fromer M, May T, Worley MJ Jr, Esselen KM, Elias KM, Lawrence M, Getz G, Smith DI, Crum CP, Meyerson M, Berkowitz RS, Wong YF. Genomic aberrations in cervical adenocarcinomas in Hong Kong Chinese women. *Int J Cancer*. 2015 Aug 15;137(4):776-83.
22. Akinyemiju T, Moore JX, **Ojesina AI**, Waterbor JW, Altekruze SF. Racial disparities in individual breast cancer outcomes by hormone-receptor subtype, area-level socio-economic status and healthcare resources. *Breast Cancer Res Treat*. 2016 Jun;157(3):575-86. PMID: PMC4912843
23. Weaver AN, Burch MB, Cooper TS, Della Manna DL, Wei S, **Ojesina AI**, Rosenthal EL, Yang ES. Notch Signaling Activation Is Associated with Patient Mortality and Increased FGF1-Mediated Invasion in Squamous Cell Carcinoma of the Oral Cavity. *Mol Cancer Res*. 2016 Sep;14(9):883-91.
24. Peadamallu CS, Bhatt AS, Bullman S, Fowler S, Freeman SS, Durand J, Jung J, Duke F, Manzo V, Cai D, Ananthakrishnan A, **Ojesina AI**, Ramachandran A, Gevers D, Xavier RJ, Bhan AK, Meyerson M, Yajnik V. Metagenomic Characterization of Microbial Communities *In Situ* Within the Deeper Layers of the Ileum in Crohn's Disease. *Cell Mol Gastroenterol Hepatol*. 2016 Sep;2(5):563-566.e5. PMID: PMC5042890
25. Li Y, Zhang X, Akinyemiju T, **Ojesina AI**, Szychowski JM, Liu N, Xu B, Yi N. A two-stage approach for combining gene expression and mutation with clinical data improves survival prediction in myelodysplastic syndromes and ovarian cancer. *J Bioinform Genom*. 2016 Sep;1(1). PMID: PMC8351588
26. Zhang X, Li Y, Akinyemiju T, **Ojesina AI**, Buckhaults P, Liu N, Xu B, Yi N. Pathway-Structured Predictive Model for Cancer Survival Prediction: A Two-Stage Approach. *Genetics*. 2017 Jan;205(1):89-100. PMID: PMC5223526
27. Cancer Genome Atlas Research Network, Analysis Working Group: Asan University, BC Cancer Agency, Brigham and Women's Hospital, Broad Institute, Brown University, Case Western Reserve University, Dana-Farber Cancer Institute, Duke University, Greater Poland Cancer Centre, Harvard Medical School, Institute for Systems Biology, KU Leuven, Mayo Clinic, Memorial Sloan Kettering Cancer Center, National Cancer Institute, Nationwide Children's Hospital, Stanford University, University of Alabama, University of Michigan, University of North Carolina, University of Pittsburgh, University of Rochester, University of Southern California, University of Texas MD Anderson Cancer Center, University of Washington, Van Andel Research Institute, Vanderbilt University, Washington University, Genome Sequencing Center: Broad Institute, Washington University in St. Louis, Genome Characterization Centers: BC Cancer Agency, Broad Institute, Harvard Medical School, Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University, University of North Carolina, University of Southern California Epigenome Center, University of Texas MD Anderson Cancer Center, Van Andel Research Institute, Genome Data Analysis Centers: Broad Institute, Brown University, Harvard Medical School, Institute for Systems Biology, Memorial Sloan Kettering Cancer Center, University of California Santa Cruz, University of Texas MD Anderson Cancer Center, Biospecimen Core Resource: International Genomics Consortium, Research Institute at Nationwide Children's Hospital, Tissue Source Sites: Analytic Biologic Services, Asan Medical Center, Asterand Bioscience, Barretos Cancer Hospital, BioreclamationIVT, Botkin

- Municipal Clinic, Chonnam National University Medical School, Christiana Care Health System, Cureline, Duke University, Emory University, Erasmus University, Indiana University School of Medicine, Institute of Oncology of Moldova, International Genomics Consortium, Invidumed, Israelitisches Krankenhaus Hamburg, Keimyung University School of Medicine, Memorial Sloan Kettering Cancer Center, National Cancer Center Goyang, Ontario Tumour Bank, Peter MacCallum Cancer Centre, Pusan National University Medical School, Ribeirão Preto Medical School, St. Joseph's Hospital & Medical Center, St. Petersburg Academic University, Tayside Tissue Bank, University of Dundee, University of Kansas Medical Center, University of Michigan, University of North Carolina at Chapel Hill, University of Pittsburgh School of Medicine, University of Texas MD Anderson Cancer Center, Disease Working Group: Duke University, Memorial Sloan Kettering Cancer Center, National Cancer Institute, University of Texas MD Anderson Cancer Center, Yonsei University College of Medicine, Data Coordination Center: CSRA Inc., Project Team: National Institutes of Health. Integrated genomic characterization of oesophageal carcinoma. *Nature*. 2017 Jan 12;541(7636):169-175. PMID: PMC5651175
