Gervaise Henry

VP, Forward Deployed Engineering · Manifold

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SCAN TO SAVE CONTACT

SUMMARY

Forward Deployed Engineering leader and computational biologist — a polymath who works across the full life-science stack: bench science, reproducible bioinformatics, cloud architecture, clinical-grade compliance, and the AI-agent layer now being built on top of it. VP, Forward Deployed Engineering at Manifold.

I've spent my career making biological data usable at every layer — running it at the bench (high-throughput screens, single-cell RNA-seq), making it reproducible and GxP/CLIA-validated in bioinformatics pipelines, scaling it in the cloud, and leading global teams that deliver genomics and multi-omics platforms to pharma and research partners. I move fluently between scientists, engineers, and operators, and I'm hands-on building the agent layer today — MCP integrations, custom skills, and automated evaluation loops — working toward making messy biological data reliably usable by AI. AWS Certified Solutions Architect & Cloud Practitioner. Certified Scrum Product Owner.

EXPERIENCE

VP, Forward Deployed Engineering

January 2026 - Present

Manifold

Lead Forward Deployed Engineering at Manifold, the enterprise agent platform for life sciences — responsible for deploying specialist agents into customer environments and owning post-sales technical delivery while staying active in pre-sales.

- Building and scaling the Forward Deployed Engineering organization, with direct reports spanning FDEs and Forward Deployed Builders, and expanding the team to meet growing customer demand for agent deployment and implementation.
- Provide technical leadership for Forward Deployed Engineers across the broader organization, guiding how they engage with customers on complex implementations even where reporting lines sit elsewhere.
- Partner with the pre-sales Solutions team across the technical customer journey — contributing to discovery, scoping, proof-of-concept development, and platform demonstrations — while owning post-sales implementation, technical delivery, and ongoing customer partnership.
- Maintain broad coverage across Manifold's customer base with concentrated focus on strategic accounts — particularly high-risk, high-reward engagements where customer problems are technically complex and platform fit requires deep scientific and architectural collaboration.
- Build proof-of-concept, reference implementation, and demo assets across three purposes: supporting pre-sales in customer acquisition, driving expansion within existing accounts, and extending platform functionality for broader customer applicability.
- Partner with Product and Engineering to translate field signal into roadmap priorities and to stress-test new capabilities against customer needs before they ship.
- Serve as a liaison between customers, sales, product, engineering, and support, ensuring customer technical and scientific needs are represented throughout the organization.

VP, Head of Data Engineering

January 2025 - January 2026

Champions Oncology, Inc.

Led data infrastructure and management strategy for Champions' research and development efforts, with responsibility for the data platform supporting multi-omics and research data workflows in alignment with FAIR principles.

- Set direction on modernizing Champions' analytic pipelines, initiating rebuilds to bring them in line with current standards for reproducibility, maintainability, and scalability.
- Migrated the analytic compute environment onto a foundation that delivered meaningful reductions in pipeline runtime and cost, improving the economics of recurring analyses.
- Initiated the build-out of data provenance, lineage, and observability infrastructure — evaluating tooling and beginning implementation of the governance layer needed to support regulated multi-omics and research data at scale.
- Owned data organization and deployment for new data commercialization efforts, structuring datasets for external availability and partnering with business stakeholders to bring data products to market.
- Supported sales efforts as the senior scientific and technical voice, providing subject-matter expertise in customer conversations and shaping the technical positioning of data offerings.
- Contributed to new assay development efforts, particularly on the analytical and data-handling side — advising on how downstream analysis requirements should shape assay design, data capture, and output structure.
- Served as the senior technical voice for data strategy, partnering with R&D and executive leadership on platform direction, tooling selection, and long-term data architecture decisions.

Head of Professional Services Engineering

June 2024 - January 2025

DNAnexus

Led the Professional Services Engineering organization — a global team of 15–20 architects, bioinformatics engineers, services engineers, and contractors across the US, Europe, and Asia — responsible for all technical services delivery on the DNAnexus platform.

