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Education and Training

2009-2013	Post-Doctoral Training University of Colorado School of Medicine
2003-2009	Ph.D. in Bioinformatics North Carolina State University, NC, USA
2000-2002	M.S. in Computer Science Gwangju Institute of Science and Technology, Gwangju, Korea
1995-1999	B.S. in Computer Science Chonnam National University, Gwangju, Korea

Positions and Employment

10/2020 – present	Project Staff , Department of Quantitative Health Sciences and Department of Neurosciences, Cleveland Clinic Lerner Research Institute, Cleveland, OH
02/2017 – 09/2020	Assistant Research Professor , Division of Medical Oncology, Department of Medicine, University of Colorado Denver School of Medicine, Aurora, CO
06/2019 – 09/2020	Co-Director , Lung SPORE Biostatistics, Informatics and Bioinformatics (BIB) Core, University of Colorado Denver School of Medicine, Aurora, CO
02/2016 – 09/2020	Member , Lung SPORE Biostatistics, Informatics and Bioinformatics (BIB) Core, University of Colorado Denver School of Medicine, Aurora, CO
02/2015 – 09/2020	Associate Member , UCCC (University of Colorado Cancer Center) Developmental Therapeutics Program, University of Colorado Cancer Center, A National Cancer Institute-Designated Consortium Comprehensive Cancer Center
02/2015 – 01/2016	Adjunct Professor , UNIST (Ulsan Institute of Science and Technology), Ulsan, S. Korea
10/2013 – 02/2017	Research Instructor of Bioinformatics , Division of Medical Oncology, Department of Medicine, University of Colorado Denver School of Medicine, Aurora, CO

07/2009 – 09/2013	Post-doc of Bioinformatics , Division of Medical Oncology, Department of Medicine, University of Colorado Denver School of Medicine, Aurora, CO
2002 – 2003	Researcher, Korean Bioinformatics Center, S. Korea

Professional Memberships

2010 – present	Member, ISCB (International Society for Computational Biology)
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Honors/Awards

2014	BRIC Hanbitsa Recommended paper, BRIC, South Korea
2014	F1000 Prime Recommended paper
2011	Best 1 st Poster Award at the 9 th Annual Rocky Mountain Bioinformatics Conference. Aspen, CO
2011	Best 3 rd Poster Award at the 9 th Annual Rocky Mountain Bioinformatics Conference. Aspen, CO
2007	Best Paper Award at 45 th ACM-SouthEast Conference, USA
2007	Supplemental Genomics Fellowship, North Carolina State University

Teaching

2013 – 2018	Instructor, CANB7640 Practical Bioinformatics for Large-Scale Genomics Data Mining, UC Denver AMC
2018 Spring	Invited lecture, The power of big data in biomedical science, Department of Anatomy and Cell Biology, Seoul National University College of Medicine
2009 (Jul 8 – 17)	Teaching Assistant, Genomics and Proteomics Workshop, Aurora CO.
2009 Spring	Teaching Assistant, Probability and Statistics for Engineers, Bioinformatics II, NCSU
2008 Fall	Teaching Assistant, Experimental Statistics For Biological Sciences, NCSU
2008 Spring	Lab Organizer and Teaching Assistant, Statistical Inference II, NCSU.
2008 Spring	Teaching Assistant, Data Mining Techniques, NCSU
2004-2007	Teaching Assistant, Introduction to Statistics, NCSU.

Mentoring

2019 – present	Mentor of a Bioinformatics Certificate Student, Sean Patrick, UC Denver AMC
2016 Fall	Mentor of a MSTP rotation student, Mindy Szeto, UC Denver AMC
2015 – 2019	Mentor of bioinformatics post-doc, melanoma bank project, UC Denver AMC
2012-2013	Mentor of winter visiting intern student of TANLAB, Minjae Yoo from Soongsil Univ.
2011	Mentor of summer visiting intern student of TANLAB, Jongbum Kim from Soongsil Univ.
2011	Mentor of visiting researcher of TANLAB, Khor Goot Heah from Universiti Teknologi MARA Selangor, Malaysia

Research Support

Current

CA210075 (Thurman)

Department of Defense

The Complement System and Liver Cancer

07/2022-06/2025

The goal of this project is to investigate the role of the complement system in hepatocellular carcinoma (HCC).

Role: Key personnel

NIH (NCI) 1R01CA219893-01 (Ghosh)

09/01/2017 – 08/31/2022

Progenitor cell malfunction, mutations and changes in microenvironment: a dynamic risk spectrum for cancer

The goal of this project is to find out a common cause of cancer mortality and a neoplasm for which there is considerable evidence supporting an origin from a premalignant field on squamous cell lung cancer (SCC)

Role : Key personnel

NIH (NINDS) R35NS097303 (Trapp)

12/01/2016-11/30/2024

Pathogenesis of Neurological Disability in Primary Diseases of Myelin

In this proposal, we are addressing three key questions: 1) How does myelin provide trophic support to axons? 2) How does demyelination affect neurons and their synaptic connections? 3) How does subpial cortical demyelination occur?

Role : Co-Investigator

NIH (NINDS) 1R21NS123546-01A1(Dutta and Mahajan)

04/01/2022-03/31/2024

Molecular correlates of sub-regional thalamic degeneration in multiple sclerosis

The goal of this grant is to understand the role of thalamic degeneration in multiple sclerosis patients.

Role : Co-Investigator

Completed

NIH (NCI) 1K08CA241071-01 (Shagisultanova)

08/01/2019 – 07/24/2020

Discovering mechanisms of sensitivity and resistance to triple combination targeted therapy in HR+/HER2+ breast cancer

The goal of this proposal is to develop a biomarker of response to triple combination targeted therapy with HER2-small molecule inhibitor tucatinib, CDK4/6 inhibitor palbociclib and aromatase inhibitor letrozole for patients with HR+/HER2+ metastatic breast cancer.

Role : Co-Investigator

AACR J&J LCISC-2018 (DeGregori)

09/01/2018 - 08/31/2021

Microenvironment-mediated Clonal Evolution and risk of Lung Adenocarcinoma

The goal of this study is to detect and understand peripheral airway field carcinogenesis at an earlier stage than previously possible and lead the way to risk determination and preventive interventions.

Role : Co-PI

V Foundation Translational Research Award (Miller)

11/01/2017- 10/31/2020

Precision Chemoprevention of Lung Cancer

In this project, our patient-derived progenitor cultures will allow a patient's own progenitor cells to be tested for response before treatment even begins in the clinic, a major step towards precision chemoprevention.

Role : Co-PI

DOD W81XWH-17-1-0344 (Heasley)

09/15/2011–09/14/2014

Identifying TME-Derived Pathways for Co-targeting with FGFR1 in Mesothelioma

The goal of this project is to define transcriptional changes in tumor cells and the TME initiated by FGFR-specific TKI treatment, and to identify signal pathways whose inhibition yields synergistic activity with

FGFR-specific TKIs in mesothelioma xenografts. My role is overall bioinformatics analysis and interpretation

Role: Co-Investigator

NIH/NCI P50 CA58187 (Bunn)

05/01/2014 - 04/30/2019

Lung SPORE Biostatistics, Informatics and Bioinformatics Core

The goal of this core is to provide biostatistics and bioinformatics support to the Lung SPORE projects and investigators.

