



Albert Tsai, M.D., Ph.D.

Assistant Professor of Pathology at the Stanford University Medical Center

CLINICAL OFFICES

- Pathology

300 Pasteur Dr Rm L235

MC 5324

Stanford, CA 94305

Tel (650) 723-5252

Fax (650) 725-6902

Bio

BIO

Dr. Tsai received his undergraduate training at the University of California, Los Angeles (B.S., Biochemistry, summa cum laude), followed by combined medical and graduate training at the University of Southern California (M.D., Ph.D., Biochemistry). He completed anatomic and clinical pathology (AP/CP) residency and hematopathology fellowship at Stanford University, receiving board certification in AP/CP and hematopathology. As an instructor, he performed clinical diagnostic duties on the hematopathology service while doing postdoctoral training in the laboratory of Dr. Sean Bendall, with funding from the Damon Runyon Cancer Research Foundation.

His current research focus is in diagnostic uses and implementation of mass immunophenotyping (mass cytometry and multiplexed ion beam imaging), particularly for blood tumors such as lymphomas and leukemias. This includes biomarker development, protocol optimization, quality control, and reducing costs using computational analysis with potential automation through artificial intelligence/machine learning. Combining his diagnostic practice with knowledge of clinical laboratory testing, access to primary patient samples, and postdoctoral work in mass immunophenotyping, he seeks to advance the routine diagnosis of hematopoietic diseases using these emerging technologies.

His clinical diagnostic duties are on the hematopathology service, primarily in the diagnosis of lymphomas, leukemias, and other hematopoietic diseases from blood, bone marrow, and tissue samples.

CLINICAL FOCUS

- Hematopathology
- Anatomic and Clinical Pathology

ACADEMIC APPOINTMENTS

- Assistant Professor - Med Center Line, Pathology

HONORS AND AWARDS

- Fellow, Damon Runyon Cancer Research Foundation (2016)

PROFESSIONAL EDUCATION

- Medical Education: University of Southern California Keck School of Medicine Registrar (2010) CA
- Fellowship: Stanford University Hemapathology Fellowship (2015) CA
- Residency: Stanford University Pathology Residency (2014) CA
- Board Certification: Hematology, American Board of Pathology (2015)
- Board Certification: Anatomic and Clinical Pathology, American Board of Pathology (2014)
- PhD, University of Southern California Keck School of Medicine , Biochemistry (2008)

Publications

PUBLICATIONS

- **Impact of somatic and germline mutations on the outcome of systemic mastocytosis.** *Blood advances*
Munoz-Gonzalez, J. I., Jara-Acevedo, M., Alvarez-Twose, I., Merker, J. D., Teodosio, C., Hou, Y., Henriques, A., Roskin, K. M., Sanchez-Munoz, L., Tsai, A. G., Caldas, C., Matito, A., Sanchez-Gallego, et al
2018; 2 (21): 2814–28
- **Bone marrow morphology is a strong discriminator between chronic eosinophilic leukemia, not otherwise specified from reactive idiopathic hypereosinophilic syndrome.** *Haematologica*
Wang, S. A., Hasserjian, R. P., Tam, W., Tsai, A. G., Geyer, J. T., George, T. I., Foucar, K., Rogers, H. J., Hsi, E. D., Rea, B. A., Bagg, A., Bueso-Ramos C, C., Arber, et al
2017
- **Targeted next-generation sequencing identifies a subset of idiopathic hypereosinophilic syndrome with features similar to chronic eosinophilic leukemia, not otherwise specified** *MODERN PATHOLOGY*
Wang, S. A., Tam, W., Tsai, A. G., Arber, D. A., Hasserjian, R. P., Geyer, J. T., George, T. I., Czuchlewski, D. R., Foucar, K., Rogers, H. J., Hsi, E. D., Rea, B. B., Bagg, et al
2016; 29 (8): 854-864
- **Targeted Next Generation Sequencing (NGS) of Chronic Eosinophilic Leukemia, Not Otherwise Specified (CEL, NOS) and of Idiopathic Hypereosinophilic Syndrome (HES)**
Wang, S., Tam, W., Tsai, A., Arber, D. A., Hasserjian, R. P., Geyer, J., George, T. I., Czuchlewski, D., Foucar, K., Rogers, H. J., Hsi, E. D., Rea, B., Bagg, et al
NATURE PUBLISHING GROUP.2016: 382A
- **Human lymphoid translocation fragile zones are hypomethylated and have accessible chromatin.** *Molecular and cellular biology*
Lu, Z., Lieber, M. R., Tsai, A. G., Pardo, C. E., Müschen, M., Kladde, M. P., Hsieh, C.
2015; 35 (7): 1209-1222
- **BCL6 breaks occur at different AID sequence motifs in Ig-BCL6 and non-Ig-BCL6 rearrangements** *BLOOD*
Lu, Z., Tsai, A. G., Akasaka, T., Ohno, H., Jiang, Y., Melnick, A. M., Greisman, H. A., Lieber, M. R.
2013; 121 (22): 4551-4554
- **Both CpG Methylation and Activation-Induced Deaminase Are Required for the Fragility of the Human bcl-2 Major Breakpoint Region: Implications for the Timing of the Breaks in the t(14;18) Translocation** *MOLECULAR AND CELLULAR BIOLOGY*
Cui, X., Lu, Z., Kurosawa, A., Klemm, L., Bagshaw, A. T., Tsai, A. G., Gemmell, N., Mueschen, M., Adachi, N., Hsieh, C., Lieber, M. R.
2013; 33 (5): 947-957
- **IgH partner breakpoint sequences provide evidence that AID initiates t(11;14) and t(8;14) chromosomal breaks in mantle cell and Burkitt lymphomas** *BLOOD*
Greisman, H. A., Lu, Z., Tsai, A. G., Greiner, T. C., Yi, H. S., Lieber, M. R.
2012; 120 (14): 2864-2867
- **Heterogeneity and Randomness of DNA Methylation Patterns in Human Embryonic Stem Cells** *DNA AND CELL BIOLOGY*

