OMB No. 3145-0279 (Expiration Date 10/31/2026)

NIH BIOGRAPHICAL SKETCH COMMON FORM

Name: Sugio, Takeshi

Persistent Identifier (PID) of the Senior/Key Person: https://orcid.org/0000-0002-4270-1943

Position Title: Instructor

Organization and Location: Stanford Medicine, Stanford, California, United States

PROFESSIONAL PREPARATION

INSTITUTION AND LOCATION	DEGREE	Start Date	Completion Date	FIELD OF STUDY
Stanford University, Stanford, California, United States	Postdoctoral Fellow	09/2021	06/2026	Hematology/Oncology
Kyushu University Hospital, Fukuoka, Not Applicable, N/A, Japan	Fellow	04/2018	08/2021	Hematology
Kyushu University, Fukuoka, Not Applicable, N/A, Japan	DOCTOR OF PHILOSOPHY	04/2014	03/2019	Hematology
Kyushu University Hospital, Fukuoka, Not Applicable, N/A, Japan	Fellow	04/2013	03/2014	Hematology
Toranomon Hospital, Tokyo, Not Applicable, N/A, Japan	Resident	04/2010	03/2012	Internal Medicine
Kyushu University, Fukuoka, Not Applicable, N/A, Japan	DOCTOR OF MEDICINE	04/2004	03/2010	Medicine

Appointments and Positions

2026 - present	Instructor, Stanford Medicine, Stanford, California, United States
2025 - present	Councillor, The Japanese Society of Hematology, Kyoto, Not Applicable, N/A, Japan
2023 - 2025	Special fellow, Leukemia Lymphoma Society, Stanford, California, United States
2023 - 2023	Overseas Research Fellowships, Japan Society for the Promotion of Science, Stanford, California, United States
2022 - present	Board Certified Attending, Japanese Society of Hematology, Fukuoka, Not Applicable, N/A, Japan
2021 - 2026	Postdoctoral Fellow, Stanford University, Stanford, California, United States
2020 - 2021	Specially Appointed Assistant Professor (Clinical), Kyushu University Hospital, Fukuoka, Not Applicable, N/A, Japan
2020 - 2021	Research Fellow, Kagoshima University, Kagoshima, Not Applicable, N/A, Japan
2018 - 2020	Clinical Fellow, Kyushu University Hospital, Fukuoka, Not Applicable, N/A, Japan
2017 - present	Board Certified Fellow, Japanese Society of Hematology, Fukuoka, Not Applicable, N/A, Japan
2013 - present	Board Certified Physician, Japanese Society of Internal Medicine, Fukuoka, Not Applicable, N/A, Japan

Products

Products Closely Related to the Proposed Project

1. Sugio T, Nesselbush M, Shukla N, Garofalo A, Mutter J, Shahrokh Esfahani M, Alig S, Shi S, Noordenbos T, Hamilton M, Rossi C, Tian F, Liu C, Olsen M, Kang X, Russler-Germain D, Horwitz S, Kato K, Ito A, Yamagishi M, Fukuda T, Akashi K, Uchimaru K, Khodadoust M, Diehn M, Mehta-Shah N, Alizadeh A. Integrating Genomic & Transcriptomic Features for Noninvasive Detection, Characterization, and Monitoring of T-Cell Lymphomas. Blood. 2024 November 05; 144(Supplement 1):454-454. Available from: https://ashpublications.org/blood/article/144/Supplement%201/454/531506/Integrating-Genomic-amp-Transcriptomic-Features DOI: 10.1182/blood-2024-206518
2. Sugio T, Shahrokh Esfahani M, Jun S, Sworder B, Hamilton M, Hosoya H, Olsen M, Kang X, Liu C, Tian F, Miklos D, Kurtz D, Diehn M, Alizadeh A. Direct Method for Estimating the Fraction of T and B/Plasma Cell-Derived DNA. Blood.