Role: Core Investigator

NIH/NCI R01 CA180175 (DeGregori)

09/01/2013 – 06/30/2018

Aging-Associated Alterations in Adaptive Landscapes and the Evolution of Leukemia

The goal of this project is to study the adaptive landscapes and evolution of leukemia related to aging.

Role: Co-Investigator

VA BX001994 (Heasley)

10/01/2013 – 09/30/2017

An FGFR1 oncogene driver pathway in head and neck cancer

The project explores the role of FGFR1 as an oncogene driver in HNSCC cell lines and directly-explanted patient tumors. In addition, the role of FGFR1 as a pathway mediating resistance to EGFR inhibitors will be tested.

Role: Key Personnel

NIH/NCI R21 CA209121 (Kern)

08/19/2016 – 07/31/2018

Kinase Dependent Chemotherapy Resistance Mechanisms In Small Cell Lung Cancer

The goal of this project is to understand the mechanisms behind acquired chemoresistance in SCLC and to exploit these vulnerabilities as therapeutic targets.

Role: Co-Investigator

American Cancer Society RSG-13-060-01 (Schweppe)

01/01/2013 – 12/31/2016

Targeting the Src Kinase Pathway in Thyroid Cancer

The goal of this project is to dissect and target Src kinase signaling pathway in thyroid cancer using genomics and proteomics approaches.

Role: Collaborator

NIH/NCI R01 CA164193 (Schweppe)

07/01/2012 – 04/30/2017

Targeting Focal Adhesion Kinase in Thyroid Cancer

The goals of this proposal are to determine when and where FAK kinase activity or protein-protein interactions are important, which will provide important information on how FAK should be targeted in the clinic.

Role: Collaborator

Doris Duke Clinical Scientist Development Award (Bernt)

07/01/2014 – 06/30/2017

Targeting DOT1L in MN1-high Acute Myeloid Leukemia

This project aims to confirm the histone methyltransferase DOT1L as a therapeutic target in acute myeloid leukemia (AML) with high expression of MN1, and at establishing criteria for a clinical trial to test the efficacy of a small molecule inhibitor of DOT1L in subtype of AML with poor prognosis.

Role: Collaborator

NIH/NCI R01 CA157850 (DeGregori)

09/26/2011 – 07/31/2016

Rationally designed targeted therapeutic approaches for NSCLC

The goal of this proposal is to perform computational analysis and systematic validation of genome-wide shRNA screening results to reveal genes and pathways whose inhibition sensitizes Non-Small Cell Lung Cancer cells to EGFR inhibition.

Role: Key Personnel

DOD W81XWH-11-1-0527 (Tan)

09/15/2011 – 09/14/2014

Collaborative Model for Acceleration of Individualized Therapy of Colon Cancer

The overall goal of this Idea Award is enhance the efficiency and speed of developing novel and individualized therapy for patients with KRAS mutant colorectal cancer (CRC) using a comprehensive bioinformatics approach and novel preclinical models of human CRC.

Role: Key Personnel

NIH/NCI P50 CA058187 Pilot Project (Kim)

11/15/2014 – 10/31/2015

A Systems Approach to Elucidating Molecular Vulnerabilities and Therapeutics in KRAS-Mutant Lung Adenocarcinoma

This project seeks to discover molecular vulnerabilities in KRAS-mutant lung cancer by integrating functional genomics and bioinformatics approaches.

Role: Principal-Investigator

Golfers Against Cancer Denver (Tan/DeGregori/Porter)

11/01/2010 – 10/31/2011

Implementation and Refinement of High Throughput Functional Genomic Screening

The goal of this project is to implement and refine the computational algorithm of high throughput genome-wide synthetic lethality screen.

Role: Key Personnel

Cancer League of Colorado (Kim)

07/01/2011 – 06/30/2012

PathCMap: Development of pathway signature system for identifying partners of synthetic lethal genes

The overall goal of this project is to develop a comprehensive computational prediction method as a powerful translational tool facilitating the understanding and overcoming resistance mechanisms to targeted therapy.

Role: Principal-Investigator

Publications

1. Hwang M, Savarin C, **Kim J**, Powers J, Towne N, Oh H, Bergmann CC. (2022). Trem2 deficiency impairs recovery and phagocytosis and dysregulates myeloid gene expression during virus-induced demyelination. *J Neuroinflammation*. 4;19(1). PMID : 36333761
2. Gurule NJ, McCoach CE, Hinz TK, Merrick DT, Van Bokhoven A, Kim J, Patil T, Calhoun J, Nemenoff RA, Tan AC, Doebele RC, Heasley LE. (2021). A tyrosine kinase inhibitor-induced interferon response positively associates with clinical response in EGFR-mutant lung cancer. *NPJ Precision Oncology*. 5(1):41. PMID: 34001994
3. Smith N, Warren BB, Smith J, Jacobson L, Armstrong J, Kim J, Di Paola J, Manco-Johnson M. (2021) Antithrombin deficiency: A pediatric disorder. *Thromb Res*. 2021 Jun;202:45-51. Epub 2021 Mar 3. PMID: 33725558
4. Korpela SP, Hinz TK, Oweida A, **Kim J**, Calhoun J, Ferris R, Nemenoff RA, Karam SD, Clambey ET, Heasley LE. Role of epidermal growth factor receptor inhibitor-induced interferon pathway signaling in the head and neck squamous cell carcinoma therapeutic response. (2021) *J Transl Med*. 2021 Jan 23;19(1):43. doi: 10.1186/s12967-021-02706-8. PMID: 33485341
5. Joshi M, **Kim J**, D'Alessandro A, Monk E, Bruce K, Elajaili H, Nozik-Grayck E, Goodspeed A, Costello JC, Schlaepfer IR. CPT1A Over-Expression Increases Reactive Oxygen Species in the Mitochondria and Promotes Antioxidant Defenses in Prostate Cancer. (2020) *Cancers (Basel)*. (2020) Nov 18;12(11):3431. doi: 10.3390/cancers12113431. PMID: 33218188
6. Bonney EA, Krebs K, **Kim J**, Prakash K, Torrance BL, Haynes L, Rincon M. Protective Intranasal Immunization Against Influenza Virus in Infant Mice Is Dependent on IL-6. (2020) *Front Immunol*. 2020 Oct 28;11:568978. doi: 10.3389/fimmu.2020.568978. eCollection 2020. PMID: 33193346
7. Lee WC, Reuben A, Hu X, McGranahan N, Chen R, Jalali A, Negrao MV, Hubert SM, Tang C, Wu CC, Lucas AS, Roh W, Suda K, **Kim J**, Tan AC, Peng DH, Lu W, Tang X, Chow CW, Fujimoto J, Behrens C, Kalhor N, Fukumura K, Coyle M, Thornton R, Gumbs C, Li J, Wu CJ, Little L, Roarty E, Song X, Lee JJ, Sulman EP, Rao G, Swisher S, Diao L, Wang J, Heymach JV, Huse JT, Scheet P,

