Serican Journal of Medicine
2025, VOL. 2, NO. 4, 24314
https://doi.org/10.17161/sjm.v2i4.24314

2025 SAU Annual Meeting Report: Unraveling the Molecular Complexities of Urologic Malignancies

Xiaoqi Liu[1], Benyi Li[2], and the SAU Conference Organization Team

[1]Department of Toxicology & Cancer Biology, The University of Kentucky College of Medicine, Lexington, KY 40536, USA;
[2]Department of Urology, The University of Kansas Medical Center, Kansas City, KS 66160, USA

The 2025 Society of Academic Urologists (SAU) annual meeting was held during Jun 15-18, 2025, and showcased the latest discoveries in urologic oncology with a particular emphasis on prostate cancer biology, epigenetic regulation, immunotherapy, and novel therapeutic targets. Featuring an exceptional lineup of keynote speakers, scientific symposia, and interactive forums, the meeting provided a dynamic platform for the exchange of ideas among researchers, clinicians, and trainees dedicated to advancing urologic science and improving patient outcomes.

Opening Session: Keynotes on Epigenetics and Transcriptional Reprogramming

The conference commenced with an evening reception and opening remarks by Dr. Benyi Li (University of Kansas Medical Center), who welcomed attendees and set the tone for a highly engaging program. The keynote session featured two pioneering researchers.

Dr. Qi Cao (Northwestern University) delivered a compelling keynote on the non-canonical function of EZH2 in prostate cancer. He presented data showing that EZH2, widely known as a histone methyltransferase, also directly interacts with the RNA-editing enzyme ADAR1. This interaction modulates A-to-I RNA editing, thereby influencing transcript stability and oncogenic signaling. Through its ability to reshape substrate selectivity of ADAR1 and suppress mRNA degradation, EZH2 emerges as a pivotal regulator of post-transcriptional gene expression. Notably, ADAR1 depletion sensitized prostate tumors to EZH2-targeted therapies, suggesting a novel combinatorial strategy for treating advanced prostate cancer [1, 2].

Dr. Qianben Wang (Banks Anderson, Dr. Distinguished Professor of Pathology at Duke University) introduced another keynote speaker, Dr. Changmeng Cai (University of Massachusetts Boston). Dr. Cai's presentation focused on the role of super-enhancers in defining molecular subtypes of metastatic castration-resistant prostate cancer (mCRPC). His team developed the Super-Enhancer Analysis for Lineages (SEAL) pipeline to classify five distinct SE programs. Among these, the AR-1 and AR-2 subtypes were associated with epithelial-to-mesenchymal transition (EMT) and metabolic reprogramming, respectively. TWIST1 and HNF1A were identified as key transcriptional drivers, with HNF1A promoting a hepatocyte-like, pro-metastatic state. These findings not only deepen our understanding of CRPC heterogeneity but also nominate actionable targets for therapeutic development [3-5].

Dr. Jianfeng Xu, MD/PhD (Endeavor Health Evanston), presented a special lecture with the title of "Germline Testing in Prostate Cancer: An Evidence-Based Approach Within and Beyond NCCN Guidelines". Approximately 50% of prostate cancer (PCa) patients meet the National Comprehensive Cancer Network (NCCN) guidelines for germline testing at diagnosis. However, the specific genes recommended for testing, their various clinical utilities, and the supporting evidence remain poorly defined in clinical adoption and complicate the interpretation of results. Additional genes and SNPs that are not included in the NCCN guidelines may also provide clinical value for the management of prostate cancer patients. In this presentation, Dr. Xu reviewed current NCCN guidelines for germline testing in PCa, including their intended clinical applications, such as identifying potential genetic causes, assessing familial risk, predicting disease prognosis, and informing treatment response [6]. He also introduced novel PCa-associated genes recently identified but not yet incorporated into current guidelines and discussed the role and limitations of polygenic risk scores in germline testing. In addition, he described GoPath ProstateNow-v2, a clinical-grade and CLIA-certified germline test that includes all NCCN-recommended genes, as well as PRS and recently discovered novel PCa genes.