2024 November 05; 144(Supplement 1):2223-2223. Available from: https://ashpublications.org/blood/article/144/Supplement%201/2223/531665/Direct-Method-for-Estimating-the-Fraction-of-T- and DOI: 10.1182/blood-2024-193441

3. Hamilton MP, Sugio T, Noordenbos T, Shi S, Bulterys PL, Liu CL, Kang X, Olsen MN, Good Z, Dahiya S, Frank MJ, Sahaf B, Mackall CL, Gratzinger D, Diehn M, Alizadeh AA, Miklos DB. Risk of Second Tumors and T-Cell Lymphoma after CAR T-Cell Therapy. N Engl J Med. 2024 Jun 13;390(22):2047-2060. PubMed Central PMCID: PMC11338600.
4. Sugio T, Miyawaki K, Kato K, Sasaki K, Yamada K, Iqbal J, Miyamoto T, Ohshima K, Maeda T, Miyoshi H, Akashi K. Microenvironmental immune cell signatures dictate clinical outcomes for PTCL-NOS. Blood Adv. 2018 Sep 11;2(17):2242-2252. PubMed Central PMCID: PMC6134219.
5. Sugio T, Kato K, Aoki T, Ohta T, Saito N, Yoshida S, Kawano I, Henzan H, Kadowaki M, Takase K, Muta T, Miyawaki K, Yamauchi T, Shima T, Takashima S, Mori Y, Yoshimoto G, Kamezaki K, Takenaka K, Iwasaki H, Ogawa R, Ohno Y, Eto T, Kamimura T, Miyamoto T, Akashi K. Mogamulizumab Treatment Prior to Allogeneic Hematopoietic Stem Cell Transplantation Induces Severe Acute Graft-versus-Host Disease. Biol Blood Marrow Transplant. 2016 Sep;22(9):1608-1614. PubMed PMID: 27220263.

Other Significant Products Highlighting Contributions to Science

1. Sugio T, Uchida N, Miyawaki K, Ohno Y, Eto T, Mori Y, Yoshimoto G, Kikushige Y, Kunisaki Y, Mizuno S, Nagafuji K, Iwasaki H, Kamimura T, Ogawa R, Miyamoto T, Taniguchi S, Akashi K, Kato K. Prognostic impact of HLA supertype mismatch in single-unit cord blood transplantation. Bone Marrow Transplant. 2024 Apr;59(4):466-472. PubMed PMID: 38238452.
2. Sugio T, Miyawaki K, Uchida N, Niemann M, Spierings E, Mori K, Ohno Y, Eto T, Mori Y, Yoshimoto G, Kikushige Y, Kunisaki Y, Mizuno S, Nagafuji K, Iwasaki H, Kamimura T, Ogawa R, Miyamoto T, Taniguchi S, Akashi K, Kato K. Indirect presentation of mismatched human leukocyte antigen-B associates with outcomes of cord blood transplantation. Br J Haematol. 2025 May;206(5):1406-1417. PubMed Central PMCID: PMC12078882.
3. Sworder BJ, Kurtz DM, Alig SK, Frank MJ, Shukla N, Garofalo A, Macaulay CW, Shahrokh Esfahani M, Olsen MN, Hamilton J, Hosoya H, Hamilton M, Spiegel JY, Baird JH, Sugio T, Carleton M, Craig AFM, Younes SF, Sahaf B, Sheybani ND, Schroers-Martin JG, Liu CL, Oak JS, Jin MC, Beygi S, Hüttmann A, Hanoun C, Dührsen U, Westin JR, Khodadoust MS, Natkunam Y, Majzner RG, Mackall CL, Diehn M, Miklos DB, Alizadeh AA. Determinants of resistance to engineered T cell therapies targeting CD19 in large B cell lymphomas. Cancer Cell. 2023 Jan 9;41(1):210-225.e5. PubMed Central PMCID: PMC10010070.
4. Sugio T, Baba S, Mori Y, Yoshimoto G, Kamesaki K, Takashima S, Urata S, Shima T, Miyawaki K, Kikushige Y, Kunisaki Y, Numata A, Takenaka K, Iawasaki H, Miyamoto T, Ishigami K, Akashi K, Kato K. Prognostic value of pre-transplantation total metabolic tumor volume on (18)fluoro-2-deoxy-D-glucose positron emission tomography-computed tomography in relapsed and refractory aggressive lymphoma. Int J Hematol. 2022 Oct;116(4):603-611. PubMed PMID: 35701707.
5. Nesselbush MC, Luca BA, Jeon YJ, Jabara I, Meador CB, Garofalo A, Binkley MS, Hui AB, van 't Erve I, Xu N, Shi WY, Liu KJ, Sugio T, Kastelowitz N, Hamilton EG, Liu CL, Olsen M, Bonilla RF, Wang YP, Jiang A, Lau B, Eichholz J, Banwait M, Schroers-Martin J, Boegeholz J, King DA, Luikart H, Esfahani MS, Mehrmohamadi M, Stehr H, Raclin T, Tibshirani R, Khush K, Srinivas S, Yu H, Rogers AJ, Nair VS, Isbell JM, Li BT, Piotrowska Z, Sequist LV, Hata AN, Neal JW, Wakelee HA, Gentles AJ, Alizadeh AA, Diehn M. An ultrasensitive method for detection of cell-free RNA. Nature. 2025 May;641(8063):759-768. PubMed Central PMCID: PMC13215214.