- Expanded scope from leading the Solutions Engineering function to leading all technical staff across Professional Services, following consistent delivery improvements under prior management.
- Oversaw services delivery across a global, distributed team — including customer-facing engineering, platform integrations, custom solution development, and data engineering for customer data ingestion.
- Managed a sizeable offshore contractor contingent alongside full-time staff, balancing delivery throughput with margin discipline as the services function reached its highest profitability during this period amid continued scaling.
- Partnered with Product Engineering and Product Management on roadmap priorities informed by customer delivery experience, and built proof-of-concept assets to support architectural decisions on new platform capabilities.
- Served as a technical liaison between sales, customers, and internal product and support teams — deployed frequently to strategic or at-risk customer engagements to resolve escalations and restore delivery trajectory.

Manager, Solutions Science Engineering

February 2023 - May 2024

DNAnexus

Managed the Solutions Engineering organization through a period of leadership transition, expanding scope mid-tenure to include a subset of the Professional Services engineering team.

- Led a team of 5–6 Solutions Engineers distributed across the US and EMEA, supporting presales engagements globally across all customer verticals.
- Took on additional management responsibility for part of the Professional Services engineering function following a leadership vacuum, tightening integration between presales and services — notably in SOW scoping accuracy and services utilization — which led to subsequent promotion to Head of PS Engineering.
- Built DNAnexus's external technical presence in Europe and North America, delivering invited oral presentations at EU Biobank Week 2024, ACMG 2024, BioTechX Europe 2023, and the Precision Medicine Leaders Summit 2023, with additional panel participation at BioIT World 2023 on precision medicine and FAIR multimodal data.
- Built and refined proof-of-concept and demo assets to demonstrate platform capabilities against customer-specific scientific and technical needs.
- Partnered with Product Engineering and Product Management on roadmap prioritization based on field signal, and served as liaison between sales, customers, product, professional services, and support.

Senior Solutions Engineer

August 2021 - February 2023

DNAnexus

Individual contributor presales engineer supporting customers globally across all verticals, with particular depth in top-5 pharma and diagnostics.

- Partnered with sales on customer discovery, scoping, and technical qualification — translating customer scientific and operational needs into platform-fit assessments and architectural proposals.
- Built proof-of-concept assets to validate the DNAnexus platform against real customer workflows, including substantial WDL and Nextflow pipeline development and lift-and-shift work.
- Delivered platform demonstrations, technical training, and white-glove technical support for strategic accounts throughout the presales cycle.
- Served as technical liaison between sales, customers, and internal product, professional services, and support teams — recognized for technical depth and customer trust that led to first-line management responsibility following departures of other team leaders.

Computational Biologist

September 2019 - July 2021

UT Southwestern Medical Center

Applied computational, cellular, and molecular techniques to investigate normal biology of the lower urinary tract and the development and progression of benign and malignant pathologies. Focused on single-cell and bulk RNA-sequencing of FACS-sorted populations to characterize normal and diseased cellular heterogeneity. Developed and deployed standardized pipelines for data analysis and exploration, including cloud-based (AWS, Azure) implementations.

Research Associate
April 2015 - September 2019

UT Southwestern Medical Center

Designed, conducted, and analyzed cellular and molecular experiments investigating normal prostate biology and the development and progression of benign prostatic hyperplasia and prostate cancer. Leveraged single-cell and bulk RNA-sequencing of FACS-sorted populations to characterize cellular heterogeneity in healthy and diseased tissue, and identified immune infiltrate signatures in primary human prostate samples to associate with cell-type-specific gene expression, epithelial dynamics, and clinical outcomes. First or co-authored eight journal publications during this period, including a first-author paper in Cell Reports (2018).

Research Associate
November 2014 - March 2015

Harbor Branch Oceanographic Institute at Florida Atlantic University

Developed high-content image-based assays for high throughput drug discovery. Optimized high throughput assays for early-stage drug discovery on marine natural products.

RA/TA
August 2012 - May 2014

American University

Used cellular and molecular biology techniques to investigate the effect of adipocytes and obesity on the multiple myeloma bone marrow tumor microenvironment. Techniques included cell culture (including co-culture), immunoblotting, ELISA, qPCR, tubulogenesis assays, invasion assays, viability assays, immunofluorescence, and confocal microscopy. Independently taught undergraduate lab courses, including design of laboratory content, assessments, grading, and student counseling.

Courses taught: Bio 200 Structure and Function of the Human Body, Bio 210 General Biology II, Bio 300 Cell Biology, Bio 356 Genetics.

Lab Technician
September 2011 - May 2012

UT Southwestern Medical Center

Investigated the relationship between the peptidyl-prolyl cis/trans isomerase Pin1 and IL13 in asthma models, using cellular, molecular, and biochemical techniques. Managed lab budget, ordering, and vendor relationships.

