유한나 Hannah Yu Ph. D, 임상유전체연구원

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깃허브: https://github.com/hannahyu-source/portfolio
링크드인: https://www.linkedin.com/in/hannah-yu-9020ab268/?skipRedirect=true
구글스칼라: https://scholar.google.com/citations?user=pQJStZ0AAAAJ&hl=ko

Qualifications profile

임상 유전체 분석과 중개 연구 분야에서 10년 이상의 연구 경험을 보유한 연구자입니다. 삼성서울병원에서는 암 환자 검체 기반 WES 및 RNA sequencing을 수행하며 임상 연구와 NGS workflow를 경험하였고, 쓰리빌리언에서는 임상 유전 과학자로서 WES/WGS 기반 변이 해석, 임상 보고서 작성 및 의료진과의 협업을 통해 희귀질환 진단을 지원하였습니다. 또한 미국 오하이오주립대학교에서 Oxford Nanopore 기반 high-fidelity sequencing 기술을 개발하여 Advanced Science(IF 14.5) 제1저자 논문을 발표하였으며, 글로벌 공동연구 및 기술 개발 경험을 보유하고 있습니다. NGS 실험, 유전체 분석, 분자생물학, 임상 유전체 해석을 아우르는 전문성을 바탕으로 연구와 임상을 연결하는 중개 연구 역량을 갖추고 있습니다.

Education

- 2010–2016: 과학기술연합대학원대학교(UST) 생물분석과학과 박사
  학위논문: *유전자 계량을 위한 기준 측정 방법 개발: 유전자 메틸화, 유전자 발현, 세균 군집 프로파일링*
  지도교수: 양인철 교수
- 2009–2010: 한국표준과학연구원 생물분석센터 인턴십
  지도교수: 양인철 교수
- 2006–2008: 충남대학교 과학교육학과(생물전공) 석사
  학위논문: *제브라피쉬에서 Farnesoid X Receptor (fxr) 유전자 분리*
  지도교수: 김철희 교수
- 2001–2006: 한동대학교 생명과학과 학사

Research Experience and Skills

쓰리빌리언 – 임상 유전 과학자 (2025.11 ~ 2026.02)

- 유전체 검사(WES/WGS)의 변이 해석 및 보고서 작성
- AI를 활용하여 희귀질환 관련 유전자 및 변이에 대한 문헌 조사 및 임상적 해석
- 의료진 및 유전상담팀과의 커뮤니케이션을 통한 증상-유전정보 통합 분석
- 유전진단 인공지능 모델 고도화 연구(AI engineer, bioinformatics 전문가들과 공동 연구)

삼성서울병원 — 박사 연구원 (2025.03 ~ 2025.09)
암 환자 샘플 기반 유전체 시퀀싱 실험 설계 및 수행
- 임상 시료에서 핵산 추출, 품질 평가, 시퀀싱 라이브러리 제작
- NovaSeq X Plus 및 AVITI24 플랫폼을 활용한 WES 및 전사체 시퀀싱 수행
- 생물정보학팀과 협업하여 데이터 처리, 분석 및 해석 진행

부산대학교 — 박사 연구원 (2024.09 ~ 2025.01)
- 국가중앙인체자원은행에서 1,017건의 혈액 및 조직 자원을 제공받아 DNA 제작 및 QC 수행 (DNA 농도·순도 평가, qPCR 기반 성별 판별, 세균/마이코플라스마 오염 검사)
- 국립보건연구원 세균질환과에서 제공받은 6종 *Mycobacterium tuberculosis* 균주의 전장 유전체 시퀀싱 수행, 배양 촉진 물질 첨가 여부에 따른 유전체 데이터 비교분석을 통해 배양 조건 차이가 시퀀싱 결과에 미치는 영향 평가

오하이오주립대학교 — 박사후 연구원 (2016.04 ~ 2024.07)
- Oxford Nanopore 기반의 high-fidelity, long-range single-molecule sequencing 기법 개발
- Circular long-read DNA constructs 및 twin random barcode 생성 기술 개발
- 개발한 기술을 활용하여:
    - 환자 및 폐수 내 SARS-CoV-2 변이 검출 및 모니터링
    - 새로운 해양 RNA 바이러스 발견
    - 항레트로바이러스제(ART) 처리된 HIV-1 변이 프로파일링
- HIV-1 변이체 in vitro 선별
- CRISPR/Cas9 기반 유전체 편집
- HIV-1 RNA 유전체 수준의 후성유전학적 변형 패턴 규명

