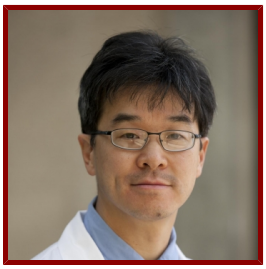
Stanford



Hanlee P. Ji

Associate Professor of Medicine (Oncology)

Medicine - Oncology

CLINICAL OFFICES

- **Medical Oncology**

  875 Blake Wilbur Dr

  Clinic A MC 6560

  Stanford, CA 94305

  Tel (650) 498-6000 **Fax** (650) 736-4167

ACADEMIC CONTACT INFORMATION

- **Alternate Contact**

  Donna Galvez - Administration Ji Research Group

  Email drgalvez@stanford.edu

  Tel 650-721-1503

Bio

CLINICAL FOCUS

- Cancer > GI Oncology
- Medical Oncology
- Oncology (Cancer)
- Gastrointestinal Neoplasms
- Inherited Cancer Disorders
- Immunotherapy in gastrointestinal cancers

ACADEMIC APPOINTMENTS

- Associate Professor, Medicine - Oncology
- Member, Bio-X
- Member, Stanford Cancer Institute

ADMINISTRATIVE APPOINTMENTS

- Senior Associate Director, Stanford Genome Technology Center, (2008- present)

HONORS AND AWARDS

- Physician-Scientist Fellowship Award, Howard Hughes Medical Institute (1998)
- American Association Cancer Research, Scholar-in-Training Award for Research Achievement (2005)
- Merit Award for Research Achievement, American Society Clinical Oncology Foundation (2006)
- Physician Scientist Early Career Award, Howard Hughes Medical Institute (2008)
- Clinical Scientist Development Award, Doris Duke Charitable Foundation (2009)
- Research Scholar Award, American Cancer Society (2013)

PROFESSIONAL EDUCATION

- Residency: University Of Iowa Hospitals and Clinics GME Training Verifications (1996) IA
- Medical Education: Johns Hopkins University School of Medicine (1994) MD
- Fellowship: Stanford University Hospital -Clinical Excellence Research Center (2005) CA
- Board Certification: Medical Oncology, American Board of Internal Medicine (2004)
- Residency: University of Washington (2001) WA
- B.A., Reed College , Biology
- M.D., Johns Hopkins University , Medicine

LINKS

- DNA Discovery - Ji Research Group: http://dna-discovery.stanford.edu/

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

To improve the lives of individuals with cancer, our research group has embarked on a research initiative to use cutting edge genetics and technology to interrogate the fundamental genetic" digital" code responsible for cancer development and overall clinical behavior.

We are pursuing projects focused on personalized medicine. Specifically, we are interested in using genetic and genomic approaches in oncology to improve targeted cancer therapy development, make accurate prognosis, prediction of cancer therapy efficacy and identify clinically relevant cancer mutations. These projects are aimed towards establishing the paradigm for individualized medicine, facilitate the introduction of these approaches into validation clinical studies and thus develop the next generation of cancer diagnostics and treatment.

Our research program is specifically focused on:

1) Discovery and validation of genetic signatures portending prognosis and therapeutic drug targets for individuals with cancer

2) Development of novel approaches for analyzing cancer genomes and identifying personalized therapeutic targets

3) Determining inherited pathogenic mutations that increase the risk of developing gastrointestinal malignancies

4) The genetic analysis of complete cancer genome sequences derived from inherited cancer

5) Technology development on novel genetic diagnostic methods to help individuals with cancer

CLINICAL TRIALS

- Clinical & Pathological Studies of Upper Gastrointestinal Carcinoma, Recruiting
- The Gastric Cancer Foundation: A Gastric Cancer Registry, Recruiting

Teaching

STANFORD ADVISEES

Postdoctoral Faculty Sponsor

Jiamin Chen, Anuja Anand Sathe

Postdoctoral Research Mentor

Jiamin Chen, Anuja Anand Sathe

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)
- Cancer Biology (Phd Program)
- Medicine (Masters Program)