Session 1: Epigenetic Regulation and Cellular Plasticity in Prostate Cancer

It was co-chaired by Chunhong Yan (Augusta) and Zhenbang Chen (Meharry Medical College), explored the multifaceted roles of chromatin and RNA modifications in tumorigenesis. Dr. Yang Yi (Northwestern University) reported on the crosstalk between EZH2 and m6A RNA methylation in driving prostate cancer progression. His data revealed that EZH2 activates an autoregulatory loop via YTHDF1, reinforcing a hyper-m6A landscape that supports tumor growth. Combining EZH2 and m6A inhibitors yielded synergistic therapeutic effects in preclinical models. Dr. Di Zhao (MD Anderson Cancer Center) presented mechanistic insights into how histone methyltransferase ASH1L primes the metastatic bone niche. His work demonstrated that ASH1L rewires H3K4 and H3K36 methylation to cooperate with HIF-1α, upregulating IGF-2 and reprogramming infiltrating monocytes into lipid-associated tumor-associated macrophages (LA-TAMs). These LA-TAMs sustain a pro-tumoral, anti-inflammatory microenvironment. Targeting the ASH1L-HIF1α axis attenuated metastasis, offering a new epigenetic target for intervention [7]. Dr. Housheng Hansen He (University of Toronto) presented a pan-omic study of m6A dysregulation in primary prostate tumors. Germline polymorphisms were shown to influence m6A deposition, which in turn modulated disease aggression and metastatic potential. VCAN emerged as a key m6A-modified transcript linked to poor prognosis [8].

Session 2: Novel Targets and Lineage Plasticity in GU Cancers

It was chaired by Pengbo Zhou (Cornell) and Jason Luo (Johns Hopkins), highlighted lineage-specific vulnerabilities in prostate cancer. Dr. Dean Tang (Roswell Park) described a population of slow-cycling prostate cancer cells (PSCCs) enriched for stem-like features and inherent therapy resistance. Using trigenic mouse models and transcriptomic analysis, his team demonstrated that PSCCs are primed for epithelial-mesenchymal transition and preferentially survive androgen deprivation and chemotherapy [9]. Dr. Dingxiao (Jerry) Zhang (Hunan University) provided a complementary perspective on the cell-of-origin in aggressive PCa. His work dissected the basal and luminal lineage hierarchies, identifying luminal progenitors as a potential source of CRPC. He also described AR+NE- transdifferentiated subtypes sensitive to SP1 or translation inhibitors [10]. Dr. Yanquan Zhang (University of Kentucky) introduced PLK1 as a novel driver of neuroendocrine prostate cancer (NEPC). PLK1-mediated phosphorylation of ASCL1 and NEUROD1 influenced protein stability and transcriptional activity. PLK1 inhibition suppressed NEPC gene programs, nominating it as a promising therapeutic target [11]. Dr. Meng Zhang (Emory University) discussed the emerging role of microproteins (<100 amino acids) in therapy resistance. Using ribosome profiling and transcriptomic data, she identified MMP24-AS1 as an ARSI-regulated microprotein critical for mCRPC cell survival [12].

Session 3: Novel Targets in GU Cancers

Chaired by Jing-tang Dong (SUSTech China) and Dinglan Wu (CUHK), this session covered several new targets in prostate cancer. The session started with a presentation by Dr. Jing-tang Dong, who described crosstalk between ZFHX3, AR, and ER in the regulation of prostate tumorigenesis, followed by Dr. Weiran Feng (Fox Chase Cancer Center), who showed cell context dependency and vulnerabilities of ERG-driven prostate cancer [13]. Dr. Dinglan Wu discussed targeting the LRG1 protein in prostate cancer bone metastasis and its potential as a liquid biopsy biomarker [14]. Dr. Houjian Cai (U of Georgia) demonstrated to use of extracellular vesicles as a vehicle to deliver CRISPR machinery for targeting castration-resistant prostate cancer [15]. Dr. Kaifu Chen (Children's Hospital at Boston) described how to map RNA modifications in prostate cancer by AI analysis of Nanopore sequencing data [16]. The session was ended by a short presentation by Dr. Xintao Qiu (Harvard Medical School) to demonstrate how to detect small cell transformation in patients through epigenomic cfDNA profiling [17].