28. Farshidfar F, Zheng S, Gingras MC, Newton Y, Shih J, Robertson AG, Hinoue T, Hoadley KA, Gibb EA, Roszik J, Covington KR, Wu CC, Shinbrot E, Stransky N, Hegde A, Yang JD, Reznik E, Sadeghi S, Padamallu CS, **Ojesina AI**, Hess JM, Auman JT, Rhie SK, Bowlby R, Borad MJ, Cancer Genome Atlas Network, Zhu AX, Stuart JM, Sander C, Akbani R, Cherniack AD, Deshpande V, Mounajjed T, Foo WC, Torbenson MS, Kleiner DE, Laird PW, Wheeler DA, McRee AJ, Bathe OF, Andersen JB, Bardeesy N, Roberts LR, Kwong LN. Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. *Cell Rep*. 2017 Mar 14;18(11):2780-2794. PMID: PMC5493145
29. Cancer Genome Atlas Research Network, Albert Einstein College of Medicine, Analytical Biological Services, Barretos Cancer Hospital, Baylor College of Medicine, Beckman Research Institute of City of Hope, Buck Institute for Research on Aging, Canada's Michael Smith Genome Sciences Centre, Harvard Medical School, Helen F. Graham Cancer Center & Research Institute at Christiana Care Health Services, HudsonAlpha Institute for Biotechnology, ILSbio, LLC, Indiana University School of Medicine, Institute of Human Virology, Institute for Systems Biology, International Genomics Consortium, Leidos Biomedical, Massachusetts General Hospital, McDonnell Genome Institute at Washington University, Medical College of Wisconsin, Medical University of South Carolina, Memorial Sloan Kettering Cancer Center, Montefiore Medical Center, NantOmics, National Cancer Institute, National Hospital, Abuja, Nigeria, National Human Genome Research Institute, National Institute of Environmental Health Sciences, National Institute on Deafness & Other Communication Disorders, Ontario Tumour Bank, London Health Sciences Centre, Ontario Tumour Bank, Ontario Institute for Cancer Research, Ontario Tumour Bank, The Ottawa Hospital, Oregon Health & Science University, Samuel Oschin Comprehensive Cancer Institute, Cedars-Sinai Medical Center, SRA International, St Joseph's Candler Health System, Eli & Edythe L. Broad Institute of Massachusetts Institute of Technology & Harvard University, Research Institute at Nationwide Children's Hospital, Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University, University of Bergen, University of Texas MD Anderson Cancer Center, University of Abuja Teaching Hospital, University of Alabama at Birmingham, University of California, Irvine, University of California Santa Cruz, University of Kansas Medical Center, University of Lausanne, University of New Mexico Health Sciences Center, University of North Carolina at Chapel Hill, University of Oklahoma Health Sciences Center, University of Pittsburgh, University of São Paulo, Ribeirão Preto Medical School, University of Southern California, University of Washington, University of Wisconsin School of Medicine & Public Health, Van Andel Research Institute, Washington University in St Louis. Integrated genomic and molecular characterization of cervical cancer. *Nature*. 2017 Mar 16;543(7645):378-384. PMID: PMC5354998
30. Cancer Genome Atlas Research Network. Electronic address: wheeler@bcm.edu, Cancer Genome Atlas Research Network. Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*. 2017 Jun 15;169(7):1327-1341.e23. PMID: PMC5680778
31. Farshidfar F, Zheng S, Gingras MC, Newton Y, Shih J, Robertson AG, Hinoue T, Hoadley KA, Gibb EA, Roszik J, Covington KR, Wu CC, Shinbrot E, Stransky N, Hegde A, Yang JD, Reznik E, Sadeghi S, Padamallu CS, **Ojesina AI**, Hess JM, Auman JT, Rhie SK, Bowlby R, Borad MJ, Cancer Genome Atlas Network, Zhu AX, Stuart JM, Sander C, Akbani R, Cherniack AD, Deshpande V, Mounajjed T, Foo WC, Torbenson MS, Kleiner DE, Laird PW, Wheeler DA, McRee AJ, Bathe OF, Andersen JB, Bardeesy N, Roberts LR, Kwong LN. Integrative Genomic Analysis of Cholangiocarcinoma Identifies

- Distinct IDH-Mutant Molecular Profiles. *Cell Rep.* 2017 Jun 27;19(13):2878-2880. PMID: PMC6141445
32. Halle MK, **Ojesina AI**, Engerud H, Woie K, Tangen IL, Holst F, Høivik E, Kusonmano K, Haldorsen IS, Vintermyr OK, Trovik J, Bertelsen BI, Salvesen HB, Krakstad C. Clinicopathologic and molecular markers in cervical carcinoma: a prospective cohort study. *Am J Obstet Gynecol.* 2017 Oct;217(4):432.e1-432.e17.
