Aik Choon Tan, Ph.D.

Vice Chair and Senior Member
E : aikchoon.tan@moffitt.org
T: 813-745-8991 F: 813-745-6107
H: http://tanlab.org

Department of Biostatistics and Bioinformatics
Moffitt Cancer Center
12902 Magnolia Drive,
Tampa, FL 33612

Research Interests:
Translational Bioinformatics, Cancer Systems Biology, Precision Oncology, Drug Repurposing and Repositioning, Drug Resistance Mechanisms, Drug Combinations, Pharmacogenomics, Kinase Signaling Networks, Big Data Analytics, Biomedical Data Science, Machine Learning, Developmental Therapeutics.

1. EDUCATION AND TRAINING

EDUCATION

2000	**B.Eng. in Chemical/Bioprocess Engineering**, University of Technology, Skudai, Johor, Malaysia. First Class Honor.
2005	**Ph.D. in Computer Science/Bioinformatics**, University of Glasgow, Glasgow, United Kingdom. Mentor: Prof. David Gilbert

TRAINING

10/2004 – 9/2007	**Post-Doctoral Research Fellow**, Institute for Computational Medicine, Center for Cardiovascular Bioinformatics and Modeling, Johns Hopkins University Whiting School of Engineering, Baltimore, MD. Mentor: Prof. Raimond L. Winslow
10/2007 – 2/2009	**Post-Doctoral Research Fellow**, Gastrointestinal Oncology Therapeutics Program, Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins University School of Medicine, Baltimore, MD. Mentor: Prof. Manuel Hidalgo

2. ACADEMIC APPOINTMENTS

8/2019 – present	**Vice Chair and Senior Member**, Department of Biostatistics and Bioinformatics, Moffitt Cancer Center, Tampa, FL.
8/2019 – present	**Associate Scientific Director**, Biostatistics and Bioinformatics Shared Resource, Moffitt Cancer Center, Tampa, FL.
11/2019 – present	**Professor**, Department of Oncologic Sciences, University of South Florida, Tampa, FL.
8/2019 – present	**Director**, Translational Bioinformatics and Cancer Systems Biology Lab, Department of Biostatistics and Bioinformatics, Moffitt Cancer Center, Tampa, FL.
8/2019 – present	**Adjoint Professor**, Division of Medical Oncology, Department of Medicine, University of Colorado Anschutz Medical Campus, Aurora, CO.
2/2018 – 8/2019	**Director**, Bioinformatics Core, Bioinformatics and Biostatistics Shared Resource, University of Colorado Cancer Center, Aurora, CO.

9/2018 – 8/2019	**Graduate Faculty**, Pharmacology Program, University of Colorado Denver, Aurora, CO.
5/2017 – 8/2019	**Graduate Faculty**, Computational Bioscience Program, University of Colorado Denver, Aurora, CO.
11/2016 – 8/2019	**Program Director**, Graduate Certificate of Biomedical Data Science, University of Colorado Anschutz Medical Campus, Aurora, CO.
10/2015 – 8/2019	**Co-Director**, Biostatistics and Bioinformatics Core, Colorado Lung Cancer SPORE, University of Colorado Cancer Center, Aurora, CO.
7/2013 – 8/2019	**Associate Professor**, Division of Medical Oncology, Department of Medicine, University of Colorado Anschutz Medical Campus, Aurora, CO.
8/2014 – 8/2019	**Associate Professor (Secondary Appointment)**, Department of Biostatistics and Informatics, Colorado School of Public Health, University of Colorado Denver, Aurora, CO.
5/2013 – 8/2019	**Co-Director**, Precision Oncology Program, Division of Medical Oncology, Department of Medicine, University of Colorado Anschutz Medical Campus, Aurora, CO.
5/2011 – present	**Graduate Faculty**, Cancer Biology Program, University of Colorado Denver, Aurora, CO.
11/2010 – 8/2019	**Graduate Faculty**, Department of Biostatistics and Informatics, Colorado School of Public Health, University of Colorado Denver, Aurora, CO.
8/2009 – 7/2014	**Assistant Professor (Secondary Appointment)**, Department of Biostatistics and Informatics, Colorado School of Public Health, University of Colorado Denver, Aurora, CO.
4/2009 – 8/2019	**Member**, Developmental Therapeutics Program, University of Colorado Cancer Center, Aurora, CO.
3/2009 – 8/2019	**Faculty Member**, Head and Neck Cancer Research Program, University of Colorado Anschutz Medical Campus, Aurora, CO.
3/2009 – 8/2019	**Director**, Translational Bioinformatics and Cancer Systems Biology Lab, Division of Medical Oncology, Department of Medicine, University of Colorado Anschutz Medical Campus, Aurora, CO.
3/2009 – 6/2013	**Assistant Professor**, Division of Medical Oncology, Department of Medicine, University of Colorado Anschutz Medical Campus, Aurora, CO.

PREVIOUS EMPLOYMENT

8/2000 – 10/2000	**Research Officer**, Bioprocess Engineering Research Laboratory, Department of Bioprocess Engineering, Faculty of Chemical and Natural Resources Engineering, University of Technology, Skudai, Johor, Malaysia.
1/2004 – 7/2004	**Teaching Fellow**, Department of Computing Science, University of Glasgow, Glasgow, United Kingdom.

3. HONORS, SPECIAL RECOGNITIONS AND AWARDS
A. AWARDS

- Winning Team for the Multi-Targeting Drug DREAM Challenge (2018).

- Winner of the International Conference of Machine Learning and Applications (ICMLA) 2008 Automated Microarray Classification Challenge, San Diego, CA. (2008).
- Winner of the Best Poster Award (First Place) at the 9th Annual Rocky Mountain Bioinformatics Conference, Aspen/Snowmass, CO. (2011).

B. TRAVEL FELLOWSHIP AWARDS

- International Society for Computational Biology (ISCB) Travel Fellowship to attend International Conference on Intelligent Systems for Molecular Biology (ISMB 2001), Copenhagen, Denmark.
- International Union of Pure and Applied Chemistry (IUPAC) Travel Fellowship to attend International Conference on Bioinformatics (InCOB 2002), Bangkok, Thailand.
- International Society for Computational Biology (ISCB) Travel Fellowship to attend International Conference on Research in Computational Biology (RECOMB 2002), Washington DC.
- International Society for Computational Biology (ISCB) Travel Fellowship to attend International Conference on Intelligent Systems for Molecular Biology (ISMB 2002), Edmonton, Canada.
- European Congress on Computational Biology Travel Fellowships to attend the 1st European Conference on Computational Biology (ECCB 2002), Saarbrucken, Germany.
- Asia Pacific Bioinformatics Network (APBioNet) Travel Fellowship to attend Asia Pacific Bioinformatics Conference (APBC 2003), Adelaide, Australia.
- The Royal Academy of Engineering International Travel Fellowship, Adelaide, Australia.
- New Zealand Bioinformatics Conference Travel Fellowship, Wellington, New Zealand.
- International Society for Computational Biology (ISCB) Travel Fellowship to attend International Conference on Intelligent Systems for Molecular Biology (ISMB 2003), Brisbane, Australia.
- European Congress on Computational Biology Travel Fellowships to attend the 2nd European Conference on Computational Biology (ECCB 2003), Paris, France.
- Japan Society of Bioinformatics (JSBi) Travel Fellowships, Yokohama, Japan.
- Center for Discrete Mathematics and Theoretical Computer Science (DIMACS) Travel Fellowship to attend Machine Learning Techniques in Bioinformatics Workshop, Rutgers, NJ.

C. STUDENTSHIP AWARDS

- Ph.D. Studentships, City University, London, United Kingdom. (2001-02).
- Ph.D. Studentships, University of Glasgow, United Kingdom. (2002-03).

4. MEMBERSHIP IN PROFESSIONAL ORGANIZATIONS

2001 – present **Member**, International Society for Computational Biology (ISCB).

2021 – present **Board of Director**, MidSouth Computational Biology and Bioinformatics Society (MCBIOS).

5. MAJOR COMMITTEE AND SERVICE RESPONSIBILITIES

A. PROFESSIONAL SERVICES

Chair or Organizer for International Conferences & Workshops

- **Organizing Committee Member**, The Joint 12th International Conference on Intelligent Systems for Molecular Biology and the 3rd European Conference on Computational Biology (ISMB/ECCB 2004), Glasgow, United Kingdom.

- **Organizer**, ICMLA Challenge, The 8th International Conference on Machine Learning and Applications (ICMLA 2009), Miami, FL.

- **Organizing Committee Member**, AI Against Cancer, Data Science Hackathon 2021, University of Alabama at Birmingham, AL.

Program Committee for International Conferences & Workshops

- **Program Committee Member**, The 11th International Conference on Intelligent Systems for Molecular Biology (ISMB 2003), Brisbane, Australia.

- **Program Committee Member**, The 4th European Conference on Computational Biology (ECCB 2005), Madrid, Spain.

- **Program Committee Member**, Workshop on Data Mining for Biomedical Applications (BioDM'06), Singapore.

- **Program Committee Member**, The 2nd International Workshop on in Biomedicine and Bioinformatics (MLBB 2008), San Diego, CA.

B. UNIVERSITY SERVICES

Moffitt Cancer Center

Chair or Director or Organizer

- **Chair**, Division of Quantitative Sciences Junior Faculty Award (2020 - present)

- **Associate Scientific Director**, Bioinformatics and Biostatistics Shared Resource (8/2019 – present)

- **Chair**, Search Committee for Bioinformatics Faculty (single cell), Department of Biostatistics and Bioinformatics (2021 - present)

- **Chair**, Search Committee for Bioinformatics Faculty (computational immunology), Department of Biostatistics and Bioinformatics (2020) -successfully recruited the faculty member.

Committee Member

- **Committee Member,** Divisions of Population and Quantitative Sciences Junior Faculty Award (2019)

- **Committee Member,** Faculty Keep Up Task Force (2019-2020)

- **Committee Member,** High-Performance Computing Steering Committee (2020-present)

- **Committee Member,** BBSR Reproducible Research Steering Committee (2020-present)

University of Colorado Anschutz Medical Campus

Chair or Director or Organizer

- **Director**, Bioinformatics Core, Bioinformatics and Biostatistics Shared Resource, University of Colorado Cancer Center, Aurora, CO. (2018 – 2019).

- **Program Director**, Graduate Certificate of Biomedical Data Science, University of Colorado Anschutz Medical Campus, Aurora, CO. (2016 – 2019).
- **Chair**, Membership Committee, Cancer Biology Training Program, University of Colorado Anschutz Medical Campus, Aurora, CO. (2016 – 2019).
- **Organizer**, Bioinformatics Journal Club, University of Colorado Anschutz Medical Campus, Aurora, CO. (Bi-weekly journal club). (2011 – 2019).
- **Co-Director**, Biostatistics and Bioinformatics Core, Colorado Lung Cancer SPORE, University of Colorado Cancer Center, Aurora, CO. (2015 – 2019).
- **Co-Director**, Precision Oncology Program, Division of Medical Oncology, Department of Medicine, University of Colorado Anschutz Medical Campus, Aurora, CO. (2013 – 2019).
- **Director**, Translational Bioinformatics and Cancer Systems Biology Lab, Division of Medical Oncology, Department of Medicine, University of Colorado Anschutz Medical Campus, Aurora, CO. (2009 – 2019).