Certification:

I certify that the information provided is current, accurate, and complete. This includes, but is not limited to, information related to current, pending, and other support (both foreign and domestic) as defined in 42 U.S.C. § 6605.

In accordance with Section 10632 of the CHIPS and Science Act of 2022 (42 U.S.C. § 19232), each individual identified as a senior/key person must certify that they are not a party to a malign foreign talent recruitment program.

Research Security Training Requirement for Federal Award Personnel: In accordance with Section 10634 of the CHIPS and Science Act of 2022 (42 U.S.C. § 19234), each individual identified as a senior/key person must certify that they have completed the requisite research security training that meets the requirements specified in Item 2 of Important Notice No. 149 within 12 months prior to proposal submission.

Misrepresentations and/or omissions may be subject to prosecution and liability pursuant to, but not limited to, 18 U.S.C. §§287, 1001, 1031 and 31 U.S.C. §§3729-3733 and 3802.

Certified by Sugio, Takeshi in SciENcv on 2026-08-26 23:19:46

NIH BIOGRAPHICAL SKETCH SUPPLEMENT

Name: Sugio, Takeshi

Persistent Identifier (PID) of the Senior/Key Person: https://orcid.org/0000-0002-4270-1943

Position Title: Instructor

Organization and Location: Stanford Medicine, Stanford, California, United States

Personal Statement

I am an M.D./Ph.D. physician-scientist and Instructor in the Division of Oncology at Stanford Medicine. Before transitioning to research, I practiced for 10 years in Japan as a hematologist, including as an attending hematologist, specializing in lymphoma, hematopoietic stem cell transplantation (HSCT), and cellular therapy for relapsed/refractory hematologic malignancies. I have been board-certified in hematology by the Japanese Society of Hematology (JSH) since 2017, became a JSH-certified supervising hematologist in 2022, and was appointed a Councilor in 2024. Working in an HTLV-1–endemic region, I treated numerous patients with adult T-cell leukemia/lymphoma (ATLL), including refractory disease, motivating my research on early detection, disease monitoring, and prediction of ATLL progression.

For the past ten years, my research has focused on T-cell lymphomas (TCLs), particularly ATLL, and HSCT. During my PhD, I developed a tumor microenvironment-based molecular classification of TCL that contributed to an investigator-initiated Phase II trial of PD-1 blockade in relapsed/refractory TCL. I participated in its implementation and treated the first patient enrolled, who achieved a durable complete response despite disease refractory to eight prior lines of therapy (Sugio et al., ASH Annual Meeting, 2025).

At Stanford, I have focused on liquid-biopsy technologies for T-cell malignancies and systemic immune profiling. I developed FIRE-Seq, a cfDNA-based approach that quantifies cellular turnover at the level of individual T- and B-cell clonotypes. The underlying technology is the subject of a published international patent application (PCT/US2026/012550; WO 2026/161805 A1), on which I am the first-named inventor. In TCL, I integrated cfDNA immune-receptor, genomic, and epigenomic profiling with cfRNA analysis to identify tumor-specific TCR clonotypes and longitudinally monitor tumor and immune dynamics. I have also applied FIRE-Seq to patients with B-cell lymphoma receiving CAR T-cell therapy, identifying systemic T-cell turnover signatures associated with therapeutic outcomes (Sugio et al., ASH Annual Meeting, 2024).