  33. Robertson AG, Kim J, Al-Ahmadie H, Bellmunt J, Guo G, Cherniack AD, Hinoue T, Laird PW, Hoadley KA, Akbani R, Castro MAA, Gibb EA, Kanchi RS, Gordenin DA, Shukla SA, Sanchez-Vega F, Hansel DE, Czerniak BA, Reuter VE, Su X, de Sa Carvalho B, Chagas VS, Mungall KL, Sadeghi S, Pedomallu CS, Lu Y, Klimczak LJ, Zhang J, Choo C, **Ojesina AI**, Bullman S, Leraas KM, Lichtenberg TM, Wu CJ, Schultz N, Getz G, Meyerson M, Mills GB, McConkey DJ, TCGA Research Network, Weinstein JN, Kwiatkowski DJ, Lerner SP. Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. *Cell.* 2017 Oct 19;171(3):540-556.e25. PMID: PMC5687509
  34. Campbell JD, Yau C, Bowlby R, Liu Y, Brennan K, Fan H, Taylor AM, Wang C, Walter V, Akbani R, Byers LA, Creighton CJ, Coarfa C, Shih J, Cherniack AD, Gevaert O, Prunello M, Shen H, Anur P, Chen J, Cheng H, Hayes DN, Bullman S, Pedomallu CS, **Ojesina AI**, Sadeghi S, Mungall KL, Robertson AG, Benz C, Schultz A, Kanchi RS, Gay CM, Hegde A, Diao L, Wang J, Ma W, Sumazin P, Chiu HS, Chen TW, Gunaratne P, Donehower L, Rader JS, Zuna R, Al-Ahmadie H, Lazar AJ, Flores ER, Tsai KY, Zhou JH, Rustgi AK, Drill E, Shen R, Wong CK, Cancer Genome Atlas Research Network, Stuart JM, Laird PW, Hoadley KA, Weinstein JN, Peto M, Pickering CR, Chen Z, Van Waes C. Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. *Cell Rep.* 2018 Apr 03;23(1):194-212.e6. PMID: PMC6002769
  35. Berger AC, Korkut A, Kanchi RS, Hegde AM, Lenoir W, Liu W, Liu Y, Fan H, Shen H, Ravikumar V, Rao A, Schultz A, Li X, Sumazin P, Williams C, Mestdagh P, Gunaratne PH, Yau C, Bowlby R, Robertson AG, Tiezzi DG, Wang C, Cherniack AD, Godwin AK, Kuderer NM, Rader JS, Zuna RE, Sood AK, Lazar AJ, **Ojesina AI**, Adebamowo C, Adebamowo SN, Baggerly KA, Chen TW, Chiu HS, Lefever S, Liu L, MacKenzie K, Orsulic S, Roszik J, Shelley CS, Song Q, Vellano CP, Wentzensen N, Cancer Genome Atlas Research Network, Weinstein JN, Mills GB, Levine DA, Akbani R. A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell.* 2018 Apr 09;33(4):690-705.e9. PMID: PMC5959730
  36. Liu Y, Sethi NS, Hinoue T, Schneider BG, Cherniack AD, Sanchez-Vega F, Seoane JA, Farshidfar F, Bowlby R, Islam M, Kim J, Chatila W, Akbani R, Kanchi RS, Rabkin CS, Willis JE, Wang KK, McCall SJ, Mishra L, **Ojesina AI**, Bullman S, Pedomallu CS, Lazar AJ, Sakai R, Cancer Genome Atlas Research Network, Thorsson V, Bass AJ, Laird PW. Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell.* 2018 Apr 09;33(4):721-735.e8. PMID: PMC5966039
  37. Thorsson V, Gibbs DL, Brown SD, Wolf D, Bortone DS, Ou Yang TH, Porta-Pardo E, Gao GF, Plaisier CL, Eddy JA, Ziv E, Culhane AC, Paull EO, Sivakumar IKA, Gentles AJ, Malhotra R, Farshidfar F, Colaprico A, Parker JS, Mose LE, Vo NS, Liu J, Liu Y, Rader J, Dhankani V, Reynolds SM, Bowlby R, Califano A, Cherniack AD, Anastassiou D, Bedognetti D, Mokrab Y, Newman AM, Rao A, Chen K, Krasnitz A, Hu H, Malta TM, Noushmehr H, Pedomallu CS, Bullman S, **Ojesina AI**, Lamb A, Zhou W, Shen H, Choueiri TK, Weinstein JN, Guinney J, Saltz J, Holt RA, Rabkin CS, Cancer Genome Atlas Research Network, Lazar AJ, Serody JS, Demicco EG, Disis ML, Vincent BG, Shmulevich I. The Immune Landscape of Cancer. *Immunity.* 2018 Apr 17;48(4):812-830.e14. PMID: PMC5982584