Screening Scientist
February 2010 - September 2011

UT Southwestern Medical Center

Conducted high-throughput compound and RNAi screens in the HTS/RNAi Core, working with a 200,000-compound library, whole-genome human siRNA, Drosophila dsRNA, and custom libraries. Primary project used compound and RNAi screens to functionally categorize NSCLC cell lines into familial groups, identifying molecular susceptibilities exploitable based on biomarkers. Contributed across all aspects of projects: assay choice and development, optimization, implementation, data analysis, bioinformatics, and follow-up experiments. Additional projects included screens for osteoclast differentiation modifiers, novel-mechanism antimicrobial agents, iron homeostasis regulators (siRNA), and miRNA sensitizers to sub-lethal chemotherapy in cancer cells with specific genetic profiles.

Summer Undergraduate Research Intern

May - August 2008

Harbor Branch Oceanographic Institution

Screened for NF-κB inhibitors using a cell-based luciferase reporter assay on a library of partially purified marine natural products. Confirmed prospective inhibitors via flow cytometry and immunoblotting, and identified active compounds using HPLC, MS, and 1D/2D NMR.

SKILLS & CERTIFICATIONS

Top Skills: Solutions Engineering Leadership, Genomics & Multi-Omics Platforms, Cloud Architecture (AWS)

AI & Agent Systems: LLM Application Development, AI Agents, MCP (Model Context Protocol), Claude Code, Agentic Workflows, LLM Evaluation

Reproducibility & Compliance: Reproducible Pipelines, GxP Validation, CLIA, HIPAA, Data Provenance & Lineage

Certifications: AWS Certified Solutions Architect - Associate, AWS Certified Cloud Practitioner, Scrum Alliance Certified Scrum Product Owner

Languages, Operating Systems & Tools: R, Python, Nextflow, WDL, Git, Linux, Bash

Website Development: Static Site Generators, Serverless Deployment, GitLab Pages, HTML5, CSS3, JavaScript

Cloud Platforms: Amazon Web Services, Azure, Google Cloud

AWS Tools: S3, EC2, Batch, Lambda, DynamoDB, API Gateway, Certificate Manager, Route53, CloudFront, CloudTrail, Athena

Container Environments: Docker, Singularity

Biological Modalities: Bulk RNA-seq, Gene Expression Microarray, scRNA-seq, scTCR-seq, Spatial Transcriptomics, Variant Calling, Proteomics (Mass Spec), Molecular Biology Techniques

EDUCATION

American University

Graduated 2014

Masters of Science, Biology

Thesis: Adipocytes, obesity and multiple myeloma

Eckerd College

Graduated 2009

Bachelors of Science, Biomedical Molecular Biology

Thesis: The Search for Novel NF-kB Inhibitors from Compounds Derived from Marine Invertebrates as Potential Anti-tumor Therapies

HONORS & AWARDS

- Bioinformatics Fellow
- American University College of Arts and Sciences Graduate Conference Travel Grant
- American University College of Arts and Sciences Graduate Student Research Support
- American University College of Arts and Sciences Graduate Student Summer Research Support
- American University Biology Department Summer Graduate Award