Session 4: Bioinformatics, AI, and New Technologies

Chaired by Xuesen Dong (UBC) and Hsin-Sheng Yang (University of Kentucky), this session showcased the integration of computational biology and experimental therapeutics. Dr. Li Liu (UT Southwestern) evaluated vascular-disrupting agents (VDAs) in kidney cancer models, highlighting their synergy with immunotherapies [18]. Dr. Zheng Xia (OHSU) presented a TCGA pan-cancer analysis linking AR activity with reduced immune cell infiltration and interferon-gamma signaling. Post-enzalutamide biopsies from mCRPC patients showed increased immune cell abundance, implying that AR inhibition may restore tumor immunogenicity. Dr. Changsheng Zhao (Emory) used Nanopore long-read sequencing to map structural variants and transposable elements in prostate cancer, revealing new layers of genome

complexity [19]. Dr. David Y. Zhang (SUNY Downstate) introduced AI-powered digital pathology platforms to enable spatial analysis, prognosis prediction, and molecular annotation in urologic cancers [20]. Dr. Wenliang Li (UTHS Houston) demonstrated how to identify and target novel kinase regulators for NEPC and cancer metastasis [21].

Session 5: Novel Therapeutic Targets in GU Cancer

It was chaired by Ming Chen (Duke) and Shang Su (LSU) and further delved into new targets. Dr. Zhiping Wang (Lanzhou University) described engineered oncolytic adenoviruses for bladder cancer, with tissue specificity and enhanced efficacy through combination with cisplatin or radiotherapy [22-24]. Dr. Jianhua Xiong (Emory) highlighted acetate as a regulator of EMT and T cell differentiation [25-28]. Dr. Jinghui Liu (Kentucky) revealed a synthetic lethal interaction between NMD components and HSP90α, with dual inhibition showing strong anti-tumor effects [29]. Dr. Zongwei Wang (Harvard/BIDMC) reported that SRD5A2 expression correlates with prostate volume and methylation status, suggesting implications for individualized BPH treatment [30].

Session 6: Tumor Microenvironment and Immunotherapy

It was co-chaired by Su Deng (Yale) and Kexin Xu (Virginia). Dr. Zhou Wang (University of Pittsburgh) discussed the modulation of androgen signaling in the context of BPH-associated inflammation, highlighting opportunities for therapeutic intervention [31]. Dr. Wang's findings suggest that low-grade prostatic inflammation could enhance the expression of androgen-responsive genes in BPH, indicating an important role for prostate inflammation in BPH pathogenesis. Dr. Zhu Wang (UC Santa Cruz) and Dr. Chin-Lee Wu (MGH/Harvard) provided critical insights into cell-of-origin models in bladder cancer [32, 33] and pathological characterization of prostate cancer subtypes, respectively [34-36]. In particular, Dr. Wang's work supports the notion that urothelial basal cells are more competitive than intermediate or umbrella cells in producing bladder tumors and are likely the cells of origin for the more aggressive bladder cancer subtype. Dr. Wu described lessons learned from the unusual pathological features.