  38. Robertson AG, Kim J, Al-Ahmadie H, Bellmunt J, Guo G, Cherniack AD, Hinoue T, Laird PW, Hoadley KA, Akbani R, Castro MAA, Gibb EA, Kanchi RS, Gordenin DA, Shukla SA, Sanchez-Vega F, Hansel DE, Czerniak BA, Reuter VE, Su X, de Sa Carvalho B, Chagas VS, Mungall KL, Sadeghi S, Pedomallu CS, Lu Y, Klimczak LJ, Zhang J, Choo C, **Ojesina AI**, Bullman S, Leraas KM, Lichtenberg TM, Wu CJ, Schultz N, Getz G, Meyerson M, Mills GB, McConkey DJ, TCGA Research Network, Weinstein JN, Kwiatkowski DJ, Lerner SP. Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. *Cell.* 2018 Aug 09;174(4):1033. PMID: PMC6297116
  39. McMaster ML, Berndt SI, Zhang J, Slager SL, Li SA, Vajdic CM, Smedby KE, Yan H, Birmann BM, Brown EE, Smith A, Kleinstern G, Fansler MM, Mayr C, Zhu B, Chung CC, Park JH, Burdette L, Hicks BD, Hutchinson A, Teras LR, Adami HO, Bracci PM, McKay J, Monnereau A, Link BK, Vermeulen RCH, Ansell SM, Maria A, Diver WR, Melbye M, **Ojesina AI**, Kraft P, Boffetta P, Clavel J, Giovannucci E, Besson CM, Canzian F, Travis RC, Vineis P, Weiderpass E, Montalvan R, Wang Z, Yeager M, Becker

- N, Benavente Y, Brennan P, Foretova L, Maynadie M, Nieters A, de Sanjose S, Staines A, Conde L, Riby J, Glimelius B, Hjalgrim H, Pradhan N, Feldman AL, Novak AJ, Lawrence C, Bassig BA, Lan Q, Zheng T, North KE, Tinker LF, Cozen W, Severson RK, Hofmann JN, Zhang Y, Jackson RD, Morton LM, Purdue MP, Chatterjee N, Offit K, Cerhan JR, Chanock SJ, Rothman N, Vijai J, Goldin LR, Skibola CF, Caporaso NE. Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for Waldenström macroglobulinemia. *Nat Commun*. 2018 Oct 10;9(1):4182. PMID: PMC6180091
40. Walker MA, Pedamallu CS, **Ojesina AI**, Bullman S, Sharpe T, Whelan CW, Meyerson M. GATK PathSeq: a customizable computational tool for the discovery and identification of microbial sequences in libraries from eukaryotic hosts. *Bioinformatics*. 2018 Dec 15;34(24):4287-4289. PMID: PMC6289130
41. Thorsson V, Gibbs DL, Brown SD, Wolf D, Bortone DS, Ou Yang TH, Porta-Pardo E, Gao GF, Plaisier CL, Eddy JA, Ziv E, Culhane AC, Paull EO, Sivakumar IKA, Gentles AJ, Malhotra R, Farshidfar F, Colaprico A, Parker JS, Mose LE, Vo NS, Liu J, Liu Y, Rader J, Dhankani V, Reynolds SM, Bowlby R, Califano A, Cherniack AD, Anastassiou D, Bedognetti D, Mokrab Y, Newman AM, Rao A, Chen K, Krasnitz A, Hu H, Malta TM, Noushmehr H, Pedamallu CS, Bullman S, **Ojesina AI**, Lamb A, Zhou W, Shen H, Choueiri TK, Weinstein JN, Guinney J, Saltz J, Holt RA, Rabkin CS, Cancer Genome Atlas Research Network, Lazar AJ, Serody JS, Demicco EG, Disis ML, Vincent BG, Shmulevich I. The Immune Landscape of Cancer. *Immunity*. 2019 Aug 20;51(2):411-412.