PUBLICATIONS

1. Broman M, Atallah NA, Vickman R, Cresswell G, Kothandaraman H, Kolliegbo A, Paez Paez JS, Glaser A, Helfand B, **Henry G**, Strand D, Franco O, Hayward S, Ratliff T. Immune cell single-cell RNA sequencing analyses link an age-associated T cell subset to symptomatic benign prostatic hyperplasia. *Frontiers in immunology* **2025**. doi.org/10.3389/fimmu.2025.1585446
2. Zhu Q, Zhu Y, Hepler C, Zhang Q, Park J, Gliniak J, **Henry GH**, Crewe C, Bu D, Zhang Z, Zhao S, Morley T, Li N, Kim D, Strand D, Deng Y, Robino JJ, Varlamov O, Gordillo R, Kolonin MG, Kusminski CM, Gupta RK, Scherer PE. Adipocyte mesenchymal transition contributes to mammary tumor progression. *Cell Reports* **2022**. doi.org/10.1016/j.celrep.2022.111362
3. Bennett C, Thornton M, Park C, **Henry G**, Zhang Y, Malladi V, Kim D. SeqWho: reliable, rapid determination of sequence file identity using k-mer frequencies in Random Forest classifiers. *Bioinformatics* **2022**. doi.org/10.1093/bioinformatics/btac050
4. Joseph DB, **Henry GH**, Malewska A, Reese JC, Mauck RJ, Gahan JC, Hutchinson RC, Mohler JL, Roehrborn CG, Strand DW. 5-alpha reductase inhibitors induce a prostate luminal to club cell transition in human benign prostatic hyperplasia. *The Journal of Pathology* **2022**. doi.org/10.1002/path.5857
5. Ruetten H, **Henry G**, Liu T, Spratt H, Ricke W, Strand D, Vezina C. A NEW Approach for Characterizing Mouse Urinary Pathophysiologies. *Physiological Reports* **2021**. doi.org/10.14814/phy2.14964
6. Joseph DB, **Henry GH**, Malewska A, Reese JC, Mauck RJ, Gahan JC, Hutchinson RC, Malladi VS, Roehrborn CG, Vezina CM, Strand DW. Single cell analysis of mouse and human prostate reveals novel fibroblasts with specialized distribution and microenvironment interactions. *The Journal of Pathology* **2021**. doi.org/10.1002/path.5751
7. Shao M, Hepler C, Zhang Q, Shan B, Vishvanath L, **Henry GH**, Zhao S, An YA, Wu Y, Strand DW, Gupta RK. Pathologic HIF1α signaling drives adipose progenitor dysfunction in obesity. *Cell Stem Cell* **2021**. doi.org/10.1016/j.stem.2020.12.008
8. Joseph DB, **Henry GH**, Malewska A, Iqbal NS, Ruetten HM, Turco AE, Abler LL, Sandhu SK, Cadena MK, Malladi VS, Reese JC, Mauck RJ, Gahan JC, Hutchinson RC, Roehrborn CG, Baker LA, Vezina CM, Strand DW. Urethral luminal epithelia are castration-insensitive cells of the proximal prostate. *The Prostate* **2020**. doi.org/10.1002/pros.24020
9. Crowell PD, Fox JJ, Hashimoto T, Diaz JA, Havarro HI, **Henry GH**, Feldmar BA, Lowe MG, Garcia AJ, Wu YE, Sajed DP, Strand DW, Goldstein AS. Expansion of Luminal Progenitor Cells in the Aging Mouse and Human Prostate. *Cell Reports* **2019**. doi.org/10.1016/j.celrep.2019.07.007
10. **Henry GH**, Malewska A, Joseph DB, Malladi VS, Lee J, Torrealba J, Mauck RJ, Gahan JC, Raj GV, Roehrborn CG, Hon GC, MacConmara MP, Reese JC, Hutchinson RC, Vezina CM, Strand DW. A cellular anatomy of the normal human prostate. *Cell Reports* **2018**. doi.org/10.1016/j.celrep.2018.11.086
11. Gerhauser C, Favero F, Risch T, Simon R, Feuerbach L, Assenov Y, Heckmann D, Sidiropoulos N, Waszak SM, Hubschmann D, Urbanucci A, Girma EG, Kuryshev V, Klimczak LJ, Saini N, Stutz AM, Weichenhan D, Bottcher LM, Toth R, Hendriksen JD, Koop C, Lutsik P, Matzk S, Warnatz HJ, Amstislavskiy V, Feuerstein C, Raeder B, Bogatyrova O, Schmitz EM, Hube-Magg C, Kluth M, Huland H, Graefen M, Lawerenz C, **Henry GH**, Yamaguchi TN, Malewska A, Meiners J, Schilling D, Reisinger E, Eils R, Schlesner M, Strand DW, Bristow RG, Boutros PC, von Kalle C, Gordenin D, Sultmann H, Brors B, Sauter G, Plass C, Yaspo ML, Korbel JO, Schlomm T, Weischenfeldt J. Molecular evolution of early-onset prostate cancer identifies molecular risk markers and clinical trajectories. *Cancer Cell* **2018**. doi.org/10.1016/j.ccell.2018.10.016