Committee Member

- **Admission Committee Member**, Computational Bioscience Program (CPBS), University of Colorado Anschutz Medical Campus, Aurora, CO. (2017 – 2019).
- **Steering Committee Member**, Cancer Biology Training Program, University of Colorado Anschutz Medical Campus, Aurora, CO. (2016 – 2019).
- **Admission Committee Member**, Medical Scientist Training Program (MSTP) Program, University of Colorado Anschutz Medical Campus, Aurora, CO. (2016 – 2019).
- **Organizing Committee Member**, Mini-Symposium on The Power of Informatics to Advance Health, University of Colorado Anschutz Medical Campus, Aurora, CO. (2013 – 2019).

Panel Member

- **Judge**, 2011 Post-doctoral Research Day, University of Colorado Denver, Aurora, CO. (2011).
- **Judge**, 2012 University of Colorado Cancer Center and Cancer Biology Program Retreat, University of Colorado Denver, Aurora, CO. (2012).

C. NATIONAL SERVICES

- **Scientific Reviewer**, ZRG1 IMST-K (70) R Study Section, National Institute of Health, Bethesda, MD. (October, 2021).
- **Scientific Reviewer**, ZRG1 BST-U (80) A Study Section, National Institute of Health, Bethesda, MD. (September, 2018).
- **Scientific Reviewer**, ZRG1 BST-U (80) A Study Section, National Institute of Health, Bethesda, MD. (March and June, 2017).
- **Scientific Reviewer**, ZRG1 BST-C (80) A Study Section, National Institute of Health, Bethesda, MD. (March and October, 2016)
- **Scientific Reviewer**, ZRG1 GGG-K (90) Computational Genomics Study Section, National Institute of Health, Bethesda, MD. (April, 2016)
- **Scientific Reviewer**, ZRG1 BST-C (80) A Study Section, National Institute of Health, Bethesda, MD. (July and November, 2015)

- **Scientific Reviewer**, ZRG1 BST-F (80) A Study Section, National Institute of Health, Bethesda, MD. (July, 2014)

6. INVENTIONS, INTELLECTUAL PROPERTY AND PATENTS HELD OR PENDING

A. PATENTS AWARDED

1. Eckhardt SG, Pitts TM, **Tan AC.** (2012). BIOLOGICAL MARKERS PREDICTIVE OF ANTI-CANCER RESPONSE TO INSULIN-LIKE GROWTH FACTOR-1 RECEPTOR KINASE INHIBITORS. United States Patent, #8,163,509. (Issued: 4/24/2012)

B. PATENT APPLICATIONS

1. Hidalgo M, Jimeno A, **Tan AC.** (2007). PREDICTIONS OF RESPONSIVENESS TO EGFR INHIBITORS. ROI to Johns Hopkins University School of Medicine Office of Technology Licensing, JHU Ref: D10140. Patent Application Ref: PCT/US2008/009594 (11/8/2008) (United States Provisional Application No. 60/964,099 filed 8/9/2007).

2. Hidalgo M, Jimeno A, **Tan AC.** (2008). METHODS TO CONNECT GENE SET EXPRESSION PROFILES TO DRUG SENSITIVITY. ROI to Johns Hopkins University School of Medicine Office of Technology Licensing, JHU Ref: C10289. Patent Application Ref: PCT/US2009/034056 (2/13/2009) (United States Provisional Application Nos. 61/118,740, 61/035,503 and 61/065,667 filed 1/12/2008, 3/11/2008 and 2/14/2008, respectively).

3. Khoo SK, **Tan AC.** (2011). CIRCULATING MICRORNAS AS BIOMARKERS FOR EARLY DETECTION OF PARKINSON'S DISEASE. IDF to Van Andel Research Institute and University of Colorado Office of Technology Transfer, University of Colorado Ref: CU2851H. Patent Application Ref: United States Provisional Application No. 61/532,718, filed 9/9/2011.

4. **Tan AC**, Eckhardt SG, Pitts TM, Arcaroli JJ. (2011). METHODS FOR IDENTIFYING RESISTANCE TO EGFR INHIBITOR. ROI to University of Colorado Office of Technology Transfer, University of Colorado Ref: CU2938H-PPA1. Patent Application Ref: United States Provisional Application No. 61/551,437, filed 10/26/2011.

C. REPORT OF INVENTIONS

1. Winslow RL, Geman D, Xu L, **Tan AC**, Naiman DQ. (2005). A Novel Statistical Method to Identify Robust Prostate Cancer Marker Genes. ROI to Johns Hopkins University School of Medicine Office of Technology Licensing, JHU Ref: 4747.

2. Winslow RL, Geman D, Anderson T, **Tan AC**, Naiman DQ. (2005). An Algorithm for the Discovery of Robust Protein Biomarkers with Application to the Design of Classification Protein Array. ROI to Johns Hopkins University School of Medicine Office of Technology Licensing, JHU Ref: 4758.

3. Hidalgo M, Jimeno A, **Tan AC.** (2008). Gemcitabine Signature: Gene expression-based fingerprints for predicting gemcitabine sensitivity in pancreatic cancer and identifying novel targets for personalized therapy. ROI to Johns Hopkins University School of Medicine Office of Technology Licensing, JHU Ref: C10288.

4. **Tan AC**, Shin J, Yoo M. (2018). A Database of Drug-Kinase Relationships. ROI to the University of Colorado, CU Innovations File No. CU4702H.

5. **Tan AC**, Hintzsche JD, Yoo M. (2018). A Database of Drug-Gene Variant. ROI to the University of Colorado, CU Innovations File No. CU4703H.

7. REVIEW AND REFEREE WORK

A. EDITORIAL BOARDS FOR JOURNALS

(On average, handling 20 manuscripts per year for these journals)

2019 – present	***Molecular Carcinogenesis***, Editorial Board Member
2005 – present	***Cancer Informatics***, Editorial Board Member
2020	***Seminars in Cancer Biology***, Special Issue Guest Editor
2014 – 2021	***Scientific Reports***, Editorial Board Member
2017 – 2020	***BMC Systems Biology***, Editorial Board Member
2015 – 2017	***Annals of Translational Medicine***, Editorial Board Member
2014 – 2015	***Biochemical Genetics***, Associate Editor

B. REVIEWER FOR JOURNALS

(Publons profile: https://publons.com/researcher/1601314/aik-choon-tan/)

🏆 Top 1% of reviewers in Cross-field (awarded in 2019 by Publons)

- *Bioinformatics*
- *BMC Bioinformatics*
- *BMC Medical Genomics*
- *BMC Medical Informatics and Decision Making*
- *Briefings in Bioinformatics*
- *Briefings in Functional Genomics*
- *Biochemical Genetics*
- *BioSystems*
- *Cancer Informatics*
- *Cancer Research*
- *Computational Biology and Chemistry*
- *Computational and Structural Biotechnology Journal*
- *Computers in Biology and Medicine*
- *Computer Methods and Programs in Biomedicine*
- *Database*
- *EBioMedicine*
- *eLife*
- *European Journal of Pharmacology*
- *Experimental and Molecular Pathology*
- *Expert Opinion on Investigational Drugs*
- *Expert Opinion on Orphan Drugs*

- *FEBS Letters*
- *Functional and Integrative Genomics*
- *Genomics Medicine*
- *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
- *International Journal of Cancer*
- *Journal of Bioinformatics and Computational Biology*
- *Journal of Medical Internet Research*
- *Journal of the Association for Information Science and Technology*
- *Journal of Visualized Experiments*
- *Medicinal Research Reviews*
- *Melanoma Research*
- *Methods*
- *Molecular BioSystems*
- *Molecular Cancer Therapeutics*
- *Molecular Carcinogenesis*
- *Molecular Oncology*
- *Nature Communications*
- *Neurocomputing*
- *Nucleic Acids Research*
- *Oncotarget*
- *Pharmacogenomics*
- *PLoS Biology*
- *PLoS ONE*
- *Quantitative Biology*
- *Scientific Data*
- *Scientific Reports*
- *Science Signaling*
- *Seminars in Cancer Biology*
- *Technology in Cancer Research and Treatment*
- *The Journal of Engineering Letters*

C. REVIEWER FOR CONFERENCES/WORKSHOPS

- The 2nd Workshop on Algorithms in Bioinformatics (WABI 2002), Rome, Italy.
- The 1st European Conference on Computational Biology (ECCB 2002), Saarbrücken, Germany.
- The 11th International Conference on Intelligent Systems for Molecular Biology (ISMB 2003), Brisbane, Australia.

- The 2nd European Conference on Computational Biology (ECCB 2003), Paris, France.
- The 4th European Conference on Computational Biology (ECCB 2005), Madrid, Spain.
- The 1st International Workshop on Data Mining for Biomedical Applications (BioDM 2006), Singapore.
- The 8th International Conference on Machine Learning and Applications (ICMLA 2009) Challenge Workshop, Miami, FL.
- Pacific Symposium on Biocomputing (PSB) 2019, Big Island, HI.

D. REVIEWER FOR GRANTS

International

- CORE Grant Scheme, Luxembourg National Research Fund (FNR), Luxembourg. (2019).
- CORE Grant Scheme, Luxembourg National Research Fund (FNR), Luxembourg. (2018).
- RESCOM Grant Scheme, Luxembourg National Research Fund (FNR), Luxembourg. (2018).
- Cancer Research UK, UK. (2017).
- RESCOM Grant Scheme, Luxembourg National Research Fund (FNR), Luxembourg. (2017).
- Austrian Science Fund, Vienna, Austria. (2016).
- AFR Grant Scheme, Luxembourg National Research Fund (FNR), Luxembourg. (2016).
- CORE Research Program, Luxembourg National Research Fund (FNR), Luxembourg. (2015).
- BBSRC, London, UK. (2014).
- Wellcome Trust Research Fellowship, London, UK. (2013).

National

- Scientific Reviewer, ZRG1 IMST-K (70) R Study Section, National Institute of Health, Bethesda, MD. (October, 2021).
- Scientific Reviewer, Harold Hamm Diabetes Center Pilot Projects, Oklahoma University College of Medicine, Oklahoma City, OK. (2021).
- Scientific Reviewer, ZRG1 BST-U (80) A Study Section, National Institute of Health, Bethesda, MD. (September, 2018).
- Scientific Reviewer, Department of Biostatistics Development Awards, Vanderbilt University School of Medicine, Nashville, TN. (2017).
- Scientific Reviewer, ZRG1 BST-U (80) A Study Section, National Institute of Health, Bethesda, MD. (March, 2017).
- Scientific Reviewer, ZRG1 BST-U (80) A Study Section, National Institute of Health, Bethesda, MD. (March and October, 2016).
- Scientific Reviewer, ZRG1 GGG-K (90) Computational Genomics Study Section, National Institute of Health, Bethesda, MD. (April, 2016).
- Scientific Reviewer, ZRG1 BST-C (80) A Study Section, National Institute of Health, Bethesda, MD. (July and November, 2015).
- Scientific Reviewer, ZRG1 BST-F (80) A Study Section, National Institute of Health, Bethesda, MD. (July, 2014).

- Scientific Reviewer, Maryland Industrial Partnerships Program, College Park, MD. (2010).