42. Behring M, Vazquez AI, Cui X, Irvin MR, **Ojesina AI**, Agarwal S, Manne U, Shrestha S. Gain of function in somatic TP53 mutations is associated with immune-rich breast tumors and changes in tumor-associated macrophages. *Mol Genet Genomic Med*. 2019 Dec;7(12):e1001. PMID: PMC6900370
43. ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium. Pan-cancer analysis of whole genomes. *Nature*. 2020 Feb;578(7793):82-93. PMID: PMC7025898
44. Li Y, Roberts ND, Wala JA, Shapira O, Schumacher SE, Kumar K, Khurana E, Waszak S, Korbel JO, Haber JE, Imielinski M, PCAWG Structural Variation Working Group, Weischenfeldt J, Beroukhim R, Campbell PJ, PCAWG Consortium. Patterns of somatic structural variation in human cancer genomes. *Nature*. 2020 Feb;578(7793):112-121. PMID: PMC7025897
45. Gerstung M, Jolly C, Leshchiner I, D'Ente SC, Gonzalez S, Rosebrock D, Mitchell TJ, Rubanova Y, Anur P, Yu K, Tarabichi M, Deshwar A, Wintersinger J, Kleinheinz K, Vázquez-García I, Haase K, Jerman L, Sengupta S, Macintyre G, Malikic S, Donmez N, Livitz DG, Cmero M, Demeulemeester J, Schumacher S, Fan Y, Yao X, Lee J, Schlesner M, Boutros PC, Bowtell DD, Zhu H, Getz G, Imielinski M, Beroukhim R, Sahinalp SC, Ji Y, Peifer M, Markowitz F, Mustonen V, Yuan K, Wang W, Morris QD, PCAWG Evolution & Heterogeneity Working Group, Spellman PT, Wedge DC, Van Loo P, PCAWG Consortium. The evolutionary history of 2,658 cancers. *Nature*. 2020 Feb;578(7793):122-128. PMID: PMC7054212
46. Rheinbay E, Nielsen MM, Abascal F, Wala JA, Shapira O, Tiao G, Hornshøj H, Hess JM, Juul RI, Lin Z, Feuerbach L, Sabarinathan R, Madsen T, Kim J, Mularoni L, Shuai S, Lanzoś A, Herrmann C, Maruvka YE, Shen C, Amin SB, Bandopadhyay P, Bertl J, Boroevich KA, Busanovich J, Carlevaro-Fita J, Chakravarty D, Chan CWY, Craft D, Dhingra P, Diamanti K, Fonseca NA, Gonzalez-Perez A, Guo Q, Hamilton MP, Haradhvala NJ, Hong C, Isaev K, Johnson TA, Juul M, Kahles A, Kahraman A, Kim Y, Komorowski J, Kumar K, Kumar S, Lee D, Lehmann KV, Li Y, Liu EM, Lochofsky L, Park K, Pich O, Roberts ND, Saksena G, Schumacher SE, Sidiropoulos N, Sieverling L, Sinnott-Armstrong N, Stewart C, Tamborero D, Tubio JMC, Umer HM, Uusküla-Reimand L, Wadelius C, Wadi L, Yao X, Zhang CZ, Zhang J, Haber JE, Hobolth A, Imielinski M, Kellis M, Lawrence MS, von Mering C, Nakagawa H, Raphael BJ, Rubin MA, Sander C, Stein LD, Stuart JM, Tsunoda T, Wheeler DA, Johnson R, Reimand J, Gerstein M, Khurana E, Campbell PJ, López-Bigas N, PCAWG Drivers and Functional Interpretation Working Group, PCAWG Structural Variation Working Group, Weischenfeldt J, Beroukhim R, Martincorena I, Pedersen JS, Getz G, PCAWG Consortium. Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*. 2020 Feb;578(7793):102-111. PMID: PMC7054214
47. Alexandrov LB, Kim J, Haradhvala NJ, Huang MN, Tian Ng AW, Wu Y, Boot A, Covington KR, Gordenin DA, Bergstrom EN, Islam SMA, Lopez-Bigas N, Klimczak LJ, McPherson JR, Morganella S, Sabarinathan R, Wheeler DA, Mustonen V, PCAWG Mutational Signatures Working Group, Getz G, Rozen SG, Stratton MR, PCAWG Consortium. The repertoire of mutational signatures in human cancer. *Nature*. 2020 Feb;578(7793):94-101. PMID: PMC7054213
48. PCAWG Transcriptome Core Group, Calabrese C, Davidson NR, Demircioğlu D, Fonseca NA, He Y, Kahles A, Lehmann KV, Liu F, Shiraiishi Y, Soulette CM, Urban L, Greger L, Li S, Liu D, Perry MD,

- Xiang Q, Zhang F, Zhang J, Bailey P, Erkek S, Hoadley KA, Hou Y, Huska MR, Kilpinen H, Korbel JO, Marin MG, Markowski J, Nandi T, Pan-Hammarström Q, Peadarallu CS, Siebert R, Stark SG, Su H, Tan P, Waszak SM, Yung C, Zhu S, Awadalla P, Creighton CJ, Meyerson M, Ouellette BFF, Wu K, Yang H, PCAWG Transcriptome Working Group, Brazma A, Brooks AN, Göke J, Rättsch G, Schwarz RF, Stegle O, Zhang Z, PCAWG Consortium. Genomic basis for RNA alterations in cancer. *Nature*. 2020 Feb;578(7793):129-136. PMID: PMC7054216