12. Hepler C, Shan B, Zhang Q, **Henry GH**, Shao M, Vishvanath L, Ghaben AL, Mobley AB, Strand DW, Hon GC, Gupta RK. Identification of functionally distinct fibro-inflammatory and adipogenic stromal subpopulations in visceral adipose tissue of adult mice. *eLife* **2018**. doi.org/10.7554/eLife.39636.001
13. **Henry GH**, Loof N, Strand DW. OMIP-040: Optimized gating of human prostate cellular subpopulations. *Cytometry Part A* **2017**. doi.org/10.1002/cyto.a.23187
14. **Henry GH**, Malewska A, Hutchinson R, Gahan J, Mauck R, Francis F, Torrealba J, Roehrborn C, Strand DW. Molecular pathogenesis of human prostate basal cell hyperplasia. *The Prostate* **2017**. doi.org/10.1002/pros.23394
15. Zhang B, Kwon OJ, **Henry G**, Malewska A, Wei X, Zhang L, Brinkley W, Zhang Y, Castro PD, Titus M, Chen R, Sayeeduddin M, Raj GV, Mauck R, Roehrborn C, Creighton CJ, Strand DW, Ittmann MM, Xin L. Non-cell-autonomous regulation of prostate epithelial homeostasis by androgen receptor. *Molecular Cell* **2016**. doi.org/10.1016/j.molcel.2016.07.025
16. Strand D W, Aaron L, **Henry G**, Franco O E, Hayward SW. Isolation and analysis of discrete human prostate cellular populations. *Differentiation* **2015**. doi.org/10.1016/j.diff.2015.10.013
17. DeCicco-Skinner KL, **Henry GH**, Cataisson C, Tabib T, Gwilliam JC, Watson NJ, Bullwinkle EM, Falkenburg L, O'Neill RC, Morin A, Wiest JS. Endothelial cell tube formation assay for the in vitro study of angiogenesis. *JoVE* **2014**. dx.doi.org/10.3791/51312
18. **Henry GH**. Adipocytes, Obesity and the Multiple Myeloma Microenvironment. *American University* **2014**. hdl.handle.net/1961/16815
19. **Henry GH**. The Search for Novel NF-κB Inhibitors from Compounds Derived from Marine Invertebrates as Potential Anti-Tumor Therapies. *Eckerd College* **2009**. eckerd.primo.exlibrisgroup.com/permalink/01ECKERD_INST/10kklq9/alma991706793406111

PRESENTATIONS

1. Mohta V, Farhi S, **Henry GH**. From Spatial Transcriptomics to Multimodal Discovery: Scaling AI Driven Genomics on Manifold. *NextGen Omics, Spatial & Data US* **2026**. (Oral Presentation)
2. Sedlakova, A, **Henry GH**. Efficiently Analyzing Population-Scale Genomics Data. *EU Biobank Week* **2024**. (Oral Presentation)
3. Szklarczyk-Smolana K, Pacewicz K, **Henry GH**. Automated Genome Interpretation Solution to Accelerate Diagnostic Decisions via Intelliseq GeneSpect™ Reporter. *ACMG* **2024**. (Oral Presentation)
4. Rao A, **Henry GH**. Bridging the Gap: Solutions for Data Integration, Security, and Collaborative Exploration in Precision Medicine. *BioTechX Europe* **2023**. (Oral Presentation)
5. **Henry GH**, Roco C. Democratizing Access to Single-Cell RNA Sequencing with the Parse Biosciences Evercode Platform. *Precision Medicine Leaders Summit: Advances in Single Cell & Spatial Biology* **2023**. (Oral Presentation)
6. Enderlein C, Clark JN, Emanuel G, **Henry GH**, Kim J. Innovation Panel: Building the Spatial Biology Ecosystem. *Precision Medicine Leaders Summit: Advances in Single Cell & Spatial Biology* **2023**. (Panelist)
7. Busby BR, Chu E, Floden E, **Henry GH**, Huitt E. Towards Precision Medicine: Datasets, Computation, and Data Integration for Patient Subsetting Research - Part I. *BioIT World* **2023**. (Panelist)
8. Busby BR, Dawson E, Gillis M, **Henry GH**, Holt R, Neilley V. Achieving FAIRness with Multimodal Data. *BioIT World* **2023**. (Panelist)