Local

- Scientific Reviewer, Cancer League of Colorado, Denver, CO. (2011-2014).
- Scientific Reviewer, University of Colorado Denver NextGen Sequencing Pilot Award, Aurora, CO. (2012).
- Scientific Reviewer, Colorado Clinical Translational Science Institute (CCTSI) CO-Pilot Award, University of Colorado Denver, Aurora, CO. (2010)

E. REVIEWER FOR FELLOWSHIPS

- Reviewer, University of Colorado Cancer Center (UCCC) Summer Student Fellowships, University of Colorado Denver, Aurora, CO. (2010 – present)

8. INVITED EXTRAMURAL LECTURES, PRESENTATIONS AND VISITING PROFESSORSHIPS

A. INTERNATIONAL (SELECTED SINCE 2009)

- "*Dissecting Kinase Dependency in Cancer*" – MidSouth Computational Biology and Bioinformatics Society (MCBIOS) and Massive Analysis and Quality Control (MAQC) Society – MCBIOS & MAQC 2021 Joint Conference, Virtual. (4/2021).
- "*Precision Oncology: Translating Big Data to Knowledge*" – Nottingham University Malaysia, Semenyih, Malaysia (6/2018).
- "*From Branch to Bedside – Translating Traditional Chinese Medicine for Cancer Treatment*" – Cancer Research Malaysia, Kuala Lumpur, Malaysia (6/2018).
- "*From Branch to Bedside – Translating Traditional Chinese Medicine for Cancer Treatment*" – Korea University, Seoul, S. Korea (10/2017).
- "*Linking Whole-Exome Cancer Sequencing Analysis with Therapeutics and Other Data Sources*" – Global Congress on Molecular Pathology (AMP GLOBAL 2017), Association for Molecular Pathology (AMP), Berlin, Germany. (4/2017).
- "*Expanding the Computational Toolbox for Interrogating Cancer Kinomes*" - Division of Cancer Biology, The Institute of Cancer Research, London, UK. (5/2016).
- "*Expanding the Computational Toolbox for Interrogating Cancer Kinomes*" - Department of Chemistry, Cambridge University, Cambridge, UK. (5/2016).
- "*Expanding the Computational Toolbox for Interrogating Cancer Kinomes*" - Department of Computer Science and Engineering, Korea University, Seoul, South Korea. (3/2016).
- "*Precision Medicine: Translating Big Data to Therapies*" – Asan Medical Center, Seoul, South Korea. (3/2015),
- "*Computational Drug Repurposing and Combination Prediction: Translating Big Data to Therapeutics*" – Soongsil University, Seoul, South Korea. (3/2015).
- "*Computational Drug Repurposing and Combination Prediction: Translating Big Data to Therapeutics*" - Cancer Research Initiatives Foundation (CARIF), Kuala Lumpur, Malaysia. (11/2014).
- "*K-Map: connecting kinases with therapeutics for drug repurposing and development*" – 22nd Annual International Conference on Intelligent Systems for Molecular Biology, ISMB 2014, Boston, MA. (7/2014).

- "*Precision Oncology: The Past, Present, and Future of Cancer Treatment*" - Faculty of Medicine, University of Malaya Medical Center, Kuala Lumpur, Malaysia. (7/2013).

- "*Exposing and Overcoming Cancer Escape Pathway*" - Cancer Research Initiatives Foundation (CARIF), Kuala Lumpur, Malaysia. (7/2013).

- "*Systems Biology in Oncology Drug Development*" - High Impact Research Center, University of Malaya, Kuala Lumpur, Malaysia. (7/2013).

- "*Dare to Dream: My Exciting Research Journey!*" - Institute of Biological Sciences, University of Malaya, Kuala Lumpur, Malaysia. (7/2013).

- "*Translational Bioinformatics: From Bytes & Bench to Bedside and Back*" - The Center for Systems and Synthetic Biology, School of Information Sciences, Computing and Mathematics, Brunel University, London, UK. (10/2011).

- "*Translational Bioinformatics: From Bytes & Bench to Bedside and Back*" - University of Tunku Abdul Rahman, Petaling Jaya, Selangor, Malaysia. (5/2010).

- "*Translational Bioinformatics: From Bytes & Bench to Bedside and Back*" - University of Technology Malaysia, Skudai, Johor, Malaysia. (4/2010).

- "*Translational Bioinformatics: From Bytes & Bench to Bedside and Back*" - Malaysia Genome Institute (MyGENOM), Bangi, Selangor, Malaysia. (4/2010).

- "*Predictive Biomarkers Developmental Strategy for Novel Targeted Cancer Therapies*" - Cancer Research Initiative Foundation (CARIF), Subang Jaya, Selangor, Malaysia. (4/2010).

- "*Translating Insights from "omic" Data into Clinical Practices*" - Bioinformatics Lecture, Oral Cancer Research & Coordinating Centre (OCRCC) and Centre of Research for Computational Sciences and Informatics in Biology, Bioindustry, Environment, Agriculture and Healthcare (CRYSTAL), University of Malaya, Kuala Lumpur, Malaysia. (4/2010).

B. NATIONAL (SELECTED SINCE 2009)

- "*Translating Big Data to Effective Cancer Therapy*" – The University of Alabama at Birmingham – Informatics Institute, Birmingham, AL. (11/2021)

- "*Translating Big Data to Effective Cancer Therapy*" – Emory University, Atlanta, GA. (11/2021)

- "*Exploiting Kinase-dependency for Cancer Therapy*" – The University of Texas Health Science Center at Houston, Houston, TX. (2/2020)

- "*Translational Bioinformatics: From Bench to Bedside and Back*" – Dartmouth College, Hanover, NH. (1/2017)

- "*Expanding the Computational Toolbox for Interrogating Cancer Kinomes*" – Moffitt Cancer Center, Tampa, FL. (11/2016).

- "*Translational Bioinformatics: Connecting Genes with Therapies*" – Systems Biology Seminar Series, Boston University, Boston, MA. (11/2013).

- "*Translational Bioinformatics: From Bytes & Bench To Bedside And Back*" - Van Andel Research Seminar Series, Van Andel Research Institute, Grand Rapids, MI. (4/2012).

- "*BiNGS!SL-seq: Computational Analytical Pipeline to Analyze and Interpret Genome-Wide Synthetic Lethal Screen*" - Next-Gen Sequencing Summit, Second Annual Sequencing Data Analysis and Interpretation Workshop, X-GEN Congress and Expo, San Diego, CA. (3/2011).

- "*Computational Analysis of Genome-wide Synthetic Lethal Screens with Targeted Therapies in Cancer using BiNGS!SL-seq*" - Genomic Targets, Therapies & Tools Summit, Inaugural Consequences of Clinical Sequencing Workshop, X-GEN Congress and Expo, San Diego, CA. (3/2011).

- "*Translational Bioinformatics: From Bytes & Bench to Bedside and Back*" - Applied Mathematics Seminar, University of Massachusetts Lowell, Lowell, MA. (11/2009).

C. LOCAL (SELECTED SINCE 2009)

- "*Translating Big Data to Effective Therapy*" – Molecular Medicine Program, Moffitt Cancer Center, Tampa, FL. (7/2021).

- "*Oncology Data Science Initiative*" – University of Colorado Cancer Center Symposium, University of Colorado Anschutz Medical Campus, Aurora, CO. (2/2018).

- "*Biomedical Data Science: Learning to Speak the Language*" – Graduate School, University of Colorado Anschutz Medical Campus, Aurora, CO. (4/2017).

- "*Translational Bioinformatics: From Bench to Bed and Back*" – University of Colorado Cancer Center Symposium, University of Colorado Anschutz Medical Campus, Aurora, CO. (1/2017).

- "*Translational Bioinformatics: From Bench to Bed and Back*" – University of Colorado Cancer Center Developmental Therapeutics Program Retreat, University of Colorado Anschutz Medical Campus, Aurora, CO. (11/2016).

- "*Expanding the Computational Toolbox for Interrogating Cancer Kinomes*" – University of Colorado Cancer Center Symposium, University of Colorado Anschutz Medical Campus, Aurora, CO. (11/2015).

- "*Computational Drug Repurposing and Repositioning*" – 2nd Annual Mini-Symposium: The Power of Informatics to Advance Health, University of Colorado Anschutz Medical Campus, Aurora, CO. (4/2015).

- "*Navigating the Kinome Space with Chemical Systems Biology for Drug Repurposing and Repositioning*" - Endocrine Research Conference, Division of Endocrinology, Metabolism and Diabetes, University of Colorado Anschutz Medical Campus, Aurora, CO. (2/2015).

- "*Translational Bioinformatics: Connecting Genes and Pathways with Therapies*" - Integrated Center for Genes, Environment, and Health, National Jewish Health, Denver, CO. (10/2013).

- "*Systems Biology in Oncology Drug Development*" - University of Colorado Cancer Center Symposium Series, University of Colorado Anschutz Medical Campus, Aurora, CO. (5/2013).

- "*Systems Biology for Oncology Drug Discovery and Development*" - Division of Renal Diseases and Hypertension Research Conference, Department of Medicine, University of Colorado School of Medicine, Aurora, CO. (2/2013).

- "*Embedding Bioinformatics in Translational Cancer Research*" - Colorado Clinical and Translational Sciences Institute Informatics Seminar Series, University of Colorado School of Medicine, Aurora, CO. (2/2013).

- "*Connecting Kinases with Therapeutics Agents*" - Head and Neck Cancer Research Seminar Series, University of Colorado School of Medicine, Aurora, CO. (2/2013).

- "*Exposing and Overcoming Escape Pathways in Cancer*" - Faculty Conference on Research and Innovation, Department of Medicine, University of Colorado School of Medicine, Aurora, CO. (6/2012).

- "*Translational Strategies to Implement Personalized Medicine: From Bytes & Bench to Bedside and Back*" - Grand Rounds, Department of Pathology, School of Medicine University of Colorado Anschutz Medical Campus, Aurora, CO. (5/2011).

- "*Bioinformatics for Genome-wide RNAi-based Synthetic Lethal Screen (BiNGS!SL-seq)*" - Hormone Related Malignancies, Division of Endocrinology, Department of Medicine, University of Colorado Anschutz Medical Campus, Aurora, CO. (12/2010).

- "*Translational Bioinformatics: From Bytes & Bench to Bedside and Back*" - Oncology SAC, University of Colorado School of Medicine, CO. (9/2009).

- "*Translational Bioinformatics: From Bytes & Bench to Bedside and Back*" - Developmental Therapeutics Group Retreat, University of Colorado Cancer Center, CO. (6/2009).

- "*Translational Bioinformatics: From Bytes & Bench to Bedside and Back*" - University of Colorado Cancer Center Symposium, University of Colorado Denver, CO. (5/2009).

- "*Translational Bioinformatics: From Bytes & Bench to Bedside and Back* PART II" - Computational Bioscience Program, University of Colorado Denver, CO. (5/2009).

- "*Translational Bioinformatics: From Bytes & Bench to Bedside and Back* PART I" - Head and Neck Cancer Research Seminar Series, University of Colorado Denver, CO. (4/2009).

D. VISITING PROFESSORSHIPS

- Visiting Professorship, Department of Computer Science and Engineering, **Korea University**, Seoul, South Korea. (4/2014-3/2016).

- Visiting Professorship, Oral Cancer Research and Coordinating Center, Faculty of Dentistry, **University of Malaya**, Kuala Lumpur, Malaysia. (7/2013).

9. TEACHING AND MENTORING RECORDS

A. TEACHING

Moffitt Cancer Center, Tampa, FL

Fellowship Program

Faculty Member, Molecular Pathology Fellowship Program (11/2019 – present)

Lectures

Genome Data Analysis (2020 – present). Lecture on "Integrative Omics" module.

University of Colorado Anschutz Medical Campus, Aurora, CO.

Program Director

Graduate Certificate of Biomedical Data Science (2016 – 2019).

Program Description: This Graduate Certificate in Biomedical Data Science (BMDS) will provide the advanced education and relevant training to students interested in pursuing careers in biomedical data science. Students enrolled in the BMDS Certificate will be equipped with the state-of-the-art training in biomedical big data analytical and data interpretation skills. Real world biomedical big data sets will be introduced and examined in the courses, and practical problem solving and effective communication skills will be taught in hands-on workshops. The BMDS Certificate Program will train the next-generation biomedical data scientists to translate biomedical big data into knowledge and applications. (Total: 15 credits)

Course Director

CANB 7640: Practical Bioinformatics for Large-Scale Genomics Data Mining (2013 – 2019).