Publications

PUBLICATIONS

- **Genomic Instability in Cancer: Teetering on the Limit of Tolerance** *CANCER RESEARCH*
  Andor, N., Maley, C. C., Ji, H. P.
  2017; 77 (9): 2179-2185
- **CRISPR-Cas9-targeted fragmentation and selective sequencing enable massively parallel microsatellite analysis** *NATURE COMMUNICATIONS*
  Shin, G., Grimes, S. M., Lee, H., Lau, B. T., Xia, L. C., Ji, H. P.
  2017; 8
- **Haplotyping germline and cancer genomes with high-throughput linked-read sequencing.** *Nature biotechnology*
  Zheng, G. X., Lau, B. T., Schnall-Levin, M., Jarosz, M., Bell, J. M., Hindson, C. M., Kyriazopoulou-Panagiotopoulou, S., Masquelier, D. A., Merrill, L., Terry, J. M., Mudivarti, P. A., Wyatt, P. W., Bharadwaj, et al
  2016; 34 (3): 303-311
- **Pan-cancer analysis of the extent and consequences of intratumor heterogeneity.** *Nature medicine*
  Andor, N., Graham, T. A., Jansen, M., Xia, L. C., Aktipis, C. A., Petritsch, C., Ji, H. P., Maley, C. C.
  2016; 22 (1): 105-113
- **The Cancer Genome Atlas Clinical Explorer: a web and mobile interface for identifying clinical-genomic driver associations.** *Genome medicine*
  Lee, H., Palm, J., Grimes, S. M., Ji, H. P.
  2015; 7 (1): 112-?
- **Emergence of Hemagglutinin Mutations During the Course of Influenza Infection.** *Scientific reports*
  Cushing, A., Kamali, A., Winters, M., Hopmans, E. S., Bell, J. M., Grimes, S. M., Xia, L. C., Zhang, N. R., Moss, R. B., Holodniy, M., Ji, H. P.
  2015; 5: 16178-?
- **A programmable method for massively parallel targeted sequencing.** *Nucleic acids research*
  Hopmans, E. S., Natsoulis, G., Bell, J. M., Grimes, S. M., Sieh, W., Ji, H. P.
  2014; 42 (10)
- **High sensitivity detection and quantitation of DNA copy number and single nucleotide variants with single color droplet digital PCR.** *Analytical chemistry*
  Miotke, L., Lau, B. T., Rumma, R. T., Ji, H. P.
  2014; 86 (5): 2618-2624
- **Metastatic tumor evolution and organoid modeling implicate TGFBR2 as a cancer driver in diffuse gastric cancer** *GENOME BIOLOGY*
  Nadauld, L. D., Garcia, S., Natsoulis, G., Bell, J. M., Miotke, L., Hopmans, E. S., Xu, H., Pai, R. K., Palm, C., Regan, J. F., Chen, H., Flaherty, P., Ootani, et al
  2014; 15 (8)
- **Systematic genomic identification of colorectal cancer genes delineating advanced from early clinical stage and metastasis.** *BMC medical genomics*
  Lee, H., Flaherty, P., Ji, H. P.
  2013; 6: 54-?
- **Improving bioinformatic pipelines for exome variant calling** *GENOME MEDICINE*
  Ji, H. P.
  2012; 4

- **Ultrasensitive detection of rare mutations using next-generation targeted resequencing** *NUCLEIC ACIDS RESEARCH*
  Flaherty, P., Natsoulis, G., Muralidharan, O., Winters, M., Buenrostro, J., Bell, J., Brown, S., Holodniy, M., Zhang, N., Ji, H. P.
  2012; 40 (1)

- **The Human OligoGenome Resource: a database of oligonucleotide capture probes for resequencing target regions across the human genome** *NUCLEIC ACIDS RESEARCH*
  Newburger, D. E., Natsoulis, G., Grimes, S., Bell, J. M., Davis, R. W., Batzoglou, S., Ji, H. P.
  2012; 40 (D1): D1137-D1143