과학기술연합대학원대학교/한국표준과학연구원 캠퍼스— 박사과정 연구원 (2010.09 ~ 2016.02)
- 유전자 계량을 위한 기준 측정법 설계 및 검증
- dNMP/NMP, human genomic DNA, miRNA, gene methylation, 16S rDNA 등 인증표준물질(CRM) 개발
- NGS 기반 실험 전략 수립 및 샘플 라이브러리 제작/시퀀싱 수행 (Illumina MiSeq)
- 첨단 분석 장비 운용:
    - NGS: DNA 메틸화 분석, 전사체 분석, metagenome 분석
    - CE: DNA 메틸화, dNMP/NMP 분석, 핵산 정량
    - MALDI-TOF: 단백질 identification, genotyping
    - FACS: 세포 분류, 단일 세포 분석
- 분자생물학 연구기술 숙련: cloning, site-directed mutagenesis, qPCR/dPCR, High Resolution Melting(HRM), bisulfite conversion, in vitro methylation, and library preparation for NGS

충남대학교 — 석사과정 연구원 (2007 ~ 2008)
- 제브라피쉬 사육 및 관리
- microinjection 과 whole-mount in situ hybridization 수행

Publications

Peer-Reviewed Research Papers – Published

1. Yu H, Golconda S, Xue D, Zhu M, Lee GE, Viola C, Dominguez-Huerta G, Bolduc B, Sullivan M and Kim S, CLAE: A High-Fidelity Nanopore Sequencing Strategy for Read-Level Viral Variant Detection and Environmental RNA Virus Discovery, ***Advanced Science***. (2025) Sep 11:305978. doi:10.1002/advs.202505978. Online ahead of print.

PMID: 40936099 ***IF:14.5***

2. Baek A, Lee GE, Golconda S, Rayhan A, Manganaris A, Chen S, Tirumuru N, Yu H *et al*., Single-molecule epitranscriptomic analysis of full-length HIV-1 RNAs reveals functional roles of site-specific m6As, ***Nature Microbiology***, (2024) May;9(5):1340-1355. PMCID: PMC11087264. ***IF:28.3***
3. Baek A, Rayhan A, Lee GE, Golconda S, Yu H *et al*., Mapping m6A Sites on HIV-1 RNA Using Oligonucleotide LC-MS/MS, ***Methods Protoc***. (2024) Jan 10;7(1). PubMed PMID: 38251200; PubMed Central PMCID: PMC10801558. doi:10.3390/mps7010007. ***IF:2.4***
4. Kim S, Shukla RK, Yu H *et al*., CD3e-immunotoxin spares CD62Llo Tregs and reshapes organ-specific T-cell composition by preferentially depleting CD3ehi T cells**,** ***Front Immunol***. (2022); 13:1011190. PubMed PMID: 36389741; PubMed Central PMCID: PMC9643874. doi: 10.3389/fimmu.2022.1011190. eCollection, ***IF: 8.8***
5. Kim S, Shukla RK, Kim E, Cressman SG, Yu H *et al*., Comparison of CD3e Antibody and CD3e-sZAP Immunotoxin Treatment in Mice Identifies sZAP as the Main Driver of Vascular Leakage, ***Biomedicines*** (2022), 10, 1221. https://doi.org/10.3390/biomedicines10061221, ***IF: 6.0***
6. Suryawanshi GW, Khamaikawin W, Wen J, Shimizu S, Arokium H, Xie Y, Wang E, Kim S, Choi H, Zhang C, Yu H *et al*., The clonal repopulation of HSPC gene modified with anti-HIV-1 RNAi is not affected by preexisting HIV-1 infection***,*** ***Science Advances***, 2020, DOI: 10.1126/sciadv.aay9206, ***IF: 13.1***
7. Yu H, Hahn Y, Park SR *et al.,* Normalization of human RNA-seq experiments using chimpanzee RNA as a spike-in standard, Sci. Rep., (2016) ***IF: 4.3***
8. Yu H, Hahn Y, and Yang I, Reference materials for calibration of analytical biases in quantification of DNA methylation, PLOS One, (2015) ***IF: 3.2***
9. Kang MJ, Yu H, Kim SK, Park SR, and Yang I, Quantification of trace-level DNA by real time whole genome amplification, PLOS One, (2011) ***IF: 3.2***

Peer-Reviewed Research Papers – Submitted

1. Lee GE, Golconda S, Yu H, Kim S, and Kim S, "Universal RNA Linearization Enables Full-Length Nanopore DRS Across Whole Transcriptomes" manuscript submitted.