Course Description: This course will introduce students to the basic concepts of bioinformatics and relevant computational tools to perform large-scale genomic data mining. A practical computer workshop will provide students with the relevant and minimal skills necessary to analyze microarray and next generation sequencing data using open source programs, to access public databases and to visualize and interpret results. (2 credits)

BSBT6111: Introduction to Biomedical Data Science (2016 – 2019).

Course Description: This course provides students with a very high level introduction of various topics in data science pertaining to biomedical informatics concept and purposes. (1 credit)

Lectures
CPBS 7711: Methods and Tools in Biomedical Informatics. (2017 – 2019). Lecture on "Gene Expression Analysis" module.

CLSC 7500: Practical Application of Molecular and Cell Biology Techniques for the Clinical Investigator (2009 – 2014). Lecture on "Bioinformatics" module.

CANB 7600: Cancer Biology (2011 – 2014). Lecture on "Bioinformatics: Cancer Biology Applications" module

University of Colorado Cancer Center Summer Fellowship Program (2010 – 2013). Lecture on "The Bioinformatics Approach" module

University of Colorado School of Medicine/Medical Oncology Fellows Meeting (2011). Lecture on "Translational Bioinformatics and Cancer Systems Biology" module

School of Computing Science, University of Glasgow, Scotland, United Kingdom

M.Sc. IT: Information Technology (2003 – 2004). Lecture on "Bioinformatics" module

B. MENTORING
Junior Faculty
Current:

Mingxiang Teng, Ph.D., Assistant Member, Department of Biostatistics and Bioinformatics, Moffitt Cancer Center (7/1/2020 – present).

Paul Stewart, Ph.D., Assistant Member, Department of Biostatistics and Bioinformatics, Moffitt Cancer Center (3/22/2021 – present).

Timothy Shaw, Ph.D., Assistant Member, Department of Biostatistics and Bioinformatics, Moffitt Cancer Center (3/15/2021 – present).

Past:

Jihye Kim, Ph.D., Assistant Research Professor, Division of Medical Oncology, Department of Medicine (10/1/2013 – 8/18/2019)

Elena Shagisultanova, M.D., Ph.D. Assistant Professor, Division of Medical Oncology, Department of Medicine (8/1/2017 – 8/18/2019) (K08A CA241071, Mentorship Team Member)

Juan-Pablo Idrovo, M.D., Assistant Professor of Surgery and Critical Care, Department of Surgery (K08 GM134185, Mentorship Team Member) (6/1/2018 – 8/18/2019)

Hyunmin Kim, Ph.D., Senior Research Instructor, Division of Medical Oncology, Department of Medicine (2/1/2017 – 8/18/2019)

Jennifer D. Hintzsche, Ph.D. Research Associate, Division of Medical Oncology, Department of Medicine (1/1/2014 – 8/18/2019)

Nikita Pozdeyev, M.D., Ph.D., Assistant Professor, Division of Endocrinology, Department of Medicine (7/1/2015 – 6/30/2018)

Jennifer Diamond, M.D., Assistant Professor, Division of Medical Oncology, Department of Medicine (K23 CA172691, Mentorship Team Member) (7/01/2013 – 6/30/2018)

Christopher Lieu, M.D., Assistant Professor, Division of Medical Oncology, Department of Medicine (K23 CA190849, Mentorship Team Member) (7/08/2015 – 6/30/2018)

Senior Faculty

Current:

Y. Ann Chen, Ph.D., Senior Member, Department of Biostatistics and Bioinformatics, Moffitt Cancer Center (7/1/2020 – present).

Brooke Fridley, Ph.D., Senior Member, Department of Biostatistics and Bioinformatics, Moffitt Cancer Center (7/1/2020 – present).

Post-Doctoral Research Fellows

Current:

Kyubum Lee, Ph.D. (3/30/2020 – present) *NIH Integrated Program in Cancer and Data Science (ICADS) T32 CA233399*

Mengyu Xie, Ph.D. (3/30/2020 – present)

Past:

Brian C. Jackson, Ph.D. (5/1/2015 – 8/18/2019) *NIH Ruth L. Kirschstein National Research Service Award T32CA174648* (co-mentor with Prof. Antonio Jimeno)

Ilyssa Summer, Ph.D. (6/1/2017 – 5/31/2018) *NIH T15 LM009451 Computational Biosciences Training Grant*

Shawna Burgett, Ph.D. (1/1/2017 – 12/31/2017) (co-mentor with Prof. Mary Evans-Weiser-Evans)

Karen A. Ryall, Ph.D. (7/1/2013 – 9/30/2016) *NIH Ruth L. Kirschstein National Research Service Award T32CA174648 – Currently, Data Scientist, Flagship Biosciences, Westminster, CO.*

David P. Astling, Ph.D. (11/1/2010 – 6/30/2013) – *Currently, Research Associate, Department of Biochemistry & Molecular Genetics, University of Colorado School of Medicine, Aurora, CO.*

Christy M. Gearheart, Ph.D. (10/1/2010 – 12/31/2013) – *Currently, Senior Software Engineer, Raytheon, Aurora, CO.*

Guoliang "Tony" Wang, Ph.D. (6/15/2013 – 9/30/2014) – *Currently, Senior Data Analyst, SRA International, Atlanta, GA.*

Jihye Kim, Ph.D. (7/1/2009 – 9/30/2013) – *Currently, Assistant Research Professor, Division of Medical Oncology, Department of Medicine, University of Colorado Anschutz Medical Campus, Aurora, CO.*

Clinical / Research Fellows

Lamees Saeed, M.D. (7/20/2020 – present)

Past:

Israel Kasago, M.D. (11/2019 – 6/2020)

Emily Simons, M.D., M.P.H. (7/2018 – 8/18/2019)

Kelly Faulk, M.D. (4/1/2017 – 2/28/2018)

Jennifer L. Salstrom, M.D., Ph.D. (12/1/2012 – 11/30/2014)

Professional Research Assistants

Past:

Minjae Yoo, M.S. (4/15/2014 – 9/30/2018) – *Currently, Senior Python Developer, Samsung Austin Semiconductor, Austin, TX.*

Jimin Shin, M.S. (10/1/2014 – 10/31/2017) – *Currently, Data Engineer, PK, Austin, TX.*

Paul Francouer, M.S. (7/1/2016 – 4/30/2017) – *Currently, Ph.D. student, Joint CMU-Pitt Ph.D. Program in Computational Biology, Carnegie Mellon University, Pittsburgh, PA.*

Carlos Henrique Cano, M.S. (9/15/2010 – 12/31/2012) – *Currently, IT Industry, Brazil.*

Tiffany Chan, B.S. (3/1/2012 – 2/28/2013) – *Currently, self-study.*

Heather M. Selby, B.S. (8/1/2009 – 6/30/2012) – *Currently, Ph.D. student, Bioinformatics Program, Boston University, Boston, MA.*

Peter J. Klauck, B.S. (6/1/2012 – 7/31/2016) – *Currently, MD student, University of Colorado School of Medicine, Aurora, CO.*

Graduate Students (Mentor)

Past:

Kelsey Wuensch, Ph.D. student, Cancer Biology Training Program (7/1/2016 – 4/22/2021) - *NIH NRSA T32CA190216 (Graduated 2021) – Currently, Scientist II, Horizon Discovery, Denver, CO.*

Justin Eagle, M.S. student, Biostatistics Program (7/1/2015 – 6/30/2017) – *Currently, Senior Bioinformatics Scientist, Verogen, San Diego, CA.*

Medical Students – Mentored Scholarly Activity (MSA) Program (Mentor)

Dillon Le, B.S. (1/2/2016 – 10/31/2016)

Amelia Kreienkamp, B.S. (6/2/2014 – 6/30/2017) – *Currently, Resident in Pediatrics, Washington University School of Medicine in St. Louis, St. Louis, MO.*

Benjamin Wendell, M.S. (12/1/2009 – 6/30/2013) – *Currently, Resident in Emergency Medicine, University of Texas Health Science Center, Houston, TX.*

Graduate Students (Thesis Committee Member)

Past:

Jenny M Samson, Ph.D. student, Cancer Biology Training Program (1/1/2017 – 10/2020, Chair)

Sean Korpela, Ph.D. student, Pharmacology Training Program (6/1/2017 – 2019)

Daniel Sisler, Ph.D. student, Cancer Biology Training Program (7/1/2017 – 2019)

Natalia Gurule, Ph.D. student, Cancer Biology Training Program (7/1/2016 – 2019)

Laura Schubert, Ph.D. student, Cancer Biology Training Program (7/1/2016 – 6/19/2019), *Currently, Medical Student, University of Colorado Anschutz Medical Campus, Aurora, CO.*

Andrew Goodspeed, Ph.D. student, Pharmacology Training Program (7/1/2015 – 9/5/2018), *Currently, Core Manager, Bioinformatics Core, University of Colorado Cancer Center, Aurora, CO.*

Katie Mishall, Ph.D. student, Cancer Biology Training Program (7/1/2015 – 7/5/2018), *Currently, Feasibility Research Fellow, IQVIA Biotech, Denver, CO.*

Kyle Smith, Ph.D. student, Computational Bioscience Training Program (7/1/2015 – 3/17/2017) – *Currently, Bioinformatician, St. Jude Children's Research Hospital, Memphis, TN.*

Jennifer M. Symonds, Cancer Biology Training Program (Graduated, 6/1/2011 – 4/30/2014) – *Currently, Post-doc in National Institute of Health, Bethesda, MD.*

Rotation/Intern/Project Students

Christopher Langouet Astrie, Graduate Student, Pharmacology Training Program (12/1/2018 – 2/28/2019)

Jaidev Bapat, Graduate Student, Cancer Biology Training Program (8/27/2018 – 11/16/2018)

Rutendo Sigauke, Graduate Student, Computational Bioscience Training Program (1/1/2018 – 3/15/2018)

Mindy Szeto, Graduate Student, Medical Scientist Training Program (9/19/2016 – 12/2/2016)

Callie Federer, Graduate Student, Computational Bioscience Training Program (1/1/2016 – 5/31/2016)

Visiting Graduate Students

Bernard Lee, Ph.D. Graduate Student, University of Malaya, Malaysia (12/6/2017 – 2/28/2018)

Goot Heah Khor, Ph.D. Graduate Student in Dentistry, University of Technology MARA, Malaysia (5/16 – 6/10/2011)

Kyubum Lee, Ph.D. Graduate Student in Computer Science, Korea University (8/1/2014 – 2/28/2015)

Minji Jeon, Ph.D. Graduate Student in Computer Science, Korea University (3/1 – 8/27/2015)

University of Colorado Cancer Center Summer Research Fellows

Daniel R. Doherty (Biomedical Engineering, Case Western Reserve University) (2013, 2014) – *Currently, MD Student, Rush Medical College, Rush University, Chicago, IL.*

Ilana M. Trumble (Engineering Honors Program, University of Colorado Boulder) (2014) – *Currently, Ph.D. Student in Biostatistics, UNC Chapel Hill, NC.*

Harrison Pielke-Lombardo (Applied Mathematics, University of Colorado Boulder) (2015) – *Currently, Ph.D. Student, Computational Bioscience Program, University of Colorado Anschutz Campus, Aurora, CO.*

Ryan Hays (Computational Biology, Massachusetts Institute of Technology) (2015)

Georgia Phillips (Computational Biology, Massachusetts Institute of Technology) (2017)

Undergraduate Interns

Tiffany Chan (University of Colorado, Boulder) (6/27– 8/1/2011)

Jong Bum Kim (Soongsil University, Seoul, Korea) (7/1 – 8/24/2011)

Byron Britt (Colorado State University) (6/1 – 8/1/2012)

Minjae Yoo (Soongsil University, Seoul, Korea) (12/6/12 – 2/26/13)

Jimin Shin (Soongsil University, Seoul, Korea) (6/2/14 – 9/30/14)

Shu Ying Ong (Colorado School of Mines) (5/21/18 – 7/31/18)

C. EXTERNAL EXAMINER

- Ph.D. Thesis Pre-Examiner, University of Helsinki, Helsinki, Finland (2021)
- Ph.D. Thesis Examiner, Faculty of Engineering and the Built Environment, University of the Witwatersrand, Johannesburg, South Africa. (2011)

10. SCHOLARSHIPS

[**H-index = 55**; i10-index: 156; >12,000 citations as of 8/31/2021, according to Google Scholar https://tinyurl.com/yckgqcps]

A. BOOKS

1. Wang J, **Tan AC**, Tian T. (Eds). (2012). *Next Generation Microarray Bioinformatics*. Methods in Molecular Biology, Volume 802, Humana Press, Springer. ISBN: 978-1-61779-399-8. [401 pages].

    o [*Book Reviewed by Lin D (2015). Briefings in Bioinformatics*. 16 (4): 732-734.]