Session 7: Cancer Etiology, Progression, and Metastasis

Co-chaired by Yuanyuan Zhang (Wake Forest) and Xiaohong Li (U of Toledo), this session addressed the molecular heterogeneity and inflammatory signaling in urologic tumors. Dr. Sean Li (Cedars-Sinai Medical Center) explored why males sex are more susceptible to cancers and presented solid evidence to show the biasing effects of the sex hormones with androgens increase bladder cancer risk through both tumor cell-intrinsic and extrinsic mechanisms [37, 38]. Dr. Shuai Gao (New York Medical College) showed how histone lactylation directs a distinct enhancer landscape to drive prostate cancer progression [5, 39]. While Dr. Jianmin Zhang (University of Toledo) focused on dissecting molecular mechanisms of breast cancer metastasis, Dr. Hai Wang (Roswell Park Cancer Center) described the metabolic symbiosis between tumor and bone cells in prostate cancer bone metastasis [40, 41]. Specifically, Dr. Zhang's work provides mechanistic insight into the importance of TAZ-CAMK1D-CTTN-mediated actin cytoskeletal regulation during breast cancer metastasis. Dr. Wang's work highlight MCT1 as a critical metabolic vulnerability in prostate cancer metastasis and suggest that targeting lactate uptake may offer a promising therapeutic strategy for this lethal disease.

Session 8: Therapy Resistance in Cancer

Co-chaired by Jason Liu (UTHSCSA) and Xuefeng Liu (OSU), this session focused on various drug resistance mechanisms. After Dr. Zhiguo Li (U of Kentucky) presented a new mechanism for docetaxel resistance [11], Dr. Feng Yang (Baylor College of Medicine) showed how COP1 regulates cellular response to taxane in prostate cancer [42]. Dr. Su Deng (Yale) demonstrated how to target lineage plasticity drivers to overcome therapy resistance in prostate cancer [43, 44]. Dr. Jianneng Li (Notre Dame University) described an unexpected mechanism of enzalutamide anti-tumor activity in prostate cancer [45]. Dr. Luksana Chaiswing (University of Kentucky) showed how to promote mitochondrial vulnerability with redox state modulating agents to enhance the efficacy of radiotherapy [46, 47]. Finally, Dr. Jia Li (Harvard Medical School) explored new synergies with PARP inhibitors in prostate cancer [48].

Career Development and Closing Forum

The evening professional development forum, chaired by Drs. Xiaohong Li and Li Liu featured a keynote by Dr. X. Shirley Liu (GV20 Therapeutics). Her presentation outlined GV20's AI-powered STEAD platform for antibody discovery. Their lead candidate, GV20-0251, an anti-IGSF8 monoclonal antibody-was developed through AI-guided selection and demonstrated monotherapy efficacy in early trials. This approach exemplifies the integration of computational prediction and biologics development. Roundtable discussions addressed career transitions, dual-career family dynamics, and strategies for becoming a rising star in academic research [49].

Keynote Presentation: Uncovering the Hidden Genetics of Disease Through Tandem Repeats

Dr. Qianben Wang (Banks Anderson, Dr. Distinguished Professor of Pathology at Duke University) introduced the third keynote speaker Dr. Wei Li, the Grace B. Bell Endowed Chair and Professor of Bioinformatics at the University of California, Irvine. Dr. Li delivered a visionary plenary lecture highlighting the overlooked but critical role of tandem repeat (TR) variations in human disease genetics. As a leader in computational genomics and creator of the widely-used MACS algorithm for ChIP-seq, Dr. Li emphasized the transformative potential of TRs-repetitive DNA elements previously neglected in GWAS and clinical diagnostics. His lab's recent efforts led to the development of two landmark resources: **TR-Atlas** [50], profiling ~1 million TRs from 340,000 individuals, and **TR-xQTL** [51], establishing the functional regulatory landscape of TRs across the human genome. Leveraging these platforms, Dr. Li presented compelling unpublished findings linking TR variants to a spectrum of complex and rare diseases-including cardiovascular disorders, neurodevelopmental anomalies, Alzheimer's disease, liver pathology, diabetes, and aggressive cancers. Notably, many associations have been experimentally validated, showcasing the clinical utility of TRs in uncovering disease mechanisms and risk genes. This presentation underscored the urgent need to integrate TR analysis into mainstream genomics pipelines and precision medicine efforts.

Conclusion

The 2025 SAU Annual Meeting successfully highlighted the latest advances across epigenetics, lineage plasticity, tumor microenvironment, and emerging therapeutics in urologic oncology. With cutting-edge technologies and a collaborative spirit, the conference reaffirmed the critical role of the SAU community in shaping the future of precision medicine and improving the lives of patients with urologic malignancies.