- Wistuba II, Gibbons DL, Futreal PA, Zhang J, Gomez D, Zhang J. (2020) Multiomics profiling of primary lung cancers and distant metastases reveals immunosuppression as a common characteristic of tumor cells with metastatic plasticity. *Genome Biol.* 2020 Nov 4;21(1):271. doi: 10.1186/s13059-020-02175-0. PMID: 33148332
8. Amato CM, Hintzsche JD, Wells K, Applegate A, Gorden NT, Vorwald VM, Tobin RP, Nassar K, Shellman YG, **Kim J**, Medina TM, Rieth M, Lewis KD, McCarter MD, Gonzalez R, Tan AC, Robinson WA. (2020) Pre-Treatment Mutational and Transcriptomic Landscape of Responding Metastatic Melanoma Patients to Anti-PD1 Immunotherapy. *Cancers (Basel)*. 2020 Jul 17;12(7):E1943. PMID: 32708981
 9. Kern JA*, **Kim J***, Foster DG, Mishra R, Gardner EE, Poirier JT, Rivard C, Yu H, Finigan JH, Dowlati A, Rudin CM, Tan AC. (2020) Role of mTOR as an essential kinase in SCLC. *Journal of Thoracic Oncology*. 2020 Jun 26:S1556-0864(20)30503-7 [Epub ahead of print] PubMed PMID : 32599072
 10. Davis SL, Ionkina A, Bagby SM, Orth JD, Gittleman B, Marcus JM, Lam ET, Corr BR, O'Bryant CL, Glode AE, Tan AC, **Kim J**, Tentler JJ, Capasso A, Dailey K, Gustafson DL, Messersmith WA, Leong S, Eckhardt SG, Pitts TM, Diamond JR. (2020). Rational Combination of TORC1/2 Inhibitor TAK-228 and Aurora A Kinase Inhibitor Alisertib in Solid Tumors: Preclinical and Dose-Finding Phase 1 Trial Results. *Clinical Cancer Research*. (Accepted 3/3/2020) [[ClinicalTrials.gov ID: NCT02719691](https://clinicaltrials.gov/ct2/show/study/NCT02719691)]
 11. Pei S, Pollyea DA, Gustafson A, Stevens BM, Minhajuddin M, Fu R, Riemondy KA, Gillen AE, Sheridan RM, **Kim J**, Costello JC, Amaya ML, Inguva A, Winters A, Ye H, Krug A, Jones CL, Adane B, Khan N, Ponder J, Schowinsky J, Abbott D, Hammes A, Myers JR, Ashton JM, Nemkov T, D'Alessandro A, Gutman JA, Ramsey HE, Savona MR, Smith CA, Jordan CT. Monocytic Subclones Confer Resistance to Venetoclax-Based Therapy in Acute Myeloid Leukemia Patients. *Cancer Discov.* 2020 Jan 23;. doi: 10.1158/2159-8290.CD-19-0710. [Epub ahead of print] PubMed PMID: 31974170.
 12. Hinz TK, Kleczko EK, Singleton KR, Calhoun J, Marek LA, **Kim J**, Tan AC, Heasley LE. Functional RNAi Screens Define Distinct Protein Kinase Vulnerabilities in EGFR-Dependent HNSCC Cell Lines. *Mol Pharmacol.* 2019 Dec;96(6):862-870. doi: 10.1124/mol.119.117804. Epub 2019 Sep 25. PubMed PMID: 31554698
 13. Capasso A, Bagby SM, Dailey KL, Currimjee N, Yacob BW, Ionkina A, Frank JG, Kim DJ, George C, Lee YB, Benaim E, Gittleman B, Hartman SJ, Tan AC, **Kim J**, Pitts TM, Eckhardt SG, Tentler JJ, Diamond JR. First-in-Class Phosphorylated-p68 Inhibitor RX-5902 Inhibits β -Catenin Signaling and Demonstrates Antitumor Activity in Triple-Negative Breast Cancer. *Mol Cancer Ther.* 2019 Nov;18(11):1916-1925. doi: 10.1158/1535-7163.MCT-18-1334. Epub 2019 Sep 5. PubMed PMID: 31488700; PubMed Central PMCID: PMC6825586.
 14. Kessler BE, Mishall KM, Kellett MD, Clark EG, Pugazhenth U, Pozdeyev N, **Kim J**, Tan AC, Schweppe RE. Resistance to Src inhibition alters the BRAF-mutant tumor secretome to promote an invasive phenotype and therapeutic escape through a FAK>p130Cas>c-Jun signaling axis. *Oncogene*. 2019 Apr;38(14):2565-2579. doi: 10.1038/s41388-018-0617-1. Epub 2018 Dec 10. PubMed PMID: 30531837; PubMed Central PMCID: PMC6450711.
 15. Yoo M, Shin J, Kim H, **Kim J**, Kang J, Tan AC. (2018). Exploring the molecular mechanisms of Traditional Chinese Medicine Components using Gene Expression Signatures and Connectivity Map. *Computer Methods and Programs in Biomedicine*. [Epub ahead of print, Apr 4, 2018] [PMID: 29650251]
 16. Suda K, Murakami I, Yu H, **Kim J**, Tan AC, Mizuuchi H, Rozeboom L, Ellison K, Rivard CJ, Mitsudomi T, Hirsch FR. (2018). CD44 facilitates epithelial to mesenchymal transition phenotypic change at acquisition of resistance to EGFR kinase inhibitors in lung cancer. *Molecular Cancer Therapeutics*. 17(10):2257-2265. [Epub ahead of print, July 26, 2018] [PMID: 30049789]
 17. Suda K*, **Kim J***, Murakami I, Rozeboom L, Shimoji M, Shimizu S, Rivard CJ, Mitsudomi T, Tan AC®, Hirsch FR®. (2018). Innate genetic evolution of lung cancers and spatial heterogeneity: analysis of treatment naive lesions. *Journal of Thoracic Oncology*. 13(10): 1496-1507. [PMID: 29933065] [COVER]
 18. Scott AJ, Arcaroli JJ, Bagby SM, Yahn R, Huber KM, Serkova NJ, Nguyen A, **Kim J**, Thorburn A, Vogel J, Quackenbush KS, Capasso A, Schreiber A, Blatchford P, Klauck PJ, Pitts TM, Eckhardt SG, Messersmith WA. (2018) Cabozantinib Exhibits Potent Antitumor Activity in Colorectal Cancer

Patient-Derived Tumor Xenograft Models via Autophagy and Signaling Mechanisms. *Molecular cancer therapeutics*. 2018; 17(10):2112-2122. [PMID:30026382]