2. **Tan AC**, Huang PH. (Eds). (2017). *Kinase Signaling Networks*. Methods in Molecular Biology, Volume 1636, Humana Press, Springer. ISBN: 978-1-4939-7154-1. [517 pages].

B. SPECIAL ISSUES

1. **Tan AC**, Huang PH. (Eds). (2020). **Translational Genomics for Rare Cancers: Challenges and Opportunity**. *Seminars in Cancer Biology*, Volume 61, 1-198.

B. BOOK CHAPTERS

1. **Tan AC**. (2012). Employing Gene Set Top Scoring Pairs to identify deregulated pathway-signatures in dilated cardiomyopathy from integrated microarray gene expression data. *Methods in Molecular Biology*. 802:389-398. [PMID: 22130895]

2. Kim J[+], **Tan AC**. (2012). BiNGS!SL-seq: A Bioinformatics Pipeline for the Analysis and Interpretation of Deep Sequencing Genome-wide Synthetic Lethality Screen. *Methods in Molecular Biology*. 802:345-361. [PMID: 22130892]

3. **Tan AC**, Leong S, Pitts TM, Tentler JJ, Eckhardt SG. (2013). New Approaches to Integration of Personalized Medicine in Early Cancer Drug Development. In: *Principles of Molecular Diagnostics and Personalized Cancer Medicine*. (Dongfeng Tan and Henry Lynch (eds)). Lippincott Williams & Wilkins. P.659-673.

4. Bradshaw-Pierce EL, **Tan AC**. (2013). Integrating "Omics" Data for Quantitative and Systems Pharmacology in Translational Oncology. In: *Micro and Nano Flow Systems for Bioanalysis*. (Michael W. Collins and Carola S. König (eds)). Springer. P.187-206.

5. <u>Hintzsche JD</u>, Robinson WA, **Tan AC**. (2021). Variant Calling in Next Generation Sequencing Data. In: ***Systems Medicine: Integrative, Qualitative and Computational Approaches***. (Olaf Wolkenhauer (ed)). Vol 1: pp. 129-140. Elsevier.

C. PEER-REVIEWED MANUSCRIPTS

NOTE:
* Denotes contributed equally to this work.
<u>Underline</u> denotes research conducted where Dr. Tan was the P.I. and mentored fellows/students (underlined) on the manuscript/abstract. Trainees are underlined.
@ Denotes co-senior/co-corresponding authors.
🏆 Highly Cited Paper Denotes **highly cited paper** according to the Clarivate Analytics, this paper received enough citations to place it in the top 1% of the academic field of Clinical Medicine based on a highly cited threshold for the field and publication year.

1. **Tan AC**, Gilbert D, Tuson A. (2002). Characterisation of FAD-family Folds using a Machine Learning Approach. In ***Proceedings of the International Conference on Bioinformatics*** *(InCoB 2002)*, Bangkok, Thailand.

2. **Tan AC**, Gilbert D. (2003). An empirical comparison of supervised machine learning techniques in bioinformatics. In ***Proceedings of the 1st Asia Pacific Bioinformatics Conference (APBC 2003)***, Adelaide, Australia. (ed. P Y-P Chen.), pp. 219-222.

3. **Tan AC**, Gilbert, D. (2003). Ensemble machine learning on gene expression data for cancer classification. ***Applied Bioinformatics***. 2(3 Suppl):S75-S83. [PMID: 15130820].

4. **Tan AC**, Gilbert D, Deville Y. (2003). Integrative machine learning approach for multi-class SCOP protein fold classification. In ***Proceedings of the German Conference on Bioinformatics (GCB2003)***. (eds. H-W Mewes, D Frishman, V Heun, S Kramer), pp. 153-159, Munich, Germany.

5. Ren T, Veeramalai M, **Tan AC**, Gilbert D. (2003). MSAT: a Multiple Sequence Alignment tool based on TOPS. In ***Proceedings of the Biological Language Conference (BLC 2003)***. (eds. J Klein-Seetharaman, R Rosenfeld, R Reddy), pp. 286-301, Pittsburgh, PA.

6. **Tan AC**, Gilbert D, Deville Y. (2003). Multi-class Protein Fold Classification using a New Ensemble Machine Learning Approach. ***Genome Informatics.*** 14:206-217. [PMID: 15706535].

7. Al-Shahib A, He C, **Tan AC**, Girolami M, Gilbert D. (2004). An assessment of feature relevance in predicting protein function from sequence. In ***Proceedings of the Fifth International Conference on Intelligent Data Engineering and Automated Learning (IDEAL 04)***. (eds. RL Yang, R Everson, H Yin), *Lecture Notes in Computer Science.* 3177:52-57. Springer-Verlag, Exeter, United Kingdom.

8. Ren T, Veeramalai M, **Tan AC**, Gilbert D. (2004). MSAT: a Multiple Sequence Alignment tool based on TOPS. ***Applied Bioinformatics.*** 3(2-3):149-158. [PMID: 15693740].

9. **Tan AC**, Naiman DQ, Xu L, Winslow RL, Geman D. (2005). Simple decision rules for classifying human cancers from gene expression profiles. ***Bioinformatics.*** 21(20):3896-3904. [PMID: 16105897]. [PMCID: PMC1987374].

10. Xu L, **Tan AC**, Naiman DQ, Geman D, Winslow RL. (2005). Robust prostate cancer marker genes emerge from direct integration of inter-study microarray data. ***Bioinformatics.*** 21(20):3905-3911. [PMID: 16131522].

11. **Tan AC**, Fan JB, Karikari C, Bibikova M, Garcia EW, Zhou L, Barker D, Serre D, Feldmann G, Hruban RH, Klein AP, Goggins M, Couch FJ, Hudson TJ, Winslow RL, Maitra A, Chakravarti A. (2008). Allele-Specific Expression in the germline of patients with familial pancreatic cancer: An unbiased approach to cancer gene discovery. *Cancer Biology and Therapy.* 7(1):137-146. [PMID: 18059179].

12. Xu L, **Tan AC**, Winslow RL, Geman D. (2008). Merging microarray data from separate breast cancer studies provides a robust prognostic test. *BMC Bioinformatics.* 9:125. [PMID: 18304324]. [PMCID: PMC2409450]. [*Highly Accessed Article*].

13. Jimeno A, **Tan AC**, Coffa J, Rajeshkumar NV, Kulesza P, Rubio-Viqueira B, Wheelhouse J, Diosdado B, Messersmith WA, Iacobuzio-Donahue C, Maitra A, Varella-Garcia M, Hirsch FR, Meijer GA, Hidalgo M. (2008). Coordinated EGFR pathway gene over-expression predicts EGFR inhibitor sensitivity in pancreatic cancer. *Cancer Research.* 68(8):2841-2849. [PMID: 18413752].

14. Geman D, Bahman A, **Tan AC**, Naiman DQ. (2008). Microarray classification from several two-gene expression comparisons. *In Proceedings of the Seventh International Conference on Machine Learning and Applications (ICMLA 08).* (eds. MA Wani, X-w Chen, D Casasent, L Kurgan, T Hu, K Hafeez) p. 583- 585. IEEE Computer Society, San Diego, CA.

15. Song D, Chaerkady R, **Tan AC**, García-García E, Nalli A, Suárez-Gauthier A, López-Ríos F, Zhang XF, Solomon A, Tong J, Read M, Fritz C, Jimeno A, Pandey A, Hidalgo M. (2008). Antitumor activity and molecular effects of the novel Hsp 90 inhibitor, IPI-504, in pancreatic cancer*. Molecular Cancer Therapeutics*. 7(10): 3275-3284. [PMID: 18852131].

16. Chen CS*, Sullivan S*, Anderson T*, **Tan AC***, Alex PJ, Brant SR, Cuffari C, Bayless TM, Talor MV, Burek CL, Wang H, Li R, Datta LW, Wu Y, Winslow RL, Zhu H, Li X. (2009). Identification of novel serological biomarkers for inflammatory bowel disease using E. coli proteome chip. *Molecular & Cellular Proteomics*. 8(8):1765-1776. [PMID: 19357087]. [PMCID: PMC2722769].

17. **Tan AC**, Jimeno A, Lin SH, Wheelhouse J, Chan F, Solomon A, Rajeshkumar NV, Rubio-Viqueira B, Hidalgo M. (2009). Characterizing methylation patterns in pancreatic cancer genome. *Molecular Oncology*. 3(5-6):425-438. [PMID: 19497796].

18. Messersmith WA, Rajeshkumar NV, **Tan AC**, Wang XF, Diesl V, Choe SE, Follettie M, Coughlin C, Boschelli F, Garcia-Garcia E, Lopez-Rios F, Jimeno A, Hidalgo M. (2009). Efficacy and pharmacodynamic effects of bosutinib, a Src/Abl inhibitor, in human pancreas cancer xenografts. *Molecular Cancer Therapeutics*. 8(6):1486-1493. [PMID: 19509264].

19. Rajeshkumar NV*, **Tan AC***, De Oliveira E, Womack C, Wombwell H, Morgan S, Warren MV, Walker J, Green TP, Jimeno A, Messersmith WA, Hidalgo M. (2009). Antitumor effects and biomarkers of activity of AZD0530, a Src inhibitor, in pancreatic cancer. *Clinical Cancer Research*. 15(12):4138-4146. [PMID: 19509160].

20. Tian Y, **Tan AC**, Sun X, Olson MT, Xie Z, Jinawath N, Chan DW, Shih IeM, Zhang Z, Zhang H. (2009). Quantitative proteomic analysis of ovarian cancer cells identified mitochondrial proteins associated with paclitaxel treatment. *PROTEOMICS – Clinical Applications.* 3(11):1288-1295*.* [PMID: 21113235].

21. Kent OA, Mullendore M, Wentzel EA, López-Romero P, **Tan AC**, Alvarez H, West K, Ochs MF, Hidalgo M, Arking DE, Maitra A, Mendell JT. (2009). A resource for analysis of miRNA expression and function in pancreatic ductal adenocarcinoma cells*. Cancer Biology and Therapy*. 8(21):2005-2016. [PMID: 20037478]. [PMCID: PMC2824894].