Acknowledgements

This event was partially supported by several industrial sponsors, including MedChemExpress US LLC, NovinoPath LLC, GoPath Global Inc., and SinoBiological US Inc. We are also grateful for the SAU Conference Organization Team, who contributed a lot of private time and energy in organizing this superb conference.

References

1. Yum C, Schaefer RA, Wang R, Wang TY, Lu X, Liu Q, Ren Y, Meng Q, Yang Y, Zhang X *et al*: **Ketone drink enhances therapeutic efficacy in prostate cancer by targeting EZH2**. *Oncogenesis* 2025, **14**(1):24.
2. Meng Q, Shen J, Ren Y, Liu Q, Wang R, Li Q, Jiang W, Wang Q, Zhang Y, Trinidad JC *et al*: **EZH2 directly methylates PARP1 and regulates its activity in cancer**. *Sci Adv* 2024, **10**(48):eadl2804.
3. Labaf M, Han W, Zhang S, Liu M, Patten ND, Li M, Patalano S, Macoska JA, Balk SP, Han D *et al*: **Heterogeneous Responses to High-Dose Testosterone in Castration-Resistant Prostate Cancer Tumors with Mixed Rb-Proficient and Rb-Deficient Cells**. *Mol Cancer Ther* 2025, **24**(5):772-783.
4. Wang Z, Townley SL, Zhang S, Liu M, Li M, Labaf M, Patalano S, Venkataramani K, Siegfried KR, Macoska JA *et al*: **FOXA2 rewires AP-1 for transcriptional reprogramming and lineage plasticity in prostate cancer**. *Nat Commun* 2024, **15**(1):4914.
5. Li M, Liu M, Han W, Wang Z, Han D, Patalano S, Macoska JA, Balk SP, He HH, Corey E *et al*: **LSD1 Inhibition Disrupts Super-Enhancer-Driven Oncogenic Transcriptional Programs in Castration-Resistant Prostate Cancer**. *Cancer Res* 2023, **83**(10):1684-1698.
6. Isaacs WB, Wei J, Gielzak M, Wang Q, Snyder NA, Zheng S, Yan G, Lu L, Engelmann V, Rabizadeh D *et al*: **Discovery of a Recurrent Frameshift Ashkenazi Jewish Founder Mutation (F722fs) in the PARP Inhibitor-sensitive MMS22L Gene Associated with Higher Risk of Prostate Cancer**. *Eur Urol Focus* 2025.
7. Meng C, Lin K, Shi W, Teng H, Wan X, DeBruine A, Wang Y, Liang X, Leo J, Chen F *et al*: **Histone methyltransferase ASH1L primes metastases and metabolic reprogramming of macrophages in the bone niche**. *Nat Commun* 2025, **16**(1):4681.
8. Xu X, Zhu H, Hugh-White R, Livingstone J, Eng S, Zeltser N, Wang Y, Pajdzik K, Chen S, Houlahan KE *et al*: **The landscape of N(6)-methyladenosine in localized primary prostate cancer**. *Nat Genet* 2025, **57**(4):934-948.
9. Kirk JS, Wang J, Long M, Rosario S, Tracz A, Ji Y, Kumar R, Liu X, Jamroze A, Singh PK *et al*: **Integrated single-cell analysis defines the epigenetic basis of castration-resistant prostate luminal cells**. *Cell Stem Cell* 2024, **31**(8):1203-1221 e1207.