49. Sieverling L, Hong C, Koser SD, Ginsbach P, Kleinheinz K, Hutter B, Braun DM, Cortés-Ciriano I, Xi R, Kabbe R, Park PJ, Eils R, Schlesner M, PCAWG-Structural Variation Working Group, Brors B, Rippe K, Jones DTW, Feuerbach L, PCAWG Consortium. Genomic footprints of activated telomere maintenance mechanisms in cancer. *Nat Commun*. 2020 Feb 05;11(1):733. PMID: PMC7002710
  50. Shuai S, PCAWG Drivers and Functional Interpretation Working Group, Gallinger S, Stein LD, PCAWG Consortium. Combined burden and functional impact tests for cancer driver discovery using DriverPower. *Nat Commun*. 2020 Feb 05;11(1):734. PMID: PMC7002750
  51. Bhandari V, Li CH, Bristow RG, Boutros PC, PCAWG Consortium. Divergent mutational processes distinguish hypoxic and normoxic tumours. *Nat Commun*. 2020 Feb 05;11(1):737. PMID: PMC7002770
  52. Zhang Y, Chen F, Fonseca NA, He Y, Fujita M, Nakagawa H, Zhang Z, Brazma A, PCAWG Transcriptome Working Group, PCAWG Structural Variation Working Group, Creighton CJ, PCAWG Consortium. High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations. *Nat Commun*. 2020 Feb 05;11(1):736. PMID: PMC7002524
  53. Rubanova Y, Shi R, Harrigan CF, Li R, Wintersinger J, Sahin N, Deshwar AG, PCAWG Evolution and Heterogeneity Working Group, Morris QD, PCAWG Consortium. Reconstructing evolutionary trajectories of mutation signature activities in cancer using TrackSig. *Nat Commun*. 2020 Feb 05;11(1):731. PMID: PMC7002414
  54. Cmero M, Yuan K, Ong CS, Schröder J, PCAWG Evolution and Heterogeneity Working Group, Corcoran NM, Papenfuss T, Hovens CM, Markowitz F, Macintyre G, PCAWG Consortium. Inferring structural variant cancer cell fraction. *Nat Commun*. 2020 Feb 05;11(1):730. PMID: PMC7002525
  55. Paczkowska M, Barenboim J, Sintupisut N, Fox NS, Zhu H, Abd-Rabbo D, Mee MW, Boutros PC, PCAWG Drivers and Functional Interpretation Working Group, Reimand J, PCAWG Consortium. Integrative pathway enrichment analysis of multivariate omics data. *Nat Commun*. 2020 Feb 05;11(1):735. PMID: PMC7002665
  56. Jiao W, Atwal G, Polak P, Karlic R, Cuppen E, PCAWG Tumor Subtypes and Clinical Translation Working Group, Danyi A, de Ridder J, van Herpen C, Lolkema MP, Steeghs N, Getz G, Morris QD, Stein LD, PCAWG Consortium. A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns. *Nat Commun*. 2020 Feb 05;11(1):728. PMID: PMC7002586
  57. Reyna MA, Haan D, Paczkowska M, Verbeke LPC, Vazquez M, Kahraman A, Pulido-Tamayo S, Barenboim J, Wadi L, Dhingra P, Shrestha R, Getz G, Lawrence MS, Pedersen JS, Rubin MA, Wheeler DA, Brunak S, Izarzugaza JMG, Khurana E, Marchal K, von Mering C, Sahinalp SC, Valencia A, PCAWG Drivers and Functional Interpretation Working Group, Reimand J, Stuart JM, Raphael BJ, PCAWG Consortium. Pathway and network analysis of more than 2500 whole cancer genomes. *Nat Commun*. 2020 Feb 05;11(1):729. PMID: PMC7002574
  58. Carlevaro-Fita J, Lanzós A, Feuerbach L, Hong C, Mas-Ponte D, Pedersen JS, PCAWG Drivers and Functional Interpretation Group, Johnson R, PCAWG Consortium. Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. *Commun Biol*. 2020 Feb 05;3(1):56. PMID: PMC7002399
  59. Yakneen S, Waszak SM, PCAWG Technical Working Group, Gertz M, Korbel JO, PCAWG Consortium. Butler enables rapid cloud-based analysis of thousands of human genomes. *Nat Biotechnol*. 2020 Mar;38(3):288-292. PMID: PMC7062635
  60. Yuan Y, Ju YS, Kim Y, Li J, Wang Y, Yoon CJ, Yang Y, Martincorena I, Creighton CJ, Weinstein JN, Xu Y, Han L, Kim HL, Nakagawa H, Park K, Campbell PJ, Liang H, PCAWG Consortium. Comprehensive molecular characterization of mitochondrial genomes in human cancers. *Nat Genet*. 2020 Mar;52(3):342-352. PMID: PMC7058535
  61. Rodriguez-Martin B, Alvarez EG, Baez-Ortega A, Zamora J, Supek F, Demeulemeester J, Santamarina M, Ju YS, Temes J, Garcia-Souto D, Detering H, Li Y, Rodriguez-Castro J, Dueso-Barroso A, Bruzos AL, Dentro SC, Blanco MG, Contino G, Ardeljan D, Tojo M, Roberts ND, Zumalave S, Edwards PA, Weischenfeldt J, Puiggròs M, Chong Z, Chen K, Lee EA, Wala JA, Raine KM, Butler A, Waszak SM,