19. Hintzsche JD, Yoo M, **Kim J**, Amato CM, Robinson WA, Tan AC. (2018). IMPACT Web Portal: Oncology Database Integrating Molecular Profiles with Actionable Therapeutics. *BMC Medical Genomics*. 11(Suppl 2): 26. [PMID: 29697364]
20. **Kim J***, Yoo M*, Shin J, Kim H, Kang J, Tan AC. (2018). Systems Pharmacology-based Approach of Connecting Disease Genes in Genome-wide Association Studies with Traditional Chinese Medicine. *International Journal of Genomics*. 2018: 7697356. [PMID: 29765977]
21. Klauck PJ, Bagby SM, Capasso A, Bradshaw-Pierce EL, Selby HM, Spreafico A, Tentler JJ, Tan AC, **Kim J**, Arcaroli JJ, Purkey A, Messersmith WA, Kuida K, Eckhardt SG, Pitts TM. (2018). Antitumor activity of the polo-like kinase inhibitor, TAK-960, against preclinical models of colorectal cancer. *BMC Cancer*. 18: 136. [PMID: 29402316]
22. Pilling A, **Kim J**, Estrada-bernal A, Zhou Q, Le A, Singleton K, Heasley LE, Tan AC, DeGregori J, Doebele RC. (2018). ALK is a critical regulator of the MYC-signaling axis in ALK positive lung cancer. *Oncotarget*. 9(10): 8823-8835. [PMID: 29507657]
23. Kim S, Park D, Choi Y, Lee K, Kim B, Jeon M, **Kim J**, Tan AC, Kang J. (2018). A Pilot Study of Biomedical Text Comprehension using an Attention-based Deep Neural Reader: Design and Experimental Analysis. *JMIR Medical Informatics*. 6(1): e2. [PMID: 29305341]
24. Ionkina AA, Tentler JJ, **Kim J**, Capasso A, Pitts TM, Ryall KA, Howison RR, Kabos P, Sartorius CA, Tan AC, Eckhardt SG, Diamond JR. (2017). Efficacy and Molecular Mechanisms of Differentiated Response to the Aurora and Angiogenic Kinase Inhibitor ENMD-2076 in Preclinical Models of p53-Mutated Triple-Negative Breast Cancer. *Frontiers in Oncology*. 7: Article 94.[PMID: 28555173]
25. Hintzsche JD, Gorden NT, Amato CM, **Kim J**, Wuensch KE, Robinson SE, Applegate AJ, Coutts KL, Medina TM, Wells KR, Wisell JA, McCarter MD, Box NF, Shellman YG, Gonzalez RC, Lewis KD, Tentler JJ, Tan AC, Robinson WA. (2017). Whole Exome Sequencing Identifies Recurrent SF3B1 R625 Mutation and Co-Mutation of NF1 and KIT in Mucosal Melanoma. *Melanoma Research*. [Epub ahead of print, Mar 14, 2017]. [PMID: 28296713]
26. Flaig TW, Salzmänn-Sullivan M, Su LJ, Zhang Z, Joshi M, Gijón MA, **Kim J**, Arcaroli JJ, Van Bokhoven A, Lucia MS, La Rosa FG, Schlaepfer IR. Lipid catabolism inhibition sensitizes prostate cancer cells to antiandrogen blockade. *Oncotarget*. 2017; 8(34):56051-56065. [PMID:28915573]
27. Suda K, Murakami I, Yu H, **Kim J**, Ellison K, Rivard CJ, Mitsudomi T, Hirsch FR. (2017) Heterogeneity in immune marker expression after acquisition of resistance to EGFR kinase inhibitors: analysis of a case with small cell lung cancer transformation. *Journal of Thoracic Oncology* [Epub ahead of print] [PMID: 28193529].
28. Dimberg LY, Towers CG, Behbakht K, Hotz TJ, **Kim J**, Fosmire S, Porter CC, Tan AC, Thorburn A, Ford HL. (2017). A genome-wide loss-of-function screen identifies SLC26A2 as a novel mediator of TRAIL resistance. *Molecular Cancer Research*. [Epub ahead of print, Jan 20, 2017]. [PMID: 28108622]
29. Zhang G, Scarborough HA, **Kim J**, Rozhok AI, Chen YA, Zhang X, Song L, Bai Y, Fang B, Liu RZ, Koomen J, Tan AC, DeGregori J, Haura EB. (2016). Coupling an EML4-ALK Centric Interactome With RNA Interference Identifies Sensitizers to ALK Inhibitors. *Science Signaling*. 9(450): rs12. [PMID: 27811184].
30. Scarborough HA, Helfrich BA, Casas-Selves M, Schuller AG, Grosskurth SE, **Kim J**, Tan AC, Chan DC, Zhang Z, Zaberezhnyy V, Bunn PA, DeGregori J. (2016). AZ1366: An inhibitor of tankyrase and the canonical Wnt pathway that limits the persistence of non-small cell lung cancer cells following EGFR inhibition. *Clinical Cancer Research*. [Epub ahead of print, Sept 23, 2016] [PMID: 27663586].
31. Gregory MA, D'Alessandro A, Alvarez-Calderon F, **Kim J**, Nemkov T, Adane B, Rozhok AI, Kumar A, Kumar V, Pollyea DA, Wempe MF, Jordan CT, Serkova NJ, Tan AC, Hansen KC, DeGregori J. (2016). ATM/G6PD-driven redox metabolism promotes FLT3 inhibitor resistance in acute myeloid