10. Zou C, Li W, Zhang Y, Feng N, Chen S, Yan L, He Q, Wang K, Li W, Li Y *et al*: **Identification of an anaplastic subtype of prostate cancer amenable to therapies targeting SP1 or translation elongation**. *Sci Adv* 2024, **10**(14):eadm7098.
11. Zhang Y, Fong KW, Mao F, Wang R, Allison DB, Napier D, He D, Liu J, Zhang Y, Chen J *et al*: **Elevating PLK1 overcomes BETi resistance in prostate cancer via triggering BRD4 phosphorylation-dependent degradation in mitosis**. *Cell Rep* 2024, **43**(7):114431.
12. Li H, Melnyk JE, Fu BXH, Shrestha R, Zhang M, Sjostrom M, Feng S, Anderson JA, Han W, Chesner LN *et al*: **Genome-wide CRISPR screens identify PTGES3 as a novel AR modulator**. *bioRxiv* 2025.
13. Fu X, Zhang Z, Chen R, A J, An N, Tian X, Dong JT: **ZFHX3 is integral to androgen/AR signaling involving protein association with AR in prostate cancer cells**. *Sci Rep* 2025, **15**(1):20931.
14. Liu P, Wang W, Wang F, Fan J, Guo J, Wu T, Lu D, Zhou Q, Liu Z, Wang Y *et al*: **Alterations of plasma exosomal proteins and motabolies are associated with the progression of castration-resistant prostate cancer**. *J Transl Med* 2023, **21**(1):40.
15. Ye C, Gosser C, Runyon ED, Zha J, Cai J, Beharry Z, Rickman CB, Klingeborn M, Liu Y, Xie J *et al*: **Src family kinases engage differential pathways for encapsulation into extracellular vesicles**. *J Extracell Biol* 2023, **2**(6).
16. Li Y, Yi Y, Gao X, Wang X, Zhao D, Wang R, Zhang LS, Gao B, Zhang Y, Zhang L *et al*: **2'-O-methylation at internal sites on mRNA promotes mRNA stability**. *Mol Cell* 2024, **84**(12):2320-2336 e2326.
17. El Zarif T, Meador CB, Qiu X, Seo JH, Davidsohn MP, Savignano H, Lakshminarayanan G, McClure HM, Canniff J, Fortunato B *et al*: **Detecting Small Cell Transformation in Patients with Advanced EGFR Mutant Lung Adenocarcinoma through Epigenomic cfDNA Profiling**. *Clin Cancer Res* 2024, **30**(17):3798-3811.
18. Wanniarachchi HI, Schuetze R, Deng Y, Hamal KB, Pavlich CI, Tankoano PEO, Tamminga C, Hammers H, Kapur P, Bueno LMA *et al*: **Evaluating Therapeutic Efficacy of the Vascular Disrupting Agent OXi8007 Against Kidney Cancer in Mice**. *Cancers (Basel)* 2025, **17**(5).
19. Lu X, Keo V, Cheng I, Xie W, Gritsina G, Wang J, Lu L, Shiau CK, He Y, Jin Q *et al*: **NKX2-1 drives neuroendocrine transdifferentiation of prostate cancer via epigenetic and 3D chromatin remodeling**. *Nat Genet* 2025, **57**(8):1966-1980.
20. Zhu M, Sali R, Baba F, Khasawneh H, Ryndin M, Leveillee RJ, Hurwitz MD, Lui K, Dixon C, Zhang DY: **Artificial intelligence in pathologic diagnosis, prognosis and prediction of prostate cancer**. *Am J Clin Exp Urol* 2024, **12**(4):200-215.