- Navarro FCP, Schumacher SE, Monlong J, Maura F, Bolli N, Bourque G, Gerstein M, Park PJ, Wedge DC, Beroukhir R, Torrents D, Korbel JO, Martincorena I, Fitzgerald RC, Van Loo P, Kazazian HH, Burns KH, PCAWG Structural Variation Working Group, Campbell PJ, Tubio JMC, PCAWG Consortium. Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nat Genet.* 2020 Mar;52(3):306-319. PMID: PMC7058536
62. Akdemir KC, Le VT, Chandran S, Li Y, Verhaak RG, Beroukhir R, Campbell PJ, Chin L, Dixon JR, Futreal PA, PCAWG Structural Variation Working Group, PCAWG Consortium. Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. *Nat Genet.* 2020 Mar;52(3):294-305. PMID: PMC7058537
63. Zapatka M, Borozan I, Brewer DS, Iskar M, Grundhoff A, Alawi M, Desai N, Sülthmann H, Moch H, PCAWG Pathogens, Cooper CS, Eils R, Ferretti V, Lichter P, PCAWG Consortium. The landscape of viral associations in human cancers. *Nat Genet.* 2020 Mar;52(3):320-330. PMID: PMC8076016
64. Cortés-Ciriano I, Lee JJ, Xi R, Jain D, Jung YL, Yang L, Gordenin D, Klimczak LJ, Zhang CZ, Pellman DS, PCAWG Structural Variation Working Group, Park PJ, PCAWG Consortium. Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nat Genet.* 2020 Mar;52(3):331-341. PMID: PMC7058534
65. Gagliardi A, Porter VL, Zong Z, Bowlby R, Titmuss E, Namirembe C, Griner NB, Petrello H, Bowen J, Chan SK, Culibrk L, Darragh TM, Stoler MH, Wright TC, Gesuwan P, Dyer MA, Ma Y, Mungall KL, Jones SJM, Nakisige C, Novik K, Orem J, Origa M, Gastier-Foster JM, Yarchoan R, Casper C, Mills GB, Rader JS, **Ojesina AI**, Gerhard DS, Mungall AJ, Marra MA. Analysis of Ugandan cervical carcinomas identifies human papillomavirus clade-specific epigenome and transcriptome landscapes. *Nat Genet.* 2020 Aug;52(8):800-810. PMID: PMC7498180
66. Li CH, Prokopec SD, Sun RX, Yousif F, Schmitz N, PCAWG Tumour Subtypes and Clinical Translation, Boutros PC, PCAWG Consortium. Sex differences in oncogenic mutational processes. *Nat Commun.* 2020 Aug 28;11(1):4330. PMID: PMC7455744
67. Inkman MJ, Jayachandran K, Ellis TM, Ruiz F, McLellan MD, Miller CA, Wu Y, **Ojesina AI**, Schwarz JK, Zhang J. HPV-EM: an accurate HPV detection and genotyping EM algorithm. *Sci Rep.* 2020 Aug 31;10(1):14340. PMID: PMC7459114
68. Bailey MH, Meyerson WU, Dursi LJ, Wang LB, Dong G, Liang WW, Weerasinghe A, Li S, Li Y, Kelso S, MC3 Working Group, PCAWG novel somatic mutation calling methods working group, Saksena G, Ellrott K, Wendl MC, Wheeler DA, Getz G, Simpson JT, Gerstein MB, Ding L, PCAWG Consortium. Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nat Commun.* 2020 Sep 21;11(1):4748. PMID: PMC7505971
69. Bailey MH, Meyerson WU, Dursi LJ, Wang LB, Dong G, Liang WW, Weerasinghe A, Li S, Li Y, Kelso S, MC3 Working Group, PCAWG novel somatic mutation calling methods working group, Saksena G, Ellrott K, Wendl MC, Wheeler DA, Getz G, Simpson JT, Gerstein MB, Ding L, PCAWG Consortium. Author Correction: Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nat Commun.* 2020 Nov 30;11(1):6232. PMID: PMC7705717
70. Sakhuja S, Fowler ME, **Ojesina AI**. Race/ethnicity, sex and insurance disparities in colorectal cancer screening among individuals with and without cardiovascular disease. *Prev Med Rep.* 2021 Mar;21:101263. PMID: PMC7773575
71. Weeks SE, Kammerud SC, Metge BJ, AlSheikh HA, Schneider DA, Chen D, Wei S, Mobley JA, **Ojesina AI**, Shevde LA, Samant RS. Inhibiting  $\beta$ -catenin disables nucleolar functions in triple-negative breast cancer. *Cell Death Dis.* 2021 Mar 04;12(3):242. PMID: PMC7933177
72. Halle MK, Sødal M, Forsse D, Engerud H, Woie K, Lura NG, Wagner-Larsen KS, Trovik J, Bertelsen BI, Haldorsen IS, **Ojesina AI**, Krakstad C. A 10-gene prognostic signature points to LIMCH1 and HLA-DQB1 as important players in aggressive cervical cancer disease. *Br J Cancer.* 2021 May;124(10):1690-1698. PMID: PMC8110544