-
- Tsai, A. G., Chen, D. M., Lin, M., Hsieh, J. C., Okitsu, C. Y., Taghva, A., Shibata, D., Hsieh, C.
2012; 31 (6): 893-907
- **t(X;14)(p22;q32)/t(Y;14)(p11;q32) CRLF2-IGH translocations from human B-lineage ALLs involve CpG-type breaks at CRLF2, but CRLF2/P2RY8 intrachromosomal deletions do not** *BLOOD*
Tsai, A. G., Yoda, A., Weinstock, D. M., Lieber, M. R.
2010; 116 (11): 1993-1994
 - **The t(14;18)(q32;q21)/IGH-MALT1 translocation in MALT lymphomas is a CpG-type translocation, but the t(11;18)(q21;q21)/API2-MALT1 translocation in MALT lymphomas is not** *BLOOD*
Tsai, A. G., Lu, Z., Lieber, M. R.
2010; 115 (17): 3640-3641
 - **Mechanisms of chromosomal rearrangement in the human genome** *International Workshop on Computational Systems Biology Approaches to Analysis of Genome Complexity and Regulatory Gene Networks*
Tsai, A. G., Lieber, M. R.
BIOMED CENTRAL LTD.2010
 - **Nonhomologous DNA end joining (NHEJ) and chromosomal translocations in humans.** *Sub-cellular biochemistry*
Lieber, M. R., Gu, J., Lu, H., Shimazaki, N., Tsai, A. G.
2010; 50: 279-296
 - **H3K4me3 Stimulates the V(D)J RAG Complex for Both Nicking and Hairpinning in trans in Addition to Tethering in cis: Implications for Translocations** *MOLECULAR CELL*
Shimazaki, N., Tsai, A. G., Lieber, M. R.
2009; 34 (5): 535-544
 - **Conformational Variants of Duplex DNA Correlated with Cytosine-rich Chromosomal Fragile Sites** *JOURNAL OF BIOLOGICAL CHEMISTRY*
Tsai, A. G., Engelhart, A. E., Hatmal, M. M., Houston, S. I., Hud, N. V., Haworth, I. S., Lieber, M. R.
2009; 284 (11): 7157-7164
 - **Human Chromosomal Translocations at CpG Sites and a Theoretical Basis for Their Lineage and Stage Specificity** *CELL*
Tsai, A. G., Lu, H., Raghavan, S. C., Muschen, M., Hsieh, C., Lieber, M. R.
2008; 135 (6): 1130-1142
 - **Unexpected complexity at breakpoint junctions in phenotypically normal individuals and mechanisms involved in generating balanced translocations t(1;22)(p36;q13)** *GENOME RESEARCH*
Gajecka, M., Gentles, A. J., Tsai, A., Chitayat, D., Mackay, K. L., Glotzbach, C. D., Lieber, M. R., Shaffer, L. G.
2008; 18 (11): 1733-1742
 - **RAGs found "not guilty": cleared by DNA evidence** *BLOOD*
Tsai, A. G., Lieber, M. R.
2008; 111 (4): 1750-1750
 - **Single-stranded DNA ligation and XLF-stimulated incompatible DNA end ligation by the XRCC4-DNA ligase IV complex: influence of terminal DNA sequence** *NUCLEIC ACIDS RESEARCH*
Gu, J., Lu, H., Tsai, A. G., Schwarz, K., Lieber, M. R.
2007; 35 (17): 5755-5762
 - **HotPatch: A statistical approach to finding biologically relevant features on protein surfaces** *JOURNAL OF MOLECULAR BIOLOGY*
Pettit, F. K., Bare, E., Tsai, A., Bowie, J. U.
2007; 369 (3): 863-879
 - **Analysis of non-B DNA structure at chromosomal sites in the mammalian genome** *DNA REPAIR, PT B*
Raghavan, S. C., Tsai, A., Hsieh, C., Lieber, M. R.
2006; 409: 301-316
-