21. Zheng D, Zhang Y, Yang S, Su N, Bakhoum M, Zhang G, Naderinezhad S, Mao Z, Wang Z, Zhou T *et al*: **Androgen deprivation induces neuroendocrine phenotypes in prostate cancer cells through CREB1/EZH2-mediated downregulation of REST**. *Cell Death Discov* 2024, **10**(1):246.
22. Cao X, Gao D, Zhang S, Yu X, Su X, Lu J, Wang Z: **Cytotoxic effect of bladder cancer oncolytic virus on bladder cancer stem-like cells via pyroptosis pathway**. *Technol Health Care* 2025:9287329251349081.
23. Zhang Y, Yang E, Zhang X, Zhang Z, Huang G, Tang B, Chen C, Lai L, Pei Z, Zhang Y *et al*: **Autophagy-related biological targets and network mechanisms of juglone against bladder cancer**. *J Cancer Res Clin Oncol* 2025, **151**(6):194.
24. Shi Y, Fan G, Yang E, Zhang Y, Ding H, Tian J, Cheng L, Wang H, Hao T, Wang B *et al*: **Enhanced efficacy of immune checkpoint inhibitors by folate-targeted multifunctional drug through synergistic therapy inducing ferroptosis and immunogenic cell death in bladder cancer**. *Mater Today Bio* 2025, **31**:101584.
25. Bronson R, Lyu J, Xiong J: **Transcriptome analysis reveals molecular signature and cell-type difference of Homo sapiens endothelial-to-mesenchymal transition**. *G3 (Bethesda)* 2023, **13**(12).
26. Lyu J, Li Z, Roberts JP, Qi YA, Xiong J: **The short-chain fatty acid acetate coordinates with CD30 to modulate T-cell survival**. *Mol Biol Cell* 2023, **34**(8):br11.
27. Jing X, Lyu J, Xiong J: **Acetate regulates GAPDH acetylation and T helper 1 cell differentiation**. *Mol Biol Cell* 2023, **34**(7):br10.
28. Lyu J, Pirooznia M, Li Y, Xiong J: **The short-chain fatty acid acetate modulates epithelial-to-mesenchymal transition**. *Mol Biol Cell* 2022, **33**(8).
29. Mao F, Kong Y, Liu J, Rao X, Li C, Donahue K, Zhang Y, Jones K, Zhang Q, Xu W *et al*: **Diptoindonesin G antagonizes AR signaling and enhances the efficacy of antiandrogen therapy in prostate cancer**. *Prostate* 2022, **82**(8):917-932.
30. Sharkey C, Gu B, Long X, Tang Y, Patsatzis N, Li S, Olumi AF, Wang Z: **Stromal SRD5A2 promotes prostate growth through WNT5A-LEF1-IGF1 signaling in benign prostatic hyperplasia**. *bioRxiv* 2025.
31. Liu TT, Igarashi T, El-Khoury N, Ihejirika N, Paxton K, Jaumotte J, Dhir R, Hudson CN, Nelson JB, DeFranco DB *et al*: **Benign prostatic hyperplasia nodules in patients treated with celecoxib and/or finasteride have reduced levels of NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, a mitochondrial protein essential for efficient function of the electron transport chain**. *Prostate* 2024, **84**(14):1309-1319.
32. Machacek ME, Wang H, Devins K, Sadow PM, Wu CL, Oliva E, Saylor PJ, Cornejo KM: **A Proposal for Revised and Simplified Renal Pelvic Urothelial Carcinoma Staging Criteria: A Clinicopathologic Study of 141 Tumors**. *Am J Surg Pathol* 2025, **49**(2):113-120.
33. Rice-Stitt T, Valencia-Guerrero A, Cornejo KM, Wu CL: **Updates in Histologic Grading of Urologic Neoplasms**. *Arch Pathol Lab Med* 2020, **144**(3):335-343.
34. Yu C, Hu K, Nguyen D, Wang ZA: **From genomics to functions: preclinical mouse models for understanding oncogenic pathways in prostate cancer**. *Am J Cancer Res* 2019, **9**(10):2079-2102.
35. Horton C, Liu Y, Wang J, Green J, Tsyporin J, Chen B, Wang ZA: **Modulation of the canonical Wnt activity by androgen signaling in prostate epithelial basal stem cells**. *Stem Cell Reports* 2023, **18**(6):1355-1370.
36. Bleeker J, Wang ZA: **Applications of Vertebrate Models in Studying Prostatitis and Inflammation-Associated Prostatic Diseases**. *Front Mol Biosci* 2022, **9**:898871.
37. Chaudhary P, Singha B, Abdel-Hafiz HA, Velegraki M, Sundi D, Satturwar S, Parwani AV, Grivennikov SI, You S, Goodridge HS *et al*: **Sex differences in bladder cancer: understanding biological and clinical implications**. *Biol Sex Differ* 2025, **16**(1):31.
38. Theodorescu D, Li Z, Li X: **Sex differences in bladder cancer: emerging data and call to action**. *Nat Rev Urol* 2022, **19**(8):447-449.
39. Yang Y, Di Ruscio A, Inoue S, Wang G, Gao S: **Editorial: Interplay between epigenetic modifiers and transcription factors in driving cancer progression**. *Front Oncol* 2023, **13**:1211537.
40. Wang X, Shen H, Chen Y, Zhang Y, Wang J, Liu S, Xu B, Wang H, Frangou C, Zhang J: **MEF2D Functions as a Tumor Suppressor in Breast Cancer**. *Int J Mol Sci* 2024, **25**(10).
41. Das A, Barry MM, Ernst CA, Dahiya R, Kim M, Rosario SR, Lo HC, Yu C, Dai T, Gugala Z *et al*: **Differential bone morphology and hypoxia activity in skeletal metastases of ER(+) and ER(-) breast cancer**. *Commun Biol* 2024, **7**(1):1545.
42. Shen T, Dong B, Meng Y, Moore DD, Yang F: **A COP1-GATA2 axis suppresses AR signaling and prostate cancer**. *Proc Natl Acad Sci U S A* 2022, **119**(43):e2205350119.
43. Jiang Y, Cheng S, Li L, Fraidenburg M, Kim IY, Deng S, Mu P: **Notch as a Driver of Lineage Plasticity and Therapeutic Target in Enzalutamide-Resistant Prostate Cancer**. *bioRxiv* 2025.