73. Chung TKH, Doran G, Cheung TH, Yim SF, Yu MY, Worley MJ Jr, Elias KM, Thorner AR, Pedamallu CS, **Ojesina AI**, Lau KM, Ducar MD, Wong RRY, Wang VW, Nag A, Wollison BM, Dalgarno A, Lee JHS, Yeung SY, Wong L, Horowitz NS, Davis MR, Leung SA, Mu Y, Mok SC, Chan PKS, Lawrence MS, Crum CP, Chiu RWK, Berkowitz RS, Wong YF. Dissection of *PIK3CA* Aberration for Cervical Adenocarcinoma Outcomes. *Cancers (Basel).* 2021 Jun 28;13(13). PMID: PMC8269188
74. Behring M, Ye Y, Elkholy A, Bajpai P, Agarwal S, Kim HG, **Ojesina AI**, Wiener HW, Manne U, Shrestha S, Vazquez AI. Immunophenotype-associated gene signature in ductal breast tumors varies by receptor subtype, but the expression of individual signature genes remains consistent. *Cancer Med.* 2021 Aug;10(16):5712-5720. PMID: PMC8366080

75. Ruiz FJ, Sundaresan A, Zhang J, Pedomallu CS, Halle MK, Srinivasasainagendra V, Zhang J, Muhammad N, Stanley J, Markovina S, Tiwari HK, Grigsby PW, Krakstad C, Schwarz JK, **Ojesina AI**. Genomic Characterization and Therapeutic Targeting of HPV Undetected Cervical Carcinomas. *Cancers (Basel)*. 2021 Sep 10;13(18). PMID: PMC8467954
76. Halle MK, Sundaresan A, Zhang J, Pedomallu CS, Srinivasasainagendra V, Blair J, Brooke D, Bertelsen BI, Woie K, Shrestha S, Tiwari H, Wong YF, Krakstad C, **Ojesina AI**. Genomic alterations associated with mutational signatures, DNA damage repair and chromatin remodeling pathways in cervical carcinoma. *NPJ Genom Med*. 2021 Oct 07;6(1):82. PMID: PMC8497615
77. Sohail M, Long DM, Batey DS, Mugavero MJ, **Ojesina AI**, Levitan EB. Partnership status and time to viral suppression and sustained viral suppression among newly diagnosed heterosexual people with HIV. *Int J STD AIDS*. 2022 Mar;33(4):347-354. PMID: PMC9364114
78. Sohail M, Long DM, Mugavero MJ, Batey DS, **Ojesina AI**, Levitan EB. Partnership status and retention in care among cisgender heterosexual newly diagnosed people with HIV: a cohort study. *AIDS Care*. 2023 Sep;35(9):1428-1436. PMID: PMC9519801
79. Sharafeldin N, Zhang J, Singh P, Bosworth A, Chen Y, Patel SK, Wang X, Francisco L, Forman SJ, Wong FL, **Ojesina AI**, Bhatia S. Genome-wide variants and polygenic risk scores for cognitive impairment following blood or marrow transplantation. *Bone Marrow Transplant*. 2022 Jun;57(6):925-933. PMID: PMC9233077
80. Galadanci NA, Sohail M, Akinyelure OP, Kanter J, **Ojesina AI**. Treatment-related Correlates of Growth in Children With Sickle Cell Disease in the DISPLACE Cohort. *J Pediatr Hematol Oncol*. 2022 Jul 01;44(5):249-254. PMID: PMC8898314
81. Mukherjee A, Ye Y, Wiener HW, Kuniholm MH, Minkoff H, Michel K, Palefsky J, D'Souza G, Rahangdale L, Butler KR, Kempf MC, Sudenga SL, Aouizerat BE, **Ojesina AI**, Shrestha S. Variations in Genes Encoding Human Papillomavirus Binding Receptors and Susceptibility to Cervical Precancer. *Cancer Epidemiol Biomarkers Prev*. 2023 Sep 01;32(9):1190-1197. PMID: PMC10472094
82. Caston NE, Franks JA, Balas N, Eltoum N, Thigpen H, Patterson M, Azuero A, **Ojesina AI**, Dent DN, Hildreth K, Lalor FR, McGowen C, Huang CS, Dionne-Odom JN, Weiner BJ, Jackson BE, Basch EM, Stover AM, Howell D, Pierce JY, Rocque GB. Evaluating Nurses' Time to Response by Severity and Cancer Stage in a Remote Symptom Monitoring Program for Patients With Breast Cancer. *JCO Clin Cancer Inform*. 2023 Jun;7:e2300015. PMID: PMC10530733
83. Kumari N, Kumari R, Dua A, Singh M, Kumar R, Singh P, Duyar-Ayerdi S, Pradeep S, **Ojesina AI**, Kumar R. From Gut to Hormones: Unraveling the Role of Gut Microbiota in (Phyto)Estrogen Modulation in Health and Disease. *Mol Nutr Food Res*. 2024 Mar;68(6):e2300688.
84. van den Berg MC, Berg HF, Stokowy T, Hoiwik EA, Woie K, Engerud H, **Ojesina AI**, Haldorsen IS, Trovik J, Bertelsen BI, Krakstad C, Halle MK. Expression patterns of mismatch repair proteins in cervical cancer uncover independent prognostic value of MSH-2. *Int J Gynecol Cancer*. 2024 Jul 01;34(7):993-1000. PMID: PMC11228214