22. Leong S, Messersmith WA, **Tan AC**, Eckhardt SG. (2010). Novel agents in the treatment of metastatic colorectal cancer. *The Cancer Journal: The Journal of Principles and Practice of Oncology*. 16(3):273-282. [PMID: 20526106].

23. Pitts TM*, **Tan AC***, Kulikowski GN, Tentler JJ, Brown AM, Flanigan SA, Leong S, Coldren CD, Hirsch FR, Varella-Garcia M, Korch C, Eckhardt SG. (2010). Development of an integrated genomic classifier for a novel agent in colorectal cancer: approach to individualized therapy in early development. *Clinical Cancer Research*. 16(12):3193-3204. [PMID: 20530704]. [PMCID: PMC2889230].

   o [*Commentated by: Douglas Yee (2010). How to Train Your Biomarker. Clinical Cancer Research. 16(12): 3091-3093*]

24. Gao D, Kim J, Kim H, Phang TL, Selby H^{+}, **Tan AC**[@], Tong T[@] (2010). A survey of statistical software for analyzing RNA-seq data. *Human Genomics*. 5(1):56-60. [PMID: 21106489].

25. Arcaroli JJ, Touban BM, **Tan AC**, Varella-Garcia M, Powell RW, Eckhardt SG, Elvin P, Gao D, Messersmith WA. (2010). Gene Array and FISH Biomarkers of Activity of Saracatinib (AZD0530), a Src Inhibitor, in a Preclinical Model of Colorectal Cancer. *Clinical Cancer Research.* 16(16):4165-4177. [PMID: 20682712].

26. Garrido-Laguna I, **Tan AC**, Uson M, Angenendt M, Ma WW, Villaroel MC, Zhao M, Rajeshkumar NV, Jimeno A, Donehower R, Iacobuzio-Donahue C, Barrett M, Rudek MA, Rubio-Viqueira B, Laheru D, Hidalgo M. (2010). Integrated preclinical and clinical development of mTOR inhibitors in pancreatic cancer. *British Journal of Cancer*. 103(5):649-655. [PMID: 20664591]. [PMCID: PMC2938261].

27. Deng Y, Liu J, Han G, Lu SL, Wang SY, Malkoski S, **Tan AC**, Deng C, Wang XJ, Zhang Q. (2010). Redox-dependent Brca1 transcriptional regulation by an NADH-sensor CtBP1. *Oncogene.* 29(50):6603-6608. [PMID: 20818429]

28. Tentler JJ, Nallapareddy S, **Tan AC**, Spreafico A, Pitts TM, Morelli MP, Selby HM, Kachaeva MI, Flanigan SA, Kulikowski GN, Leong S, Arcaroli JJ, Messersmith WA, Eckhardt SG. (2010). Identification of Predictive Markers of Response to the MEK1/2 Inhibitor Selumetinib (AZD6244) in KRAS-Mutated Colorectal Cancer. *Molecular Cancer Therapeutics.* 9(12):3351-3362. [PMID: 20923857]. [*Highlights of this issue*].

29. Camidge DR, Kono SA, Flacco A, **Tan AC**, Doebele RC, Zhou Q, Crino L, Franklin WA, Varella-Garcia M. (2010). Optimizing the detection of lung cancer patients harboring Anaplastic Lymphoma Kinase (ALK) gene rearrangements potentially suitable for ALK inhibitor treatment. *Clinical Cancer Research.* 16(22):5581-5590. [PMID: 21062932]. 🏆 Highly Cited Paper

30. Flanigan SA, Pitts TM, Eckhardt SG, Tentler JJ, **Tan AC**, Thorburn A, Leong S. (2010). The IGF-1R/IR Tyrosine Kinase Inhibitor, PQIP, Exhibits Enhanced Anti-Tumor Effects in Combination with Chemotherapy Against Colorectal Cancer Models. *Clinical Cancer Research.* 16(22):5436-5446. [PMID: 20943761].

31. Kim H, Kim J, Selby H, Gao D, Tong T, Phang TL, **Tan AC**. (2011). A Short Survey of Computational Analysis Methods in Analyzing ChIP-seq Data. *Human Genomics.* 5(2):117-123. [PMID: 21296745].

32. Jones LK[@], Zou F, Kheifets A, Rybnikov K, Berry D, **Tan AC**[@]. (2011). Confident Predictability: Identifying reliable gene expression patterns for individualized tumor classification using a local minimax kernel algorithm. *BMC Medical Genomics.* 4:10. [PMID:21261972]. [PMCID: PMC3038886].

33. Xiong Y, Li Z, Ji M, **Tan AC**, Bemis J, Tse JV, Huang G, Park J, Ji C, Chen J, Bemis LT, Bunting KD, Tse. (2011). Mir-29b regulates expression of AF1q, an MLL fusion partner and low miR-29b/high AF1q associates with adverse cytogenetics and poor overall survival in AML. *British Journal of Haematology.* 153(6):753-757. [PMID: 21496004].

34. Huang Q, Li F, Liu X, Li W, Shi W, Liu FF, O'Sullivan B, He Z, Peng Y, **Tan AC**, Zhou L, Shen J, Han G, Wang XJ, Thorburn J, Thorburn A, Jimeno A, Raben D, Bedford JS, Li CY. (2011). Caspase 3-mediated stimulation of tumor cell repopulation during cancer radiotherapy. ***Nature Medicine.*** 17(7):860-866. [PMID: 21725296].

   o [*Commented by: Connell, PP and Weichselbaum, RR (2011). A downside to apoptosis in cancer therapy? Nature Medicine 17(7):780-782*]

   o [*Commented by: Hutchinson L. (2011). Radiotherapy: Repopulating tumor cells-dying for caspase 3. Nat Rev Clin Oncol. 8(9):508*]

35. Garrido-Laguna I, Uson M, Rajeshkumar NV, **Tan AC**, De Oliveira E, Karikari C, Villaroel MC, Solomon A, Taylor G, Sharma R, Hruban RH, Maitra A, Laheru D, Rubio-Viqueira B, Jimeno A, Hidalgo M. (2011). Tumor engraftment in nude mice and enrichment in stroma-related gene pathways predicts poor survival and resistance to gemcitabine in patients with pancreatic cancer. ***Clinical Cancer Research.*** 17(17):5793-5800. [PMID: 21742805].

36. Lyons TR, O'Brien J, Borges VF, Conklin MW, Keely PJ, Eliceiri KW, Marusyk A, **Tan AC**, Schedin P. (2011). Postpartum mammary gland involution drives progression of ductal carcinoma *in situ* through collagen and COX-2. ***Nature Medicine.*** 17(9):1109-1115. [PMID: 21822285].[***Cover Article***]

   o [*Commented by: Tlsty TD (2011). Tissue states provide novel insights into attributes that drive metastasis. Cancer Cell. 2011 20(3):285-286*]

37. Khoo SK, Petillo D, Parida M, **Tan AC**, Resau JH, Obaro SK. (2011). Host response transcriptional profiling reveals extracellular components and ABC (ATP-binding cassette) transporters gene enrichment in typhoid fever-infected Nigerian children. ***BMC Infectious Diseases.*** 11(1):241. [PMID: 21914192]. [***Highly Accessed Article***].

38. Liu X, Li F, Stubblefield EA, Blanchard B, Richards TL, Larson GA, He Y, Huang Q, **Tan AC**, Zhang D, Benke TA, Sladek JR, Zahniser NR, Li CY. (2012). Direct reprogramming of human fibroblasts into dopaminergic neuron-like cells. ***Cell Research.*** 22:321-332. [PMID: 22105488]. [PMCID: PMC3271588].

39. Morelli MP, Tentler JJ, Kulikowski GN, **Tan AC**, Bradshaw-Pierce EL, Pitts TM, Brown AM, Nallapareddy S, Arcaroli JJ, Serkova NJ, Hidalgo M, Ciardiello F, Eckhardt SG. (2012) Preclinical Activity of the Rational Combination of Selumetinib (AZD6244) in Combination with Vorinostat in KRAS Mutant Colorectal Cancer Models. ***Clinical Cancer Research.*** 18(4):1051-1062. [PMID: 22173548].

40. Fernandez AF, Assenov Y, Martin-Subero JI, Balint B, Siebert R, Taniguchi H, Yamamoto H, Hidalgo M, **Tan AC**, Galm O, Ferrer I, Sanchez-Cespedes M, Villanueva A, Carmona J, Sanchez-Mut JV, Berdasco M, Moreno V, Capella G, Monk D, Ballestar E, Ropero S, Martinez R, Sanchez-Carbayo M, Prosper F, Agirre X, Fraga MF, Graña O, Perez-Jurado L, Mora J, Puig S, Prat J, Badimon L, Puca AA, Meltzer SJ, Lengauer T, Bridgewater J, Bock C, Esteller M. (2012). A DNA methylation fingerprint of 1,628 human samples. ***Genome Research.*** 22(2):407-419. [PMID: 21613409].

41. Haughian JM, Pinto MP, Harrell JC, Bliesner BS, Joensuu KM, Dye WW, Sartorius CA, **Tan AC**, Heikkilä P, Perou CM, Horwitz KB (2012). Maintenance of Hormone Responsiveness in Luminal Breast Cancers by Suppression of Notch. ***Proceedings of the National Academy of Sciences of the United States of America.*** 109(8):2742-2747. [PMID: 21969591]. [PMCID: PMC3287001].

42. 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].

43. Smith AL, Iwanaga R, Drasin DJ, Micalizzi DS, Vartuli RL, **Tan AC**, Ford HL. (2012). The miR-106b-25 cluster targets Smad7, activates TGF-β signaling, and induces EMT and tumor initiating cell characteristics downstream of Six1 in human breast cancer. *Oncogene.* 31(50): 5162-5171. [PMID: 22286770]. [PMCID: PMC3342483].

44. Arcaroli JJ, Powell RW, Varella-Garcia M, McManus M, **Tan AC**, Quackenbush KS, Pitts TM, Gao D, Spreafico A, Dasari A, Touban BM, Messersmith WA (2012). ALDH+ Tumor-Initiating Cells Exhibiting Gain in Notch1 Gene Copy Number have Enhanced Regrowth Sensitivity to a γ-Secretase Inhibitor and Irinotecan in Colorectal Cancer. *Molecular Oncology.* 6(3):370-381. [PMID: 22521243].

45. Tentler JJ, **Tan AC**, Weekes CD, Jimeno A, Leong S, Pitts TM, Arcaroli JJ, Messersmith WA, Eckhardt SG. (2012). Patient-derived tumour xenografts as models for oncology drug development. *Nature Reviews Clinical Oncology.* 9(6):338-350. [PMID: 22508028]. [*Cover Article*].

🏆 Highly Cited Paper

46. Arcaroli JJ, Quackenbush KS, Powell RW, Pitts TM, Spreafico A, Varella-Garcia M, Bemis L, **Tan AC**, Reinemann JM, Touban BM, Dasari A, Eckhardt SG, Messersmith WA. (2012). Common PIK3CA mutants and a novel 3' UTR mutation are associated with increased sensitivity to saracatinib. *Clinical Cancer Research.* 18(9):2704-2714. [PMID: 22553375].

47. 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 non-genotoxic activation of p53. *Nature Chemical Biology.* 8(7):646-654. [PMID: 22660439].

48. Casás-Selves M, Kim J, Zhang Z, Helfrich BA, Gao D, Porter CC, Scarborough HA, Bunn PA Jr, Chan DC, **Tan AC**, Degregori. (2012). Tankyrase and the canonical Wnt pathway protect lung cancer cells from EGFR inhibition. *Cancer Research.* 72(16):4154-4164. [PMID: 22738915].