44. Jiang Y, Cheng S, Kim IY, Deng S, Mu P: **Pan-cancer Analysis Identified Ectopic RUNX1T1 Associated with Lineage Plasticity**. *bioRxiv* 2025.
45. Cui D, Li J, Zhu Z, Berk M, Hardaway A, McManus J, Chung YM, Alyamani M, Valle S, Tiwari R *et al*: **Cancer-associated fibroblast-secreted glucosamine alters the androgen biosynthesis program in prostate cancer via HSD3B1 upregulation**. *J Clin Invest* 2023, **133**(7).
46. Miller CE, Xu F, Zhao Y, Luo W, Zhong W, Meyer K, Jayswal R, Weiss HL, St Clair WH, St Clair DK *et al*: **Hydrogen Peroxide Promotes the Production of Radiation-Derived EVs Containing Mitochondrial Proteins**. *Antioxidants (Basel)* 2022, **11**(11).
47. Banadaki MD, Rummel NG, Backus S, Butterfield DA, St Clair DK, Campbell JM, Zhong W, Mayer K, Berry SM, Chaiswing L: **Extraction of redox extracellular vesicles using exclusion-based sample preparation**. *Anal Bioanal Chem* 2024, **416**(28):6317-6331.
48. Gui F, Jiang B, Jiang J, He Z, Tsujino T, Takai T, Arai S, Pana C, Kollermann J, Bradshaw GA *et al*: **Acute BRCAness induction and AR pathway blockage through CDK12/7/9 degradation enhances PARP inhibitor sensitivity in prostate cancer**. *Sci Adv* 2025, **11**(17):eadu0847.
49. Nicol PB, Paulson D, Qian G, Liu XS, Irizarry R, Sahu AD: **Robust identification of perturbed cell types in single-cell RNA-seq data**. *Nat Commun* 2024, **15**(1):7610.
50. Cui Y, Ye W, Li JS, Li JJ, Vilain E, Sallam T, Li W: **A genome-wide spectrum of tandem repeat expansions in 338,963 humans**. *Cell* 2024, **187**(22):6411-6412.
51. Cui Y, Arnold FJ, Li JS, Wu J, Wang D, Philippe J, Colwin MR, Michels S, Chen C, Sallam T *et al*: **Multi-omic quantitative trait loci link tandem repeat size variation to gene regulation in human brain**. *Nat Genet* 2025, **57**(2):369-378.