9. Binoy Joseph D, **Henry GH**, Malewska A, Reese JC, Mauck RJ, Gahan J, Hutchinson RC, Mohler JL, Roehrborn CG, Strand DW. Spatial transcriptomics reveals a transition from a prostate luminal to club-like cell state in 5-alpha reductase inhibitor treated BPH patients. *Collaborating for the Advancement of Interdisciplinary Research in Benign Urology: Meeting* **2021**. (Poster Presentation)
10. Binoy Joseph D, **Henry GH**, Malewska A, Reese JC, Mauck RJ, Gahan J, Hutchinson RC, Mohler JL, Roehrborn CG, Strand DW. Spatial transcriptomics reveals a transition from a prostate luminal to club-like cell state in 5-alpha reductase inhibitor treated BPH patients. *Society for Basic Urologic Research: Annual Meeting* **2021**. (Poster Presentation)
11. Broman MM, Lanman NA, Vickman RE, Cresswell GM, **Henry G**, Strand D, Hayward SW, Ratliff TL. Immune cell Single cell RNA sequencing and interaction analyses suggest a prominent role for T cells and T cell-macrophage interactions in Benign Prostatic Hyperplasia. *Society for Basic Urologic Research: Annual Meeting* **2021**. (Poster Presentation)
12. Amado N, Mathews J, **Henry G**, Fusco A, Egeland T, Malewska A, Cantrel B, Strand D, Baker L. Understanding Prune Belly Syndrome at Single Cell Resolution. *American Urological Association: Annual Meeting* **2021**. (Poster Presentation)
13. Binoy Joseph D, **Henry G**, Malewska A, Reese JC, Mauck RJ, Gahan J, Hutchinson RC, Roehrborn CG, Strand DW. Characterization of 5ARI treatment response at the single cell level. *American Urological Association: Annual Meeting* **2021**. (Poster Presentation)
14. Binoy Joseph D, **Henry GH**, Malewska A, Wegner K, Rees JC, Hutchinson RC, Roehrborn CG, Strand DW. Decoding Stromal Heterogeneity Across BPH Phenotypes. *Collaborating for the Advancement of Interdisciplinary Research in Benign Urology: Meeting* **2020**. (Poster Presentation)
15. Ruetten H, **Henry G**, Strand D, Vezina C. A Phenome-Based Approach for Characterizing Mouse Urinary Pathophysiologies. *Collaborating for the Advancement of Interdisciplinary Research in Benign Urology: Meeting* **2020**. (Poster Presentation)
16. Binoy Joseph D, **Henry GH**, Malewska A, Wegner K,Reese JC, Hutchinson RC, Roehrborn CG, Strand DW. Decoding Stromal Heterogeneity across BPH Phenotypes. *Society for Basic Urologic Research: Annual Meeting* **2020**. (Poster Presentation)
17. Broman MM, Lanman NA, Vickman RE, Franco OE, Hayward SW, **Henry GH**, Strand DW, Ratliff TL. Immune Cell Interactions in Benign Prostatic Hyperplasia. *Collaborating for the Advancement of Interdisciplinary Research in Benign Urology: Meeting* **2019**. (Poster Presentation)
18. Binoy Joseph D, **Henry GH**, Malewska A, Wegner K, Rees JC, Hutchinson RC, Roehrborn CG, Vezina CM, Strand DW. Identification of Cognate Proximal Cell Types of the Mouse and Human Prostate and Their Enrichment in Human Benign Prostatic Hyperplasia. *Collaborating for the Advancement of Interdisciplinary Research in Benign Urology: Meeting* **2019**. (Poster Presentation)
19. **Henry GH**, Malewska A, Malladi VS, Lee J, Gahan JC, Reese J, Strand DW. A Cellular Atlas of Human Prostate Disease. *Cold Spring Harbor: Single Cell Analysis* **2019**. (Poster Presentation)
20. Binoy Joseph D, **Henry G**, Malewska A, Wegner K,Reese J, Hutchinson R, Roehrborn C, Vezina C, Strand D. Identification of cognate proximal cell types of the mouse and human prostate and their enrichment in human Benign Prostatic Hyperplasia. *Society for Basic Urologic Research: Annual Meeting* **2019**. (Poster Presentation)
21. Broman MM, Lanman NL, Vickman RE, Hayward SW, **Henry G**, Strand DW, Ratliff TL. Immune Cell Interactions in Benign Prostatic Hyperplasia. *Society for Basic Urologic Research: Annual Meeting* **2019**. (Poster Presentation)