Peer-Reviewed Research Papers – In preparation

1. Yu H, Golconda S, Baek A, Kim S and Kim S, Novel twin barcoding for ultra-high-accuracy, Nanopore sequencing for HIV-1 whole genome analysis, manuscript in preparation
2. Yu H, Golconda S, Baek A, Kim S and Kim S, Recombination-free, long-range PCR for full-length HIV-1 DNA genotyping, manuscript in preparation
3. Kim S, Yu H, Golconda S, Reneu J, Hanel W and Kim S, "Treatment resistance of Follicular T helper cells in T-cell-targeting antibody and immunotoxin therapies" manuscript in preparation
4. Golconda S, Lee GE, Yu H, Kim S and Kim S, "Context dependent and HIV-1-specific regulation of RNA and protein expression by HIV-1's site specific m6A RNA modifications" manuscript in preparation.

Peer-reviewed Abstracts

1. Yu H, Baek A, Golconda S and Kim S, "*Novel twin barcoding for ultrahigh-accuracy, Nanopore sequencing for HIV-1 whole genome analysis*."; NHGRI Advanced Genomic Technology Development Meeting, 2019, Boston, MA.
2. Yu H, Baek A, Golconda S and Kim S, "*Ultra-high-accuracy Nanopore target-sequencing for innovations in HIV diagnosis and surveillance*."; NHGRI Advanced Genomic Technology Development Meeting, 2019, Boston, MA.

Patents

1. Yang I, Yu H, Yang HJ, Kim SK, Park SR, Quantitative analysis method using

microorganism 16S rDNA gene having single nucleotide polymorphism, US Patent 10,253,378, (2019)
2. Kim S, Yu H, Baek A, Methods of making and using tandem, twin barcode molecules, PCT/US2018/049203, (2018)
3. Yang I, Kang MJ, Yu H, Park SR, Kim SK, Methods and kits for the quantification of nucleic acids, US/9,297,038 (2016)
4. Yang I, Yu H, Yang H, Kim SK, Park SR, Bacterial 16s rDNA sequences with defined single nucleotide polymorphisms, PCT/KR2014/011040, (2014)
5. Yang I, Kang MJ, Yu H, Park SR, Kim SK, Methods and kits for the quantification of nucleic acids, PCT/KR2011/008494, (2011)

Research Fund

1. 2018 – 2024 NHGRI R01 (PI: Kim S) “On-site, high-fidelity target sequencing and absolute quantitation for HIV-1 surveillance”
2. 2019 – 2023 Department of Energy (PI: Sullivan M; Co-I: Kim S) “Virus in soils: key modulators of microbiomes and nutrient cycling?”
3. 2018 – 2022 NHGRI R21 (PI: Kim S) ”High-accuracy, long-range sequencing for HIV genotyping”

Conference

1. 2019 Advanced Genomic Technology Development Meeting, Boston, USA, short talk
2. 2018 Nanopore Community Meeting, San Francisco, USA, Poster
3. 2016 Nanopore Community Meeting, New York, USA, Poster
4. 2013 Nucleic Acid Summit, San Francisco, USA, Poster

AI & Data Science Training

1. 2026.04 – 2026.05 | AI 융합 데이터 분석 전문인력 양성과정 (WISET × AWS)
   Python(Google Colab) 기반 데이터 분석, 데이터 수집·전처리, API 활용, 데이터 시각화 및 대시보드 구현, AWS 기반 데이터 분석 프로젝트 및 멘토링
2. 2026.06 – 2026.07 | 생성형 AI 전문강사 양성과정 (WISET × AWS)
   프롬프트 엔지니어링, RAG, MCP, Agentic AI, AI Coding Agent, AWS 기반 생성형 AI 활용, AI 교육 콘텐츠 개발 및 팀 프로젝트 수행
3. 2026.07 – 2026.08 (수강 중) | AI 활용 실무 훈련 (WISET × 상상력집단)
   ChatGPT·Claude·Gemini 활용 업무 생산성 향상, Python·Colab 기반 데이터 분석, AI 업무 자동화, 연구·실험 데이터 분석 프로젝트, GitHub·Notion 포트폴리오 제작