49. Arcaroli JJ, Quackenbush KS, Dasari A, Powell RW, McManus M, **Tan AC**, Foster NR, Picus J, Wright J, Nallapareddy S, Erlichman C, Hidalgo M, Messersmith WA. (2012). Biomarker-Driven Trial in Metastatic Pancreas Cancer: Feasibility in a Multi-Center Study of Saracatinib, an Oral Src Inhibitor, in Previously Treated Pancreatic Cancer. *Cancer Medicine.* 1(2):207-217.

50. Giles ED, Wellberg EA, Astling DP[+], Anderson SM, Thor AD, Jindal S, **Tan AC**, Schedin PS, MacLean PS. (2012). Obesity and Overfeeding Affecting Both Tumor and Systemic Metabolism Activates the Progesterone Receptor to Contribute to Postmenopausal Breast Cancer. *Cancer Research.* 72(24):6501-6512. [*Cover Article*].

51. Khoo SK[@], Petillo D, Kang UJ, Resau JH, Berryhill B, Linder J, Forsgren L, Neuman LA, **Tan AC**[@]. (2012). Plasma-based Circulating MicroRNA Biomarkers for Parkinson's Disease. *Journal of Parkinson's Disease.* 2(4):321-331.[PMID: 23938262].

52. Diamond JR, Eckhardt SG, **Tan AC**, Newton TP, Selby HM, Brunkow KL, Kachaeva MI, Varella-Garcia M, Pitts TM, Bray MR, Fletcher GC, Tentler JJ. (2013). Predictive Biomarkers of Sensitivity to the Aurora and Angiogenic Kinase Inhibitor ENMD-2076 in Preclinical Breast Cancer Models. *Clinical Cancer Research.* 19(1): 19:291-303. [PMID: 23136197]. [*Cover Article*].

53. Singleton KR, Kim J, Hinz TK, Marek L, Casás-Selves M, Hatheway C, **Tan AC**, DeGregori J, Heasley LE. (2013). A Receptor Tyrosine Kinase Network Comprised of FGFRs, EGFR, ERBB2 and MET Drives Growth and Survival of Head and Neck Squamous Carcinoma Cell Lines. *Molecular Pharmacology.* 83(4):882-893. [PMID: 23371912].

54. Bradshaw-Pierce EL, Pitts TM, McPhillips KL, Hasley C, Gustafson DL, **Tan AC**, Nguyen L, West M, Fisher T, Kan JL, Murray BW, Eckhardt SG. (2013). Tumor P-glycoprotein Correlates with Efficacy of PF-03758309 in In Vitro and In Vivo models of Colorectal Cancer. *Frontiers in Pharmacology.* 4:22. [PMID: 23524533].

55. Pitts TM, Kulikowski GN, **Tan AC**, Murray BW, Carley W, Smeal T, Guo C, Arcaroli JJ, Powell RW, Tentler JJ, Spreafico A, Selby HM, Kachaeva MI, McPhillips K, Im EK, Bradshaw-Pierce EL, Messersmith WA, Eckhardt SG. (2013). Association of Biomarkers of the Epithelial-to-Mesenchymal Transition (EMT) Phenotype with Responsiveness to the p21-Activated Kinase Inhibitor, PF-3758309, in Colorectal Cancer Models. *Frontiers in Pharmacology.* 4:35. [PMID: 23543898].

56. Harvell DME, Kim J, O'Brien J, **Tan AC**, Borges VF, Schedin P, Jacobsen BM, Horwitz KB. (2013). Genomic Signatures of Pregnancy-Associated Breast Cancer Epithelia and Stroma and their Regulation by Estrogens and Progesterone. *Hormone and Cancer.* 4(3):140-153. [PMID:23479404].

57. Ware KE, Hinz TK, Kleczko E, Singleton KR, Marek LA, Helfrich BA, Cummings CT, Graham DK, Astling D[+], **Tan AC**, Heasley LE. (2013). A mechanism of resistance to gefitinib mediated by cellular reprogramming and the acquisition of an FGF2-FGFR1 autocrine growth loop. *Oncogenesis.* 2: e39. [PMID: 23552882].

58. Schlegel J, Sambade MJ, Sather S, Moschos SJ, **Tan AC**, Winges A, Deryckere D, Carson CC, Trembath DG, Tentler JJ, Eckhardt SG, Kuan PF, Hamilton RL, Duncan LM, Miller CR, Nikolaishvili-Feinberg N, Midkiff BR, Liu J, Zhang W, Yang C, Wang X, Frye SV, Earp HS, Shields JM, Graham DK. (2013). MERTK receptor tyrosine kinase is a therapeutic target in melanoma. *The Journal of Clinical Investigation.* 23(5):2257-2267. [PMID:23585477].

59. Keysar SB*, Astling DP*, Anderson RT*, Vogler BW, Bowles DW, Morton JJ, Paylor JJ, Glogowska MJ, Le PN, Eagles-Soukup JR, Kako SL, Takimoto SM, Sehrt DB, Umpierrez A, Pittman MA, Macfadden SM, Helber RM, Peterson S, Hausman DF, Said S, Leem TH, Goddard JA, Arcaroli JJ, Messersmith WA, Robinson WA, Hirsch FR, Varella-Garcia M, Raben D, Wang XJ, Song JI, **Tan AC**, Jimeno A. (2013). A patient tumor transplant model of squamous cell cancer identifies PI3K inhibitors as candidate therapeutics in defined molecular bins. *Molecular Oncology.* 7(4): 776-790. [PMID:23607916].

60. 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]. [PMCID: PMC3733554].

61. 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].

62. Maller O, Hansen KC, Lyons TR, Acerbi I, Weaver VM, Prekeris R, **Tan AC**, Schedin P. (2013). Collagen architecture in pregnancy-induced protection from breast cancer. *Journal of Cell Science.* 126:4108-4110. [PMID: 23843613].

63. Linger RM, Lee-Sherick AB, Deryckere D, Cohen RA, Jacobsen KM, McGranahan A, Brandão LN, Winges A, Sawczyn KK, Liang X, Keating AK, **Tan AC**, Earp HS, Graham DK. (2013). Mer receptor tyrosine kinase is a therapeutic target in pre-B-cell acute lymphoblastic leukemia. *Blood.* 122(9):1599-1609. [PMID: 23861246]. [PMCID: PMC3757372].

64. Arcaroli JJ, Quackenbush KS, Purkey A, Powell RW, Pitts TM, Bagby S, **Tan AC**, Cross B, McPhillips K, Song EK, Tai WM, Winn RA, Bikkavilli K, Vanscoyk M, Eckhardt SG, Messersmith WA. (2013). Tumours with elevated levels of the Notch and Wnt pathways exhibit efficacy to PF-03084014, a γ-secretase inhibitor, in a preclinical colorectal explant model. *British Journal of Cancer.* 109(3): 667-675. [PMID: 23868008]. [PMCID: PMC3738122].

65. Anderson RT, Keysar SB, Bowles DW, Glogowska MJ, Astling DP, Morton JJ, Le P, Umpierrez A, Eagles-Soukup J, Gan GN, Vogler BW, Sehrt DB, Takimoto SM, Aisner DL, Wilhem F, Frederick BA,

Varella-Garcia M, **Tan AC**, Jimeno A. (2013). The dual pathway inhibitor rigosertib is effective in direct-patient tumor xenografts of head and neck squamous cell carcinomas. *Molecular Cancer Therapeutics.* 12(10):1994 - 2005. [PMID: 23873848].

66. Lieu CH, **Tan AC**, Leong S, Diamond JR, Eckhardt SG. (2013). From Bench to Bedside: Assessing the Impact of Preclinical Studies on Targeted Agent Development in Oncology. *Journal of the National Cancer Institute.* 105(19):1441–1455. [PMID: 24052618].

   o [*Commented by: Bertotti A, Trusolino L. (2013). From Bench to Bedside: does Preclinical Practice in Translational Oncology Need Some rebuilding? Journal of the National Cancer Institute. 105 (19):1426-1427.*]

67. Khor GH, Froemming GRA, Zain RB, Abraham MT, Omar E, Tan SK, **Tan AC**, Vincent-Chong VK, Thong KL. (2013). DNA Methylation Profiling Revealed Promoter Hypermethylation-induced Silencing of p16, DDAH2 and DUSP1 in Primary Oral Squamous Cell Carcinoma. *International Journal of Medical Sciences.* 10(12):1727 - 1739. [PMID: 24155659].

68. Flanigan SA, Pitts TM, Newton TP, Kulikowski GN, **Tan AC**, McManus MC, Spreafico A, Kachaeva MI, Selby HM[+], Tentler JJ, Eckhardt SG, Leong S. (2013). Overcoming IGF1R/IR Resistance Through Inhibition of MEK Signaling in Colorectal Cancer Models. *Clinical Cancer Research.* 9(22):6219-6229. [PMID: 24045180].

69. Kim J[*], Yoo M[*], Kang J, **Tan AC**. (2013). K-Map: Connecting kinases with therapeutics for drug repurposing and development. *Human Genomics.* 7:20. [PMID: 24060470]. [*Highly Accessed Article*].

70. Davies KD, Mahale S, Astling D, Aisner DL, Le AT, Vaishnavi A, **Tan AC**, Camidge DR, Varella-Garcia M, Doebele RC. (2013). Resistance to ROS1 Inhibition Mediated by EGFR Pathway Activation. *PLoS ONE.* 8(12):e82236. [PMID:24349229].

71. Jeon M, Lee S, Lee K, **Tan AC**, Kang J. (2014). BEReX: Biomedical Entity-Relationship eXplorer. *Bioinformatics.* 30(1):135-136. [PMID: 24149052].

72. Saha A, **Tan AC**, Kang J. (2014). Automiatic Context-Specific Subnetwork Discovery from Large Interaction Networks. *PLoS ONE.* 9(1):e84227. [PMID: 24392115].

73. Bowles DW, Diamond JR, Lam ET, Weekes CD, Astling DP, Anderson RT, Leong S, Gore L, Varella-Garcia M, Vogler BW, Keysar SB, Freas E, Aisner DL, Ren C, **Tan AC**, Wilhelm F, Maniar M, Eckhardt SG, Messersmith WA, Jimeno A. (2014). Phase I Study of Oral Rigosertib (ON 01910.Na), a Dual Inhibitor of the PI3K and Plk1 Pathways, in Adult Patients with Advanced Solid Malignancies. *Clinical Cancer Research.* 20: 1656 - 1665. [PMID: 24493827].

74. Morrison JA, Pike LA, Sams SB, Sharma V, Zhou Q, Severson JJ, **Tan AC**, Wood WM, Haugen BR. (2014). Thioredoxin interacting protein (TXNIP) is a novel tumor suppressor in thyroid cancer. *Molecular Cancer.* 13: 62. [PMID: 24645981]. [*Highly Accessed Article*].

75. Wynes MW, Hinz TK, Gao D, Martini M, Marek L, Ware KE, Edwards MG, Bohm D, Perner S, Helfrich BA, Dziadziuszko R, Jassem J, Wojtylak S, Sejda A, Gozgit JM, Bunn PA Jr, Camidge DR, **Tan AC**, Hirsch FR, Heasley LE. (2014). FGFR1 mRNA and Protein Expression, not Gene Copy Number, Predict FGFR TKI Sensitivity Across All Lung Cancer Histologies. *Clinical Cancer Research.* 20(12): 3299-3309. [PMID: 24771645].

76. 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.* 30(17):2393-2398. [PMID: 24812339]. [*F1000 Recommended*].