- leukemia. *Proceedings of the National Academy of Sciences USA*. 113(43):E6669-E6678. [PMID: 27791036].
32. Helfrich BA, **Kim J**, Gao D, Chan DC, Zhang Z, Tan AC, Bunn Jr PA. (2016). Barasertib (AZD1152), a small molecule Aurora B inhibitor, inhibits the growth of SCLC cell lines in vitro and in vivo. *Molecular Cancer Therapeutics*. 15(10): 2314-2322. [PMID: 27496133].
 33. Keysar SB, Le PH, Miller B, Jackson BC, Eagles JR, Nieto C, **Kim J**, Tang B, Glogowska MJ, Morton JJ, Padilla-Just N, Gomez K, Warnock E, Reisinger J, Arcaroli JJ, Messersmith WA, Wakefield LM, Gao D, Tan AC, Serracino H, Vasiliou V, Roop DR, Wang XJ, Jimeno. (2016). PI3K signaling regulates SOX2 enabling cancer stem cell properties in head and neck cancer. *Journal of the National Cancer Institute*. [PMID: 27634934]
 34. Cavalli G, Koenders M, Kalabokis V, **Kim J**, Tan AC, Mantovani A, Garlanda C, Dagna L, Joosten LAB, Dinarello CA. (2016). Treating experimental arthritis with the innate inflammation inhibitor IL 37 reduces joint and systemic inflammation. *Rheumatology*. 55(12):2220-2229. [PMID: 27567100].
 35. Bagby S, Messersmith WA, Pitts TM, Capasso A, Varella-Garcia M, Klauck P, **Kim J**, Tan AC, Eckhardt SG, Tentler JJ, Arcaroli JJ. (2016). Development and Maintenance of a Preclinical Patient Derived Tumor Xenograft Model for the Investigation of Novel Anti-Cancer Therapies. *The Journal of Visualized Experiments*. 115: e54393. [PMID: 27768028].
 36. Quackenbush KS, Bagby S, Tai WM, Messersmith WA, Schreiber A, Greene J, **Kim J**, Wang G, Purkey A, Pitts TM, Nguyen A, Gao D, Blatchford P, Capasso A, Schuller AG, Eckhardt SG, Arcaroli JJ. (2016). The novel tankyrase inhibitor (AZ1366) enhances irinotecan activity in tumors that exhibit elevated tankyrase and irinotecan resistance. *Oncotarget*. 7(19):28273-28285. [PMID: 27070088].
 37. Beadnell TC, Mishall KM, Zhou Q, Riffert SM, Wuensch KE, Kessler BE, Corpus ML, Jing X, **Kim J**, Wang G, Tan AC, Schweppe RE. (2016). The Mitogen Activated Protein Kinase Pathway Facilitates Resistance to the Src Inhibitor, Dasatinib, in Thyroid Cancer. *Molecular Cancer Therapeutics*. 15(8): 1952-1963. [PMID: 27222538].
 38. Hintzsche J, **Kim J**, Amato CM, Yadav V, Robinson SE, Seelenfreund E, Shellman Y, Wisell J, Applegate A, McCarter M, Box N, Tentler J, De S, Robinson WA, and Tan AC. (2016) "IMPACT: Whole-Exome Sequencing Analysis Pipeline of Integrating Molecular Profiles with Actionable Therapeutics in Clinical Samples," *Journal of the American Medical Informatics Association*. 23(4): 721-730. [PMID: 27026619].
 39. Towers CG, Guarnieri AL, Micalizzi DS, Harrell JC, Gillen AE, **Kim J**, Wang CA, Oliphant MUJ, Drasin DJ, Guney MA, Kabos P, Sartorius CA, Tan AC, Perou CM, Espinosa JM, Ford HL. (2015). The Six1 oncoprotein downregulates p53 via concomitant regulation of RPL26 and microRNA-27-a-3p. *Nature Communications*. 6:10077. [PMID: 26687066].
 40. Ryall KA, **Kim J**, Klauck PJ, Shin J, Yoo M, Ionkina A, Pitts TM, Tentler JJ, Diamond JR, Eckhardt SG, Heasley LE, Kang J, Tan AC. (2015). An integrated bioinformatics analysis to dissect kinase dependency in triple negative breast cancer. *BMC Genomics*. 16 (Suppl 12):S2. (Proceedings of the 1st Joint GIW/InCoB Conference, Tokyo, Japan). [PMID: 26681397].
 41. Henry C, Casas-Selves M, **Kim J**, Zaberezhnyy V, Aghili L, Daniel AE, Jimenez L, Azam T, McNamee EN, Clambey ET, Klawitter J, Serkova NJ, Tan AC, Dinarello CA, DeGregori J. (2015). Aging-associated inflammation promotes selection for adaptive oncogenic events in B cell progenitors. *The Journal of Clinical Investigation*. 125(12):4666-4680. [PMID: 26551682].
 42. Singleton KR, Hinz TK, Kleczko EK, Marek LA, Kwak J, Harp T, **Kim J**, Tan AC, Heasley LE. (2015) Kinome RNAi Screens Reveal Synergistic Targeting of MTOR and FGFR1 Pathways for Treatment of Lung Cancer and HNSCC. *Cancer Research*. 2015 Oct 15;75(20):4398-406. [PMID: 26359452]
 43. Ryall KA, Shin J, Yoo M, Hinz TK, **Kim J**, Kang J, Heasley LE, Tan AC. (2015) Identifying kinase dependency in cancer cells by integrating high-throughput drug screening and kinase inhibition data. *Bioinformatics*. 31(23):3799-3806. [PMID: 26206305].
 44. Davis EM, **Kim J**, Menasche BL, Sheppard J, Liu X, Tan AC, Shen J. (2015) Comparative Haploid Genetic Screens Reveal Divergent Pathways in the Biogenesis and Trafficking of

Glycophosphatidylinositol-Anchored Proteins. *Cell Rep.* 2015 Jun 23;11(11):1727-36 [PMID: 26074080].

45. Göke F, Franzen A, Hinz TK, Marek LA, Yoon P, Sharma R, Bode M, Mässenhausen A, Lankat-Buttgereit B, Göke A, Golletz C, Kirsten R, Boehm D, Vogel W, Kleczko EK, Eagles J, Hirsch FR, Bremen TV, Bootz F, Schröck A, **Kim J**, Tan AC, Jimeno A, Heasley LE, Perner S. (2015). FGFR1 expression levels predict BGJ398-sensitivity of FGFR1-dependent head and neck squamous cell cancers. *Clinical Cancer Research*. 21(19): 4356-4364. [PMID: 26015511].
46. Yoo M*, Shin J*, **Kim J**, Ryall KA, Lee K, Lee S, Jeon M, Kang J, Tan AC. (2015). DSigDB: Drug Signatures Database for Gene Set Analysis. *Bioinformatics*. 31(18): 3069-3071. [PMID: 25990557].
47. Kleczko EK, **Kim J**, Keysar SB, Heasley LR, Eagles-Soukup J, Simon M, Marshall ME, Singleton KR, Jimeno A, Tan AC, Heasley LE. (2015). An Inducible TGFB2-TGFBR Pathway Modulates the Sensitivity of HNSCC Cells to Tyrosine Kinase Inhibitors Targeting Dominant Receptor Tyrosine Kinases. *PLoS ONE*. 10(5):e0123600. [PMID: 25946135].
48. Drasin DJ, Guarnier AL, Neelakantan D, **Kim J**, Cabrera JH, Wang CA, Zaberezhnyy V, Gasparini P, Cascione L, Huebner K, Tan AC, Ford HL. (2015). Twist1-induced microRNA-424 reversibly drives mesenchymal programming while inhibiting tumor initiation. *Cancer Research*. 75(9): 1908-1921. [PMID: 25716682].
49. Yonekawa T, Gamez G, **Kim J**, Tan AC, Thorburn J, Gump J, Thorburn A, Morgan MJ. (2015). RIP1 Negatively Regulates Basal Autophagic Flux through TFEB to Control Sensitivity to Apoptosis. *EMBO Reports*. 16:700-708. [PMID: 25908842].
50. Fleenor CJ, Rozhok AI, Zaberezhnyy V, Mathew D, **Kim J**, Tan AC, Bernstein ID, DeGregori J. (2014). Contrasting Roles for C/EBPa and Notch in Irradiation-Induced Multipotent Hematopoietic Progenitor Cell Defects. *Stem Cells*. 33(4):1345-1358. [PMID: 25546133].
51. Seelenfreund E, Robinson WA, Amato CM, Tan AC, **Kim J**, Robinson SE. (2014). Long term storage of dry versus frozen RNA for next generation molecular studies. *PLoS ONE* 9(11): e111827. [PMID: 25380187].
52. **Kim J**, Vasu VT, Mishra R, Singleton KR, Yoo M, Leach SM, Farias-Hesson E, Mason RJ, Kang J, Ramamoorthy P, Kern JA, Heasley LE, Finigan JH, Tan AC. (2014). Bioinformatics-driven discovery of rational combination for over-coming EGFR-mutant lung cancer resistance to EGFR therapy. *Bioinformatics*. 2014 Sep 1;30(17):2393-8. [PMID: 24812339], **F1000 recommended**
53. **Kim J**, Yoo M, Kang J, Tan AC. (2013). K-Map: connecting kinases with therapeutics for drug repurposing and development. *Hum Genomics*. 7(1):20. [PMID: 24060470]
54. Spreafico A, Tentler JJ, Pitts TM, Tan AC, Gregory MA, Arcaroli JJ, Klauck PJ, McManus MC, Hansen RJ, **Kim J**, Micel LN, Selby HM, Newton TP, McPhillips K, Gustafson DL, Degregori JV, Messersmith WA, Winn RA, Eckhardt SG. (2013). Rational Combination of a MEK Inhibitor, Selumetinib, and the Wnt/Calcium Pathway Modulator, Cyclosporin A, in Preclinical Models of Colorectal Cancer. *Clinical Cancer Research* 19(15):4149 - 4162. [PMID: 23757356]
55. Andrysik Z, **Kim J**, Tan AC, Espinosa JM. (2013). A Genetic Screen Identifies TCF3/E2A and TRIAP1 as Pathway-Specific Regulators of the Cellular Response to p53 Activation. *Cell Reports* 3(5):1346-1354. [PMID:23684607].
56. Harvell D, **Kim J**, O'Brien J, Tan AC, Borges VF, Shedin P, Jacobsen BM, Horwitz KB. (2013) Genomic Signatures of Pregnancy – Associated Breast Cancer Epithelia and Stroma and their Regulation by Estrogens and Progesterone. *Hormones and Cancer*. 4(3):140-153. [PMID: 23479404].
57. Singleton KR, **Kim J**, Hinz TK, Marek LA, Casas-Selves M, Hatheway C, Tan AC, Degregori J, Heasley LE. (2013). A Receptor Tyrosine Kinase Network Composed of Fibroblast Growth Factor Receptors, Epidermal Growth Factor Receptor, v-erb-b2 Erythroblastic Leukemia Viral Oncogene Homolog 2, and Hepatocyte Growth Factor Receptor Drives Growth and Survival of Head and Neck Squamous Carcinoma Cell Lines. *Molecular Pharmacology*. 83(4):882-893. [PMID: 23371912].