- **Quantitative and Sensitive Detection of Cancer Genome Amplifications from Formalin Fixed Paraffin Embedded Tumors with Droplet Digital PCR.** *Translational medicine (Sunnyvale, Calif.)*
  Nadauld, L., Regan, J. F., Miotke, L., Pai, R. K., Longacre, T. A., Kwok, S. S., Saxonov, S., Ford, J. M., Ji, H. P.
  2012; 2 (2)

- **Efficient targeted resequencing of human germline and cancer genomes by oligonucleotide-selective sequencing** *NATURE BIOTECHNOLOGY*
  Myllykangas, S., Buenrostro, J. D., Natsoulis, G., Bell, J. M., Ji, H. P.
  2011; 29 (11): 1024-U95

- **A Flexible Approach for Highly Multiplexed Candidate Gene Targeted Resequencing** *PLOS ONE*
  Natsoulis, G., Bell, J. M., Xu, H., Buenrostro, J. D., Ordonez, H., Grimes, S., Newburger, D., Jensen, M., Zahn, J. M., Zhang, N., Ji, H. P.
  2011; 6 (6)

- **Targeted deep resequencing of the human cancer genome using next-generation technologies** *BIOTECHNOLOGY AND GENETIC ENGINEERING REVIEWS, VOL 27*
  Myllykangas, S., Ji, H. P.
  2010; 27: 135-158

- **HOTSPOTS FOR UNSELECTED TY1 TRANSPOSITION EVENTS ON YEAST CHROMOSOME-III ARE NEAR TRANSFER-RNA GENES AND LTR SEQUENCES** *CELL*
  Ji, H., Moore, D. P., BLOMBERG, M. A., Braiterman, L. T., Voytas, D. F., Natsoulis, G., Boeke, J. D.
  1993; 73 (5): 1007-1018

- **Tandem Oligonucleotide Probe Annealing and Elongation To Discriminate Viral Sequence** *ANALYTICAL CHEMISTRY*
  Taskova, M., Uhd, J., Miotke, L., Kubit, M., Bell, J., Ji, H. P., Astakhova, K.
  2017; 89 (8): 4363-4366

- **A genome-wide approach for detecting novel insertion-deletion variants of mid-range size.** *Nucleic acids research*
  Xia, L. C., Sakshuwong, S., Hopmans, E. S., Bell, J. M., Grimes, S. M., Siegmund, D. O., Ji, H. P., Zhang, N. R.
  2016; 44 (15)

- **Emergence of Hemagglutinin Mutations During the Course of Influenza Infection** *SCIENTIFIC REPORTS*
  Cushing, A., Kamali, A., Winters, M., Hopmans, E. S., Bell, J. M., Grimes, S. M., Xia, L. C., Zhang, N. R., Moss, R. B., Holodniy, M., Ji, H. P.
  2015; 5

- **The Cancer Genome Atlas Clinical Explorer: a web and mobile interface for identifying clinical-genomic driver associations** *GENOME MEDICINE*
  Lee, H., Palm, J., Grimes, S. M., Ji, H. P.
  2015; 7

- **Enzyme-Free Detection of Mutations in Cancer DNA Using Synthetic Oligonucleotide Probes and Fluorescence Microscopy** *PLOS ONE*
  Miotke, L., Maity, A., Ji, H., Brewer, J., Astakhova, K.
  2015; 10 (8)

- **Allele-specific copy number profiling by next-generation DNA sequencing.** *Nucleic acids research*
  Chen, H., Bell, J. M., Zavala, N. A., Ji, H. P., Zhang, N. R.
  2015; 43 (4)