22. Crowell PD, Fox JJ, Hashimoto T, Diaz JA, **Henry GH**, Lowe MG, Wu YE, Strand DW, Goldstein AS. Expansion of Luminal Progenitor Cells in the Aging Mouse and Human Prostate. *Society for Basic Urologic Research: Annual Meeting* **2019**. (Poster Presentation)
23. Binoy Joseph D, **Henry G**, Malewska A, Strand D. Urethral Hillock Epithelia Extend into the Proximal Prostate Stem Cell Niche. *Prostate Cancer Foundation: Annual Scientific Retreat* **2019**. (Poster Presentation)
24. Shih T, **Henry G**, Malladi V, Loof N. Cloud-based cytometry workflow for big data analysis. *International Society for Advancement of Cytometry: CYTO* **2019**. (Poster Presentation)
25. **Henry G**, Malewska A, Binoy Joseph D, Roehrborn C, Hutchinson R, Vezina C, Strand D. Cellular pathogenesis of human BPH. *American Urological Association: Annual Meeting* **2019**. (Poster Presentation)
26. **Henry GH**, Malewska A, Joseph DB, Malladi VS, Lee J, Torrealba J, Mauck RJ, Gahan JC, Raj JV, Roehrborn CG, Hon GC, MacConmara MP, Reese JC, Hutchinson RC, Vezina CM, Strand DW. Building a comprehensive cellular anatomy of the normal and diseased human prostateia. *Collaborating for the Advancement of Interdisciplinary Research in Benign Urology: Meeting* **2018**. (Poster Presentation)
27. Iqbal N, Kern A, Jascur T, **Henry GH**, Edwards A, Wong D, Sanchez EJ, Baker L. Global Transcriptional Dynamics Identify Key Functional Pathways Involved in the Pathogenesis of Prune Belly Syndrome. *Society for Basic Urologic Research: Annual Meeting* **2018**. (Poster Presentation)
28. Blatt EB, Sonavane R, **Henry GH**, Ekoue DN, Strand DW, Raj GV. Characterizing the metabolic effect of enzalutamide on prostate cancer. *Society for Basic Urologic Research: Annual Meeting* **2018**. (Poster Presentation)
29. **Henry G**, Malewska A, Binoy Joseph D, Malladi V, Lee J, Gahan J, Mauck R, Raj G, Roehrborn C, Hon G, Reese J, Hutchinson R, Vezina C, Strand D. A Cellular Anatomy of the Normal Human Prostate and BPH. *Society for Basic Urologic Research: Annual Meeting* **2018**. (Poster Presentation)
30. **Henry GH**. Determining Cellular Heterogeneity in Human Prostate using the Chromium™ Single Cell 3' Solution. *10x Genomics User Group Meeting: Houston* **2018**. (Oral Presentation)
31. **Henry GH**. Determining cellular heterogeneity in human prostate with flow cytometry and single-cell RNA-sequencing. *FlowTex Conference* **2018**. (Oral Presentation)
32. **Henry GH**. Determining cellular heterogeneity in human prostate with flow cytometry and single-cell RNA-sequencing. *North Texas Flow Cytometry Conference* **2017**. (Oral Presentation)
33. **Henry G**, Malewska A, Hutchinson R, Gahan J, Mauck R, Torrealba J, Francis F, Roehrborn C, Strand D. Pathogenesis of Inflammation in Human BPH. *Society for Basic Urologic Research: Annual Meeting* **2017**. (Poster Presentation)
34. **Henry GH**. Deconstructing BPH Phenotypes: Molecular Pathogenesis of Basal Hyperplasia. *North Texas Flow Cytometry Conference* **2016**. (Oral Presentation)
35. **Henry G**, Malewska A, Mauck R, Torrealba J, Roehrborn C, Strand D. Deconstructing BPH phenotypes. *Society for Basic Urologic Research: Annual Meeting* **2016**. (Poster Presentation)
36. **Henry G**, Malewska A, Mauck R, Roerborn C, Strand D. Cell-specific responses to inflammation in BPH. *Society for Basic Urologic Research: Annual Meeting* **2015**. (Poster Presentation)
37. **Henry GH**, Watson NJ, O'Neill R, Tabib T, Bullwinkle EM, DeCicco-Skinner KL. Adipocytes, Obesity and the Multiple Myeloma Microenvironment. *American Association of Cancer Research: Annual Meeting* **2014**. (Poster Presentation)