58. Casás-Selves M, **Kim J**, Zhang Z, Helfrich BA, Gao D, Porter CC, Scarborough HA, Bunn PA Jr, Chan DC, Tan AC, DeGregori J. (2012) Tankyrase and the canonical Wnt pathway protect lung cancer cells from EGFR inhibition. *Cancer Research*. 72(16):4154-64. [PMID: 22738915].
59. Sullivan KD, Padilla-Just N, Henry RE, Porter CC, **Kim J**, Tentler JJ, Eckhardt SG, Tan AC, Degregori J, Espinosa JM. (2012). ATM and MET kinases are synthetic lethal with nongenotoxic activation of p53. *Nature Chemical Biology*. 8(7): 646-654. [PMID: 22660439].
60. Porter CC, **Kim J**, Fosmire S, Gearheart CM, van Linden A, Baturin D, Zaberezhnyy V, Patel PR, Gao D, Tan AC, Degregori J. (2012). Integrated genomic analyses identify WEE1 as a critical mediator of cell fate and a novel therapeutic target in acute myeloid leukemia. *Leukemia*. 26(6):1266-1276. [PMID: 22289989].
61. **Kim J**, Tan AC. (2012) BiNGS!SL-seq: a bioinformatics pipeline for the analysis and interpretation of deep sequencing genome-wide synthetic lethal screen. *Methods Mol Biol*. 802:389-398. [PMID: 22130895]
62. Kim H, **Kim J**, Selby H, Gao D, Tong T, Phang TL, Tan AC. (2011) A short survey of computational analysis methods in analysing ChIP-seq data. *Human Genomics*. 5(2):117-123. [PMID: 21296745]
63. Gao D, **Kim J**, Kim H, Phang TL, Selby H, Tan AC, Tong T. (2010) A survey of statistical software for analysing RNA-seq data. *Human Genomics*. 5(1):56-60. [PMID: 21106489]
64. **Kim J**, Zhao S, Howard BE, Heber S. (2009). Mining of *cis*-regulatory motifs associated with tissue-specific alternative splicing. *Lecture Notes in Bioinformatics (LNBI)*: 5542, p. 260-271.
65. Zhao S, **Kim J**, Heber S. (2009). Analysis of *cis*-regulatory motifs in cassette exons. *Lecture Notes in Bioinformatics (LNBI)*: 5542, p. 272-283.
66. Zhao S., **Kim J**, Heber S. (2007). Large-scale discovery of regulatory motifs involved in alternative splicing. *Proceeding of IEEE 7th International Conference of Bioinformatics and BioEngineering* 2007:1399-1403.
67. **Kim J**, Zhao S, Heber S. (2007). Finding association rules of *cis*-regulatory elements involved in alternative splicing. *Proceeding of ACM Southeast Regional Conference* 2007: 232-237

Invited Presentations

1. Mitochondrial Engineering Lab Seminar, Department of Biotechnology at CHA University, Seongnam, S. Korea (2022)
2. Annual Computational Systems Biology Seminar, Chonnam National University, Gwangju, S. Korea (2022)
3. Annual Computational Systems Biology Seminar, Chonnam National University, Gwangju, S. Korea (2021)
4. Lung SPORE workshop, UT southwestern, Dallas, TX, USA (2018)
5. The 5th annual mini-symposium on The power of Informatics to Advance Health, University of Colorado Anschutz Medical Campus, Aurora, CO (2018)
6. Translational Bioinformatics in Cancer Research, Nov 11, 2017, Chungbuk National University Hospital, Cheongju-si, South Korea (2017)
7. Bioinformatics Journal Club, CCTSI, University of Colorado AMC, Aurora, CO (2015)
8. School of Information and Communications, Gwangju Institute of Science and Technology (GIST), Gwangju, S. Korea (2015)
9. School of Medicine, Chonbuk National University, Jeonju, S. Korea (2015)
10. Dental Science Research Institute, Chonnam National University, Gwangju, S. Korea (2015)
11. Biomedical Engineering, Ulsan National Institute of Science and Technology (UNIST), Gwangju, S. Korea (2015)
12. School of Life Science, Gwangju Institute of Science and Technology (GIST), Gwangju, S. Korea (2015)
13. BRIC Hanbitsa Webinar Seminar (2014)

14. Chonnam National University Hospital, Seoul, S. Korea (2014)
15. Cancer Biology Program, University of Colorado AMC, Aurora, CO (2013)
16. Invited Speaker Presentation in KOGO Winter Symposium. YongPyung, S. Korea (2012)
17. School of Systems Biomedical Science, Soongsil University, Seoul, S. Korea (2012)
18. Dental Science Research Institute, Chonnam National University, Gwangju, S. Korea (2012)
19. School of Life Science, Gwangju Institute of Science and Technology (GIST), Gwangju, S. Korea (2012)
20. Computational Bioscience Program, University of Colorado AMC, Aurora, CO (2009)