- **Allele-specific copy number profiling by next-generation DNA sequencing.** *Nucleic acids research*
  Chen, H., Bell, J. M., Zavala, N. A., Ji, H. P., Zhang, N. R.
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- **Enzyme-Free Detection of Mutations in Cancer DNA Using Synthetic Oligonucleotide Probes and Fluorescence Microscopy.** *PloS one*
  Miotke, L., Maity, A., Ji, H., Brewer, J., Astakhova, K.
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- **Oncogenic transformation of diverse gastrointestinal tissues in primary organoid culture** *NATURE MEDICINE*
  Li, X., Nadauld, L., Ootani, A., Corney, D. C., Pai, R. K., Gevaert, O., Cantrell, M. A., Rack, P. G., Neal, J. T., Chan, C. W., Yeung, T., Gong, X., Yuan, et al
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- **A programmable method for massively parallel targeted sequencing.** *Nucleic acids research*
  Hopmans, E. S., Natsoulis, G., Bell, J. M., Grimes, S. M., Sieh, W., Ji, H. P.
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- **MendeLIMS: a web-based laboratory information management system for clinical genome sequencing.** *BMC bioinformatics*
  Grimes, S. M., Ji, H. P.
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- **MendeLIMS: a web-based laboratory information management system for clinical genome sequencing.** *BMC bioinformatics*
  Grimes, S. M., Ji, H. P.
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  Natsoulis, G., Zhang, N., Welch, K., Bell, J., Ji, H. P.
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- **RVD: a command-line program for ultrasensitive rare single nucleotide variant detection using targeted next-generation DNA resequencing.** *BMC research notes*
  Cushing, A., Flaherty, P., Hopmans, E., Bell, J. M., Ji, H. P.
  2013; 6: 206-?

- **DETECTING MUTATIONS IN MIXED SAMPLE SEQUENCING DATA USING EMPIRICAL BAYES** *ANNALS OF APPLIED STATISTICS*
  Muralidharan, O., Natsoulis, G., Bell, J., Ji, H., Zhang, N. R.
  2012; 6 (3): 1047-1067

- **Identification of a novel deletion mutant strain in Saccharomyces cerevisiae that results in a microsatellite instability phenotype.** *BioDiscovery*
  Ji, H. P., Morales, S., Welch, K., Yuen, C., Farnam, K., Ford, J. M.
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- **The Human OligoGenome Resource: a database of oligonucleotide capture probes for resequencing target regions across the human genome.** *Nucleic acids research*
  Newburger, D. E., Natsoulis, G., Grimes, S., Bell, J. M., Davis, R. W., Batzoglou, S., Ji, H. P.
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- **Performance comparison of whole-genome sequencing platforms** *NATURE BIOTECHNOLOGY*
  Lam, H. Y., Clark, M. J., Chen, R., Chen, R., Natsoulis, G., O'Huallachain, M., Dewey, F. E., Habegger, L., Ashley, E. A., Gerstein, M. B., Butte, A. J., Ji, H. P., Snyder, et al
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- **A cross-sample statistical model for SNP detection in short-read sequencing data** *NUCLEIC ACIDS RESEARCH*
  Muralidharan, O., Natsoulis, G., Bell, J., Newburger, D., Xu, H., Kela, I., Ji, H., Zhang, N.
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- **Targeted sequencing library preparation by genomic DNA circularization** *BMC BIOTECHNOLOGY*
  Myllykangas, S., Natsoulis, G., Bell, J. M., Ji, H. P.
  2011; 11

- **Genetic-based biomarkers and next-generation sequencing: the future of personalized care in colorectal cancer** *PERSONALIZED MEDICINE*
  Kim, R. Y., Xu, H., Myllykangas, S., Ji, H.
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- **Identification of Novel LNK Mutations In Patients with Chronic Myeloproliferative Neoplasms and Related Disorders** *52nd Annual Meeting and Exposition of the American-Society-of-Hematology (ASH)*

Oh, S. T., Zahn, J. M., Jones, C. D., Zhang, B., Loh, M. L., Kantarjian, H., Simonds, E. F., Bruggner, R. V., Abidi, P., Natsoulis, G., Bell, J., Buenrostro, J., Nolan, et al