OPEN SOURCE CONTRIBUTIONS

Open Source Visualizations

1. cellxgene: Single cell analysis of mouse and human prostate reveals novel fibroblasts with specialized distribution and microenvironment interactions. **2021**. cellxgene.cziscience.com/collections/4b54248f-2165-477c-a027-dd55082e8818
2. cellxgene: Urethral luminal epithelia are castration-insensitive cells of the proximal prostate. **2020**. cellxgene.cziscience.com/collections/fbc5881f-1ee3-4ffe-8095-35e15e1a08fc
3. cellxgene: A Cellular Anatomy of the Normal Adult Human Prostate and Prostatic Urethra. **2018**. cellxgene.cziscience.com/collections/e2a4a67f-6a18-431a-ab9c-6e77dd31cc80

Open Source Code

1. RNA-seq Analytic Pipeline for GUDMAP/RBK. **2021**. doi.org/10.5281/zenodo.4429315
2. Strand Lab analysis of single-cell RNA sequencing. **2020**. doi.org/10.5281/zenodo.3687064
3. Single-Cell RNA-Seq Image Generation Pipeline for GUDMAP/RBK. **2019**. doi.org/10.5281/zenodo.2652611
4. BICF Cellranger mkfastq Analysis Workflow. **2019**. doi.org/10.5281/zenodo.2652611
5. BICF Cellranger count Analysis Workflow. **2019**. doi.org/10.5281/zenodo.2652611
6. Determining cellular heterogeneity in the human prostate with single-cell RNA sequencing. **2018**. doi.org/10.5281/zenodo.2652611

Open Source Data

1. GEO: Single cell RNA-sequencing of verumontanum region and peripheral zone of normal human prostate. **2021**. www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE179312
2. GEO: Human prostate luminal epithelia adopt a club-like state in response to low androgen levels. **2021**. www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE178934
3. GUDMAP: Single cell analysis of mouse and human prostate reveals novel fibroblasts with specialized distribution and microenvironment interactions. **2021**. doi.org/10.25548/17-DRBC
4. GEO: Single-cell RNA-sequencing of adult mouse lower urinary tracts v2. **2021**. www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE173096
5. GEO: Single-cell RNA-sequencing of adult human normal and BPH (glandular and stroma) prostates and urethra. **2021**. www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE172357
6. GEO: Bulk RNA-sequencing of fibroblasts isolated by FACS from normal human prostate. **2021**. www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE172347
7. GUDMAP: Urethral luminal epithelia are castration-insensitive cells of the proximal prostate. **2020**. doi.org/10.25548/16-WM8C
8. GEO: Single-cell RNA-sequencing of adult mouse lower urinary tracts. **2020**. www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE145929
9. GEO: Single-cell RNA-sequencing of adult human prostates and urethra (normal and diseased). **2020**. www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE145928
10. GEO: Single Cell RNA-sequencing of cell types isolated by FACS from normal human prostates. **2018**. www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE117403
11. GEO: Bulk RNA-sequencing of cell types isolated by FACS from normal human prostates. **2018**. www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE117271

12. FLOWRepository: OMIP-040: Optimized gating of human prostate cellular subpopulations. **2018**. flowrepository.org/id/FR-FCM-ZY6D
13. GUDMAP: Determining cellular heterogeneity in the human prostate with single-cell RNA sequencing. **2018**. doi.org/10.25548/w-r8cm

Projects

1. GUDMAP/RBK Analytics. **2021**. Design and manage the Agile group responsible for creating analytics for data stored on the NIH consortiums GUDMAP and RBK. This analytics are not only best-practices pipelines written in Nextflow, …
2. Nextflow in the Cloud. **2020**. Manage a small agile team to create a proof of concept AWS architecture to run Nextflow pipelines in the cloud. It utilizes low-cost, highly-availability queueing, compute, and storage resources.
3. Pipeline Run Tracking. **2019**. Creating a pipeline run tracking tool for the Bioinformatics Core Facility at UT Southwestern Medical Center. This tool utilizes AWS serverless offerings, including REST-API and a website for run …
4. Strand Lab Internal Data Website. **2019**. Developed the internal Strand Lab website and manage the server used explore and share pre-publication single-cell RNA-sequencing data.
5. Strand Lab External Website. **2019**. The Strand Lab website was designed to not only provide a location to share information about the lab, but also provide a means to showcase the lab's data and biorepository. The single-cell data is …
6. BICF Pipelining. **2018**. Creating analytics for the Bioinformatics Core Facility at UT Southwestern Medical Center, using the pipelining language Nextflow.