Certification

2026.06.05 데이터분석준전문가(ADsP)

Universal RNA Linearization Enables Full-Length Nanopore DRS Across Whole Transcriptomes

(revision for *Nature Methods*, 2026)

Abstract
We present universal reverse transcription methods (UmRT and UmRT+) that enhance Nanopore direct RNA sequencing of long and structured RNAs. These protocols enable high-efficiency, full-length recovery of challenging transcripts—including the 20 Kb XIST RNA—and resolve isoform-specific expression, m6A modifications, and poly(A) tail variation. This advancement enables high-resolution profiling of native RNAs, with broad utility in transcriptomics, virology, and RNA-based diagnostics.

Novel twin barcoding for ultra-high-accuracy, Nanopore sequencing for HIV-1 whole genome analysis
(manuscript in preparation)

Abstract
Human Immunodeficiency Virus Type-1 (HIV-1) genotyping has been hindered by short read-length and errors in the current sequencing platforms. We have developed a novel twin-barcoding approach to improve long-range sequencing for HIV-1 genotyping using Nanopore sequencing. Nanopore sequencing can read extremely long nucleotide sequences (company record: 2 Mb), but its application is significantly limited by high error rates (approximately 5-10%). Conventional "single" barcoding is impractical for the error-prone Nanopore sequencing because of the high error rates already associated with reading the short barcodes themselves; for example, when using 10-20bp barcodes, nearly all the barcodes in Nanopore data will have read errors. Our twin-barcoding approach uses a library of Tandem Twin Barcode (TTB) DNA, in which every TTB DNA molecule has two identical barcodes placed next to each other in the same direction. After Nanopore $1D^2$ (or 2D) sequencing of TTB-labeled DNA, barcode read errors can be recognized and removed by comparing 4 identical barcodes in the same double-stranded DNA. Given that chemical synthesis of a high-quality TTB is practically impossible, we have developed a novel twin-barcode preparation method that mimics the DNA duplication steps of retroviral integration. With 10^{14} copies of starting materials (single barcode oligos), we can generate $>10^{11}$ twin-barcode molecules with 10^9 variants. To minimize PCR bias, no PCR is included until the last step. The quality of the TTB library was tested with both Sanger and Illumina sequencing methods, showing > 90% twins in the current TTB library. Using a TTB library specific for HIV-1 *nef*, HIV-1 plasmid and cellular proviral DNA (NL4-3 strain) were sequenced and up to 99.99% accuracy was achieved in our preliminary study. Our twin barcoding approach enables high-accuracy, full-genome HIV-1 sequencing. When using a portable Nanopore sequencer (MinION), our approach has the potential to significantly improve point-of-care HIV diagnosis and real-time surveillance even in resource-limited settings.

Recombination-free, long-range PCR for full-length HIV-1 DNA genotyping
(manuscript in preparation)

Abstract
Given the rapid development of 3rd generation Nanopore sequencing, long-range single molecule target sequencing is expected to deliver great advancements in genomic research. Single molecule target sequencing often requires a PCR step for high-sensitivity and high-accuracy sequencing. However, a long-range PCR (e.g. 9 Kb HIV DNA amplification) is challenging. Previous studies identified that PCR recombination occurs as frequently as 5-40% depending on PCR conditions and template types. These events are difficult to identify and correct during sequence analysis. We have extensively tested different lengths (1-3-6-9Kb) of PCR for HIV DNA and found that PCR recombination occurs more frequently with longer-range PCR. Modifying PCR conditions can partially reduce the recombination events, but such modifications were not effective in full-length PCR for the HIV genome. In order to effectively reduce PCR recombination in long-range PCR, we employed a droplet digital PCR (ddPCR) system that partitions the PCR reaction to 20,000 separate droplets. This in turn enabled single target molecule amplification in nano-liter volume droplets with adjusted input template copy numbers. We compared the DNA sequencing results from regular PCR with those from ddPCR and demonstrated that ddPCR can effectively resolve the PCR recombination issue. With this new PCR approach, we were able to sequence full-length, individual HIV DNA molecules in a high-throughput fashion without PCR-induced recombination. The new approach will help accurately assess the HIV proviral genome in reservoir cells and identify critical information that has been inaccessible with conventional short-read genotyping, including intact vs. defective viruses; recombination hotspots at the whole genome level; and non-drug target mutations.