Conference Presentations

1. **Kim J**, Suda K, Murakami I, Rozeboom L, Rivard CJ, Mitsudomi T, Hirsche FR, Tan AC, Tracing the Innate Genetic Evolution and Spatial Heterogeneity in Treatment Naive Lung Cancer Lesions, 15th Annual Rocky Mountain Bioinformatics Conference, Aspen/Snowmass, CO, USA (2017), **invited to Oral presentation**
2. Hintzsche J, Yoo M, **Kim J**, Amato C, Robinson W, Tan AC, IMPACT Web Portal: An Oncology Database Integrating Molecular Profiles with Actionable Therapeutics from Next Generation Sequencing Data, 15th Annual Rocky Mountain Bioinformatics Conference, Aspen/Snowmass, CO, USA (2017), **invited to Oral presentation**
3. Hintzsche JD, Yoo M, **Kim J**, Amato CM, Robinson WA, Tan AC, IMPACT Web Portal: Oncology Database of Integrating Molecular Profiles with Actionable Therapeutics, GIW/BIOINFO 2017, Seoul, Korea (2017)
4. Suda K, Murakami I, Yu H, **Kim J**, Mizuuchi H, Ellison K, Rivard CJ, AC Tan, Mitsudomi T, Hirsch FR, CD44 confers EMT phenotypic change following resistance to EGFR-TKIs in lung cancer, IASLC chicago meeting 2017
5. Tentler J, Frank JG, Kim DJ, Geroge C, Lee YB, Benaim E, Tan AC, Kim J, Pitts TM, Capasso A, Dailey K, Diamond JR, Preclinical Studies of RX-5902, a Beta-catenin Modulator, in Triple Negative Breast Cancer, SABCS 2017, San Antonio, TX, USA
6. Diamond JR, Orth JD, Ionkina A, Dailey K, Pitts TM, Capasso A, Marcus JM, Burke RT, Davis SL, **Kim J**, Tan AC, Eckhardt SG, Tentler JJ, Rational combination of mTOR and Aurora kinase A inhibition in preclinical models of triple-negative breast cancer, AACR-NCI-EORTC International Conference, Philadelphia, PA, USA
7. Kim H, **Kim J**, Bentley D (2016). Computational pipelines for the analysis of premature cleavage and polyadenylation, ISMB, Orlando, FL, USA (2016)
8. Meyer JE, Serebriiskii I, Lieu CH, Frampton GM, Bailey M, Ennis R, Tan AC, **Kim J**, Golemis E, "Genomic distinctions between colon and rectal cancer in young patients", 2016 ASCO Annual Meeting, Chicago, IL, USA (2016)
9. Lieu CH, Pitts TM, **Kim J**, Tan AC, Messersmith WA, You YN, Eng C, Eckhardt SG, "Emerging transcriptional landscape and putative therapeutic targets in young patients with metastatic colorectal cancer (CRC)", 2016 Gastrointestinal Cancers Symposium, ASCO, San Francisco, CA, USA (2016)
10. ISMB 2014 Poster Oral Presentation in ISMB 2014. Boston, CO. USA (2014)
11. Workshop Presentation in the 9th Annual Rocky Mountain Bioinformatics Conference. Aspen, CO. USA (2011)
12. Paper presentation in the 5th international Symposium on Bioinformatics Research and Applications. Ft. Lauderdale, FL, USA (2009)
13. Paper presentation in the 45th ACM-SouthEast conference, Winston-Salem, NC, USA (2007)
14. Workshop presentation in the 3rd Rocky Mountain Regional Bioinformatics Conference, Aspen, CO, USA (2005)

Poster Presentations

1. Kim H, Nassar K, Hintzsche J, **Kim J**, Tan AC. SALSA: Systematic Alternative Splicing Analysis Pipeline for Detecting Cryptic 3' Splice Site Usage in SF3B1 Mutant Cancer RNA-seq, 15th Annual Rocky Mountain Bioinformatics Conference, Aspen/Snowmass, CO, USA (2017)

2. Kim H, **Kim J**, Bentley D. Computational pipelines for the analysis of premature cleavage and polyadenylation, ISMB, Orlando, FL, USA (2016)
3. Meyer JE, Serebriiskii I, Lieu CH, Frampton GM, Bailey M, Ennis R, Tan AC, **Kim J**, Golemis E, "Genomic distinctions between colon and rectal cancer in young patients", 2016 ASCO Annual Meeting, Chicago, IL, USA (2016)
4. Lieu CH, Pitts TM, **Kim J**, Tan AC, Messersmith WA, You YN, Eng C, Eckhardt SG, "Emerging transcriptional landscape and putative therapeutic targets in young patients with metastatic colorectal cancer (CRC)", 2016 Gastrointestinal Cancers Symposium, ASCO, San Francisco, CA, USA (2016)
5. Kim H, **Kim J**, Fong N, Bentley D. A comprehensive, flexible pipelines for alternative polyadenylation, CSH Genomics & Informatics, Cold spring harbor, NY, USA (2015)
6. Gregory MA, D'Alessandro A, Alvarez-Calderon F, **Kim J**, Nemkov T, Tan AC, Hansen KC, DeGregori J, "ATM/G6PD-dependent metabolic pathways promote mitochondrial redox homeostasis and resistance to FLT3 inhibition in acute myeloid leukemia", AACR-NCI-EORTC International Conference, Boston, MA, USA (2015)
7. Hintzsche JD, Amato CM, Seelenfreund E, Robinson SE, Turner JA, Applegate AJ, Gonzalez R, Nooruddin Z, Coutts KL, **Kim J**, Shellman YG, Wisell J, McCarter MD, Box NF, Tentler JJ, Tan AC, Robinson WA, "Characterizing the Mutational Landscape of 418 Melanoma Tumors Using Whole Exome Sequencing", the Society for Melanoma Research, San Francisco, CA, USA (2015)
8. Mishall KM, Beadnell TC, Keunzi B, Kessler BE, **Kim J**, Superti-Furga G, Rix U, Tan AC, Schweppe R, "A CHEMICAL PROTEOMICS APPROACH TO IDENTIFY MECHANISMS OF RESISTANCE TO THE SRC INHIBITOR, DASATINIB", 15th International Thyroid Congress and 85th Annual Meeting of the ATA, Lake Buena Vista, FL, USA (2015)
9. Kim H, **Kim J**, Fong N, Bentley, D, "Comprehensive, flexible pipeline for alternative polyadenylation analysis", Cold Spring Harbor Meeting 2015 Genomic Informatics, Cold Spring Harbor, NY, USA (2015)
10. **Kim J**, Foster D, Mishra R, Kern JA, Tan AC, Finigan JH, "Kinome RNAi Screens Identify Essential Genes and Therapeutics in "Driver Negative" Non-Small Cell Lung Cancer", IASLC 2015, Denver, CO, USA (2015)
11. **Kim J**, Yoo M, Kang J, Tan AC, "K-Map: Connecting Kinases with Therapeutics for Drug Repurposing and Development", ISMB 2014, Boston, MA, USA (2014) (Oral Presentation)
12. Beadnell TC, Mishall KM, Zhou Q, Strait AA, Corpuz ML, **Kim J**, Wang G, Tan AC, Schweppe RE. "Elucidating Mechanisms of Resistance to Src Inhibition in Thyroid Cancer." In Thyroid Neoplasia, pp. *Presented in the Endocrine Society's 96th Annual Meeting and Expo*, Chicago, IL. USA (2014)
13. Dimberg LY, Cabrera J, Menke C, **Kim J**, Porter CC, Tan AC, Behbakht K, Thorburn A, Ford HL., Use of a genome-wide loss-of-function screen to identify novel mechanisms of resistance to TRAIL induced apoptosis. *Presented in the EORTC-NCI-AACR Symposium on Molecular Targets and Cancer Therapeutics*, Boston, MA. USA. *Mol Cancer Ther* 2013;12(11 Suppl):B115. (2013)
14. **Kim J**, Cano C, Tan AC, "Consensus Gene Ranking Method for Genome-wide Functional Genetic Screens", Annual Rocky Mountain Bioinformatics Conference 2012, Aspen, CO, USA (2012)
15. Singleton KR, Tan AC, **Kim J**, Heasley LE. "Abstract B35: Alternate receptor tyrosine kinases provide protection from FGFR inhibition in HNSCC cells as identified by genome-wide shRNA screening." *Clinical Cancer Research* 18, no. 10 Supplement (2012): B35-B35.
16. Gregory, MA, Tan AC, **Kim J**, DeGregori J. "165 RNAi Screen Identifies ATM-directed Metabolic Pathway as Synthetic Lethal with FLT3 Inhibition in AML." *European Journal of Cancer* 48 (2012): 50-51.