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  Zhang, N. R., Siegmund, D. O., Ji, H., Li, J. Z.
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- **Oncogenic BRAF Mutation with CDKN2A Inactivation Is Characteristic of a Subset of Pediatric Malignant Astrocytomas** *CANCER RESEARCH*
  Schiffman, J. D., Hodgson, J. G., VandenBerg, S. R., Flaherty, P., Polley, M. C., Yu, M., Fisher, P. G., Rowitch, D. H., Ford, J. M., Berger, M. S., Ji, H., Gutmann, D. H., James, et al
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- **Identification of a biomarker panel using a multiplex proximity ligation assay improves accuracy of pancreatic cancer diagnosis** *JOURNAL OF TRANSLATIONAL MEDICINE*
  Chang, S. T., Zahn, J. M., Horecka, J., Kunz, P. L., Ford, J. M., Fisher, G. A., Le, Q. T., Chang, D. T., Ji, H., Koong, A. C.
  2009; 7

- **Molecular inversion probes reveal patterns of 9p21 deletion and copy number aberrations in childhood leukemia** *CANCER GENETICS AND CYTOGENETICS*
  Schiffman, J. D., Wang, Y., McPherson, L. A., Welch, K., Zhang, N., Davis, R., Lacayo, N. J., Dahl, G. V., Faham, M., Ford, J. M., Ji, H. P.
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- **Disperse-a software system for design of selector probes for exon resequencing applications** *BIOINFORMATICS*
  Stenberg, J., Zhang, M., Ji, H.
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- **Molecular inversion probe assay for allelic quantitation.** *Methods in molecular biology (Clifton, N.J.)*
  Ji, H., Welch, K.
  2009; 556: 67-87

- **Next-generation DNA sequencing** *NATURE BIOTECHNOLOGY*
  Shendure, J., Ji, H.
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- **Gene-specific delineation of copy number aberrations in follicular lymphoma with molecular inversion probes** *49th Annual Meeting of the American-Society-of-Hematology*
  Ji, H. P., Welch, K. M., Wang, Y., Faham, M., Akasaka, T., Czerwinski, D., Davis, R. W., Levy, R.
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- **Multigene amplification and massively parallel sequencing for cancer mutation discovery** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
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- **Multiplex amplification of all coding sequences within 10 cancer genes by Gene-Collector** *NUCLEIC ACIDS RESEARCH*
  Fredriksson, S., Baner, J., Dahl, F., Chu, A., Ji, H., Welch, K., Davis, R. W.
  2007; 35 (7)

- **Multiplexed protein detection by proximity ligation for cancer biomarker validation** *NATURE METHODS*
  Fredriksson, S., Dixon, W., Ji, H., Koong, A. C., Mindrinos, M., Davis, R. W.
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- **Under-expression of Kalirin-7 increases iNOS activity in cultured cells and correlates to elevated iNOS activity in Alzheimer's disease hippocampus** *JOURNAL OF ALZHEIMERS DISEASE*
  Youn, H., Ji, I., Ji, H. P., Markesbery, W. R., Ji, T. H.
  2007; 12 (3): 271-281

- **Reproducibility Probability Score - incorporating measurement variability across laboratories for gene selection** *NATURE BIOTECHNOLOGY*
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  Ji, H., Davis, R. W.
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- **The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements** *NATURE BIOTECHNOLOGY*
  Shi, L., Reid, L. H., Jones, W. D., Shippy, R., Warrington, J. A., Baker, S. C., Collins, P. J., de Longueville, F., Kawasaki, E. S., Lee, K. Y., Luo, Y., Sun, Y. A., Willey, et al
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- **Molecular inversion probe analysis of gene copy alterations reveals distinct categories of colorectal carcinoma** *CANCER RESEARCH*
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- **A functional assay for mutations in tumor suppressor genes caused by mismatch repair deficiency** *HUMAN MOLECULAR GENETICS*
  Ji, H. P., King, M. C.
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- **Spondyloepimetaphyseal dysplasia with joint laxity (SEMDJL): Presentation in two unrelated patients in the United States** *AMERICAN JOURNAL OF MEDICAL GENETICS*
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- **Molecular classification of the inherited hamartoma polyposis syndromes: Clearing the muddied waters** *AMERICAN JOURNAL OF HUMAN GENETICS*
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