Through collaboration with the Joint Study on Predisposing Factors of ATL Development (JSPFAD), a nationwide longitudinal cohort of HTLV-1 carriers in Japan, I have access to longitudinal plasma collected before ATLL development. These specimens enable characterization of molecular and clonal evolution from asymptomatic HTLV-1 infection to ATLL and development of machine-learning models for individualized risk prediction. I am expanding this effort through collaborations in other HTLV-1–endemic regions, including Peru and Brazil, to validate these approaches across geographically diverse populations and develop globally applicable strategies for risk-adapted surveillance and ultimately ATLL prevention and interception.

I was recently awarded an NIH/NCI K99/R00 Pathway to Independence Award and appointed as an Instructor at Stanford. As an independent physician-scientist, I aim to build an academic program centered on T-cell lymphomas that integrates focused lymphoma clinical care with translational investigation of tumor and immune biology. By connecting questions arising from patient care with biological investigation and prospective clinical studies, I seek to advance early detection, precision treatment, and ultimately lymphoma interception.

Honors

2026 - 2031	NIH/NCI K99/R00 Pathway to Independence Award, National Cancer Institute
2025	The ASH Abstract Achievement Award, American Society of Hematology
2024	The ASH Abstract Achievement Award, American Society of Hematology
2023	The ASH Abstract Achievement Award, American Society of Hematology
2023 - 2025	Special fellow, Leukemia Lymphoma Society, United States, Leukemia Lymphoma Society
2023 - 2023	JSH Young Investigator's Award, Japanese Society of Hematology
2023 - 2023	Postdoctoral Fellowship for Research Abroad, Japan Society for the Promotion of Science
2022	The ASH Abstract Achievement Award, American Society of Hematology

2020	Clinical Medical Research Award, Medical Care Education Research Foundation
2020 - 2023	Postdoctoral Fellowship for Research in Japan , Japan Society for the Promotion of Science
2019	Research Grant, The Shinnihon Foundation of Advanced Medical Treatment Research
2017	JSH International Symposium, Best presentation award, Japanese Society of Hematology

Contributions to Science

1. Developing Disease Monitoring Systems and Identifying Immunologic Determinants of Lymphoma Progression for Personalized Treatment

   As a Ph.D. student, I used gene-expression profiling to reclassify biologically heterogeneous lymphomas, including diffuse large B-cell lymphoma and peripheral T-cell lymphoma, and identified tumor microenvironment-associated programs linked to prognosis. These findings contributed to the development of an investigator-initiated Phase II trial of PD-1 blockade for relapsed/refractory T-cell lymphoma (TCL), in which I participated in trial implementation and treated the first enrolled patient.
   At Stanford, I extended this work by developing multimodal liquid-biopsy approaches to characterize TCL noninvasively. In an international study of 204 patients across five cohorts, I integrated cfDNA genomic, immune-receptor, and epigenomic profiling with circulating tumor cell and cfRNA analyses. This framework enabled molecular classification and longitudinal disease monitoring, identified occult circulating disease associated with poor outcomes, and demonstrated that end-of-treatment ctDNA predicts relapse, including among PET-negative responders. cfRNA further captured subtype-specific transcriptional programs. This work establishes a framework for integrating tumor and immune signals to improve risk stratification, disease monitoring, and personalized treatment of TCL.