17. Spreafico AP, Klauck J, Tentler JJ, Pitts TM, Tan AC, **Kim J**, Gregory MA, McManus MC, Arcaroli JJ. "485 Targeting the MAP Kinase and Wnt Signaling Pathways in Preclinical Models of Colorectal Cancer." *European Journal of Cancer* 48 (2012): 150
18. Almeida AR, Partyka KA, Tan AC, **Kim J**, Porter CC, Casas M, Gregory M et al., "A genome-wide shRNA screen identified the WNT pathway as a potential target for combination treatments with BRAF inhibitors in melanoma." In *Journal of Investigative Dermatology*, vol. 132, pp. S128-S128. NATURE PUBLISHING GROUP, 2012.
19. Pilling AB, Le AT, Tan AC, **Kim J**, Singleton KR, Heasley LE, Helfrich B, DeGregori J, Doebele RC., ALK-driven lung cancer: Potential therapeutic strategies for treatment and prevention of drug resistance. *Presented in the 103rd American Association for Cancer Research Annual Meeting 2012*, Chicago, IL (2012)
20. **Kim J**, Cano C, Tan AC, "PathCMap : Development of pathway signature system for identifying druggable partners of synthetic lethal genes in cancer", *Annual Rocky Mountain Bioinformatics Conference 2011*, Aspen, CO, USA (2011)
21. Astling D, Chan T, **Kim J**, Tan AC, "Opportunities and challenges associated with computational RNAseq data analysis", *Annual Rocky Mountain Bioinformatics Conference 2011*, Aspen, CO, USA (2011)
22. Porter CC, **Kim J**, Fosmire S, Gearheart CM⁺, van Linden A, Zaberezhnyy V, Gao D, Tan AC, DeGregori J., Genome wide shRNA screening identifies WEE1 as a critical mediator of cell fate and novel therapeutic target in AML. *Presented in American Society of Hematology Annual Meeting 2011*, San Diego, CA (2011)
23. Shellman YG, Partyka KA, Porter C, Casas M, Tan AC, **Kim J**, Gregory M, et al., "Using a RNAi-based screen to identify targets lobe combined with BRAF inhibitors for treating melanomas." In *JOURNAL OF INVESTIGATIVE DERMATOLOGY*, vol. 131, pp. S85-S85. 75 VARICK ST, 9TH FLR, NEW YORK, NY 10013-1917 USA: NATURE PUBLISHING GROUP, 2011.
24. Phang TL, Kim H, **Kim J**, Gao D, Tong T, Selby H, Tan AC., "An Analysis Workflow for Loss-of-function RNA Interference Whole-Genome Screening using the Next Generation Sequencing Technology". *Presented in the 53rd Annual Meeting Thomas L. Petty Aspen Lung Conference*, Aspen, CO (2010)
25. **Kim J**, Kim H, Gao D, Gregory M, Selby H, Tong T, Phang TL, DeGregori J, Tan AC, "Computational Analysis of Genome-wie Synthetic Lethal Screen with a tyrosine kinase inhibitor in Leukemia cell using BiNGS!SL-seq", *ISMB 2010*, Boston, MA, USA (2010)
26. Kim H, **Kim J**, Phang TL, Gao D, Tong T, Selby H, Zhang Q, Wang XJ, Bently D, Tan AC, "A Case Study for Genome-wide Smad4 Binding Sites Using BiNGS!ChiP-seq" *ISMB 2010*, Boston, MA, USA (2010)
27. Selby H, **Kim J**, Tentler J, Diamond J, Pitts T, Leong S, Messersmith W, Eckhardt G, Tan AC, Jimeno A, "A systemes Biology Strategy to Accelerate the Development of Predictive Biomarkers for Novel Anti-cancer Agents", *ISMB 2010*, Boston, MA, USA (2010)
28. Gao D, **Kim J**, Kim H, Selby H, Phang TJ, Tan AC, Tong T, "Comparative Statistical Analysis on Identifying Differentially Expressed Reads in Next Generation Sequencing Data", *ISMB 2010*, Boston, MA, USA (2010)
29. Phang TL, Kim H, **Kim J**, Gao D, Tong T, Selby H, Gregory H, DeGregori J, Tan AC, " A Computational Analysis Workflow for Whole-Genome RNA Interference Screening Using the Next Generation Seugencing Technology", *ISMB 2010*, Boston, MA, USA (2010)
30. **Kim J**, Henry C, DeGregori J, Tan AC, "Genome-wide Survey of Age-related Gene Expression Patterns Relative to Binding Sites for the Global Regulator of Chromatin CTCF", *MGED 12 meeting*, Phoenix, AZ, USA (2009)

31. Goth J, Williams-DeVane C, **Kim J**, “Gene Classification by Decision Tree Data Mining Methods: Identification of Genes Likely to be Involved in Human Genetic Disease”, Annual Rocky Mountain Bioinformatics Conference 2005, Aspen, CO, USA (2005)

Software and Computational tools/resources

1. **BiNGS!SL-seq. Bioinformatics for Next Generation Sequencing – synthetic lethal screen analysis module.** The BiNGS! (Bioinformatics for Next Generation Sequencing) program is an innovative bioinformatics analysis pipeline for analyzing and interpreting genome-wide shRNA deep sequencing data.

2. **IMPACT.** IMPACT is a whole-exome sequencing (WES) analysis pipeline of Integrating Molecular Profiles with Actionable Therapeutics in Clinical Samples. IMPACT analysis pipeline integrates four analytical modules for WES analysis: (1) variant detection, (2) copy number estimation, (3) drug prediction, and (4) tumor heterogeneity analysis. IMPACT is available at: <http://tanlab.ucdenver.edu/IMPACT>. (Currently not available. The webpage is moving).

3. **K-Map.** K-Map is a novel and user-friendly web-based program that systematically connects a set of query kinases to kinase inhibitors based on quantitative profiles of the kinase inhibitor activities. Users can use K-Map to find kinase inhibitors for a set of query kinases (obtained from high-throughput “omics” experiments) or to reveal new interactions between kinases and kinase inhibitors for rational drug combination studies. <http://tanlab.ucdenver.edu/kMap>. (Currently not available. The webpage is moving).

4. **DSigDB.** Drug Signatures Database (DSigDB) is a new gene set resource that relates drugs/compounds and their target genes, for gene set enrichment analysis. DSigDB currently holds 22,527 gene sets, consists of 17,389 unique compounds covering 19,531 genes. We also developed an online DSigDB resource that allows users to search, view, and download drugs/compounds and gene sets. DSigDB gene sets provide seamless integration to GSEA software for linking gene expressions with drugs/compounds for drug repurposing and translational research. DSigDB is freely available for non-commercial use at <http://tanlab.ucdenver.edu/DSigDB>. (Currently not available. The webpage is moving).

5. **KAR.** Kinase Addiction Ranker (KAR) is an algorithm that integrates high-throughput drug screening data, comprehensive kinase inhibition data and gene expression profiles to identify kinase dependency in cancer cells. <http://tanlab.ucdenver.edu/KAR/>. (Currently not available. The webpage is moving).