2. Identification of Prognostic Determinants for Hematopoietic Stem Cell Transplantation

   As a Ph.D. student, I retrospectively analyzed the data of patients with acute T-cell leukemia/lymphoma (ATLL) who received allogeneic stem cell transplantation (allo-HSCT). As a result, I identified that the CCR4 inhibitor, which was expected as pre-transplant therapy due to its high remission induction rate, induced lethal GvHD when it was used before allo-HSCT. The results of my study have led to a significant revision of the treatment strategy for ATLL and contributed to improved prognosis
   During the clinical fellowship, I performed translational research on HSCT patients. I analyzed the function of mismatched HLA from two angles: 1) antigen-presenting function of mismatched HLA and 2) antigenicity of mismatched HLA. As a result, I found that 1) GVL effect is effectively induced in cases with matched mismatched HLA supertypes, dramatically lowering disease recurrence, 2) mismatched HLA-B derived epitopes are associated with pre-engraftment immune reaction leading to engraft failure in cord blood transplantation. The results of these studies were significant for the development of new donor selection criteria.
   As a postdoctoral fellow, I conducted a retrospective analysis of the prognostic impact of PET-CT prior to HSCT for R/R lymphoma and identified that low TMTV is associated with better prognosis both in autologous and allogeneic hematopoietic stem cell transplantations. Moreover, For R/R B-cell lymphoma, I also performed retrospective analysis of Japanese registry data for patients treated with HSCT and made a prognostic index that can identify a subgroup of DLBCL patients who benefit from allo-HSCT.

3. Identification and Preclinical Validation of Therapeutic Targets and Development of Patient-Derived Cancer Models

   During my Ph.D., I investigated therapeutic vulnerabilities in hematologic malignancies using complementary molecular and patient-derived models. I identified BIRC5 as a potential therapeutic target in PTCL based on its increased expression in patients with poor outcomes and validated BIRC5 dependency through shRNA- and CRISPR-mediated perturbation in vitro and pharmacologic inhibition in PTCL patient-derived xenograft (PDX) models established by renal-capsule transplantation. I also investigated metabolic vulnerabilities across hematologic malignancies, including PAICS and other de novo purine synthesis pathways in DLBCL and AML, validating therapeutic activity in cell lines and PDX models. In parallel, I evaluated the efficacy and safety of KHK2823, a non-fucosylated fully human anti–IL-3Rα monoclonal antibody, in AML PDX models and contributed to studies identifying BCAA metabolism as a therapeutic vulnerability in leukemic stem cells.
   More recently, I have extended my experience with patient-derived models to organoid systems. In preliminary studies using patient-derived organoids (PDOs) from pancreatic, gastrointestinal, and lung cancers, I analyzed cfDNA released into culture supernatants and found that epigenomic profiling can recover tumor-associated molecular signals from these models. These findings provide preliminary support for using cell-free nucleic acids as nondestructive molecular readouts of patient-derived experimental systems. Building on this work, I aim to integrate PDO and PDX models with longitudinal cell-free molecular profiling to monitor biological responses to therapeutic perturbation without relying solely on destructive endpoint measurements.

4. Cell-Free Molecular Profiling of Immune Dynamics and Lymphoid Malignant Evolution

   I have developed complementary cell-free molecular approaches to longitudinally profile systemic and tissue-associated immune dynamics. I developed FIRE-Seq, which integrates fragment-aware T- and B-cell receptor profiling with quantitative measurement of lymphocyte-derived cfDNA to determine the contribution and turnover of individual lymphocyte clones. In parallel, I have applied cfDNA epigenomic profiling, cfRNA expression analysis, and immune-receptor repertoire analysis to characterize immune states and tumor–immune dynamics from plasma.
   I applied FIRE-Seq across 2,267 samples from 730 patients spanning cancer, infection, and immune-mediated diseases, demonstrating that lymphocyte-derived cfDNA captures systemic and tissue-associated immune dynamics across diverse clinical contexts. In patients with B-cell lymphoma receiving CAR19 therapy, cell-free immune profiling identified pretreatment immune states associated with clinical outcome and post-infusion T-cell dynamics that tracked CAR-T expansion. In complementary studies, I identified clonal hematopoiesis as a predisposing factor for secondary T-cell malignancies following CAR-T therapy. Longitudinal cell-free profiling further revealed clonal and immune evolution preceding T-cell malignancies, including the transition from asymptomatic HTLV-1 infection to overt ATLL. Beyond hematologic malignancies, urinary cfDNA profiling identified local T-cell immune states associated with response to BCG immunotherapy in bladder cancer.
   The FIRE-Seq immune-monitoring technology is the subject of a published international patent application (PCT/US2026/012550; WO 2026/161805 A1), on which I am the first-named inventor. Together, these studies establish cell-free molecular profiling as a broadly applicable framework for longitudinally tracking immune dynamics, therapeutic response, and malignant evolution.

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