○ [*Samudrala R, Sethi G. (2014). F1000Prime – Recommended*]

77. Wang CA, Drasin D, Pham C, Jedlicka P, Zaberezhnyy V, Guney M, Li H, Nemenoff R, Costello JC, **Tan AC**, Ford HL. (2014). Homeoprotein Six2 Promotes Breast Cancer Metastasis via Transcriptional and Epigenetic Control of E-Cadherin Expression. *Cancer Research.* 74(24):7357-7370. [PMID: 25348955].

78. 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].

79. Pitts TM, Newton TP, Bradshaw-Pierce EL, Addison R, Arcaroli JJ, Klauck PJ, Bagby SM, Hyatt SL, Purkey A, Tentler JJ, **Tan AC**, Messersmith WA, Eckhardt SG, Leong S. (2014). Dual Pharmacological Targeting of the MAP Kinase and PI3K/mTOR Pathway in Preclinical Models of Colorectal Cancer. *PLoS ONE.* 9(11):e113037. [PMID: 25401499].

80. Song EK, Tai W, Messersmith WA, Bagby S, Purkey A, Quackenbush KS, Pitts TM, Wang G, Blatchford P, Yahn R, Kaplan J, **Tan AC**, Atreya CE , Eckhardt G, Kelley RK, Venook A, Kwak EL, Ryan D, Arcaroli JJ. (2015). Potent antitumor activity of cabozantinib, a c-MET and VEGFR2 inhibitor, in a colorectal cancer patient-derived tumor explant model. *International Journal of Cancer.* 136(8):1967 - 1975. [PMID: 25242168].

81. Micel LN, Tentler JJ, **Tan AC**, Selby HM, Brunkow KL, Robertson KM, Davis SL, Klauck PJ[+], Pitts TM, Gangolli E, Fabrey R, O'Connell SM, Vincent PW, Eckhardt SG. (2015). Antitumor Activity of the MEK Inhibitor TAK-733 Against Melanoma Cell Lines and Patient-Derived Tumor Explants. *Molecular Cancer Therapeutics.* 14(2): 317-325. [PMID: 25376610].

○ [Selected in the "*2015 Must Read Collections*" of *Molecular Cancer Therapeutics*]

82. Fleenor CJ, Rozhok AI, Zaberezhnyy V, Mathew D, Kim J, **Tan AC**, Bernstein ID, DeGregori J. (2015). Contrasting Roles for C/EBPalpha and Notch in Irradiation-Induced Multipotent Hematopoietic Progenitor Cell Defects. *Stem Cells.* 33(4):1345-1358. [PMID: 25546133]. [PMCID: PMC4376650].

83. Petillo D, Orey S, **Tan AC**, Forsgren L, Khoo SK. (2015). Parkinson's Disease-related Circulating microRNA Biomarkers - a Validation Study. *AIMS Medical Science.* 2(1): 7-14.

84. Ryall KA, **Tan AC**. (2015). Systems Biology Approaches For Advancing The Discovery Of Effective Drug Combinations. *Journal of Cheminformatics.* 7:7. [PMID: 25741385]. [PMCID: PMC4348553]. [*Highly Accessed Article*].

85. 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]. [PMCID: PMC4417413].

86. Tentler JJ, Ionkina A, **Tan AC**, Newton TP, Pitts TM, Glogowska MJ, Kabos P, Sartorius CA, Sullivan KD, Espinosa JM, Eckhardt SG, Diamond JD. (2015). p53 Family Members Regulate Phenotypic Response to Aurora Kinase A Inhibition in Triple-Negative Breast Cancer. *Molecular Cancer Therapeutics.* 4(5):1117-1129. [PMID: 25758253]. [PMCID: PMC4425647].

87. 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]. [PMCID: PMC4422719].

88. 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].

> o [*Commented by: Green DR (2015). Another face of RIPK1. EMBO Reports. 16:674-675.*]

89. 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].

90. Göke F, Franzen A, Hinz TK, Marek LA, Yoon P, Sharma R, Bode M, von Mäessenhausen A, Lankat-Buttgereit B, Göke A, Golletz C, Kirsten R, Boehm D, Vogel W, Kleczko EK, Eagles JR, Hirsch FR, Van Bremen T, 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].

91. Davis EM, Kim J, Menasche B, Sheppard J, Liu X, **Tan AC**, Shen J. (2015). Comparative haploid genetic screens reveal divergent pathways in the biogenesis of glycophosphatidylinositol-anchored proteins. ***Cell Reports***. 11(11):1727-1736. [PMID: 26074080].

92. Davis SL, Robertson KM, Pitts TM, Tentler JJ, Bradshaw-Pierce EL, Klauck PJ, Bagby SM, Hyatt SL, Selby HM, Spreafico A, Ecsedy JA, Arcaroli JJ, Messersmith WA, **Tan AC**, Eckhardt SG. (2015). Combined inhibition of MEK and Aurora A kinase in KRAS/PIK3CA double-mutant colorectal cancer models. ***Frontiers in Pharmacology***. 6:120. [PMID: 26136684].

93. Saha A, Jeon M, **Tan AC**, Kang J. (2015). iCOSSY: an online tool for context-specific subnetwork discovery from gene expression data. ***PLoS ONE***. 10(7): e0131656. [PMID: 26147457].

94. 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. [PMID:26681397].

95. 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].

96. 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***. 75(20):4398-4406. [PMID: 26359452].

97. Lieu CH, Klauck PJ, Henthron PK, Tentler JJ, **Tan AC**, Spreafico A, Selby HM, Britt BC, Bagby SM, Arcaroli JJ, Messersmith WA, Pitts TM, Eckhardt SG. (2015). Antitumor Activity of a Potent MEK Inhibitor, TAK-733, Against Colorectal Cancer Cell Lines and Patient Derived Xenografts. ***Oncotarget***. 6(33):34561-34572 [PMID: 26439693].

98. Henry C, Casas-Selves M, Kim J, Zaberezhnvv V, Aghili L, Daniel A, Jimenez L, Azam T, McNamee EN, Clambey E, Klawitter J, Serkova N, **Tan AC**, Dinarello C, DeGregori J. (2015). Aging-associated inflammation promotes selection for adaptive oncogenic events in B-progenitors. ***The Journal of Clinical Investigation***. 125(12):4666-4680. [PMID: 26551682].

99. 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].

100. Arcaroli JJ, Tai WM, McWilliams R, Bagby S, Blatchford PJ, Varella-Garcia M, Purkey A, Quackenbush KS, Song EK, Pitts TM, Gao D, Lieu C, McManus M, **Tan AC**, Zheng X, Zhang Q,

Ozeck M, Olson P, Jiang ZQ, Kopetz S, Jimeno A, Keysar S, Eckhardt G, Messersmith WA. (2016). A NOTCH1 Gene Copy Number Gain is a Prognostic Indicator of Worse Survival and a Predictive Biomarker to a Notch1 Targeting Antibody in Colorectal Cancer. *International Journal of Cancer*. 138(1):195-205. [PMID: 26152787].

101. **Tan AC**, Ryall KA, Huang PH. (2016). Expanding the Computational Toolbox for Interrogating Cancer Kinomes. *Pharmacogenomics*. 17(2):95-97. [PMID: 26666839].

102. Bowles DW, Keysar SB, Eagles JR, Wang G, Glogowska MJ, McDermott JD, Le PN, Gao D, Ray CE, Rochon PJ, Roop DR, **Tan AC**, Serracino HS, Jimeno A. (2016). A pilot study of cetuximab and the hedgehog inhibitor IPI-926 in recurrent/metastatic head and neck squamous cell carcinoma. *Oral Oncology*. 53: 74-79. [PMID: 26705064].

103. Fornetti J, Flanders K, Henson PM, **Tan AC**, Borges V, Schedin P. (2016). Mammary epithelial cell phagocytosis downstream of TGF-B3 is characterized by adherens junction reorganization. *Cell Death and Differentiation*. 23(2): 185-196. [PMID: 26113040].

104. Morton J, Bird G, Keysar S, Astling D, Lyons T, Anderson R, Glogowska M, Estes P, Eagles J, Le P, Gan G, McGettigan B, Fernandez P, Padilla-Just N, Garcia M, Song J, Bowles D, Schedin P, **Tan AC**, Roop DR, Wang XJ, Refaeli Y, Jimeno A. (2016). XactMice: humanizing mouse bone marrow enables microenvironment reconstitution in a patient-derived xenograft model of head and neck cancer. *Oncogene*. 35:290-300. [PMID: 25893296].

105. Symonds JM, Ohm AM, **Tan AC**, Reyland ME. (2016). PKCδ regulates integrin αVβ3 expression and transformed growth of K-ras dependent lung cancer cells. *Oncotarget*. 7(4): 17905-17919. [PMID: 26918447].

106. Lee K, Lee S, Park S, Kim S, Kim S, Choi K, **Tan AC**[@], Kang J[@]. (2016). BRONCO: Biomedical entity Relation Oncology Corpus for Extracting Gene-Variant-Disease-Drug Relations. *DATABASE*. 2016:baw043. [PMID: 27074804]. [[@]Co-corresponding authors].

107. Hintzsche J, Kim J, Yadav Y, Amato C, Robinson SE, Seelenfreund E, Shellman Y, Wisell J, Applegate A, McCarter M, Box N, Tentler J, De S, Robinson WA, **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].

108. Hidayatullah Fadlullah MZ, Chiang IK, Dionne KR, Yee PS, Gan CP, Sam KK, Tiong KH, Wen Ng AK, Martin D, Lim KP, Kallarakkal TG, Wan Mustafa WM, Lau SH, Abraham MT, Zain RB, Abdul Rahman ZA, Molinolo A, Patel V, Gutkind JS, **Tan AC**, Cheong SC. (2016). Genetically-defined novel oral squamous cell carcinoma cell lines for the development of molecular therapies. *Oncotarget*. 7(19):27802-27818. [PMID: 27050151].

109. Pitts TM, Bradshaw-Pierce E, Bagby S, Hyatt S, Selby H, Spreafico A, Tentler J, McPhillips K, Klauck P, Capasso A, Diamond JR, Davis SL, **Tan AC**, Arcaroli J, Purkey A, Messersmith WA, Ecsedy J, Eckhardt SG. (2016). Antitumor Activity of the Aurora A Selective Kinase Inhibitor, Alisertib, Against Preclinical Models of Colorectal Cancer. *Oncotarget*. 7(31): 50308-50319. [PMID:27385211].

110. 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].

111. Pozdeyev N, Yoo M, Mackie R, Schweppe RE, **Tan AC**[*], Haugen BR[*]. (2016). Integrating Heterogeneous Drug Sensitivity Data from Cancer Pharmacogenomic Studies. *Oncotarget*. 7(32): 51619-51625. [PMID:27322211]. ([*]Co-senior author).

112. Lee K, Shin W, Kim B, Lee S, Choi Y, Kim S, Jeon M, **Tan AC**[@], Kang J[@]. (2016). HiPub: Translating PubMed and PMC Texts to Networks for Knowledge Discovery. ***Bioinformatics***. 32(18):2886-2888. [PMID: 27485446].

113. 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].

114. Bagby S, Messersmith WA, Pitts TM, Capasso A, Varella-Garcia M, Klauck P, Kim J, **Tan AC**, Eckhardt SG, 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 (JoVE)***.115:e54393. [PMID:27768028].

115. Todd JR*, Ryall KA*, Vyse S*, Wong JP, Natrajan RC, Yuan Y, **Tan AC**, Huang PH. (2016). Systematic analysis of tumour cell-extracellular matrix adhesion identifies independent prognostic factors in breast cancer. ***Oncotarget***. 7(39):62939-62953. [PMID: 27556857]. (*contributed equally).

116. Lee S*, Kim D*, Lee K, Choi J, Kim S, Jeon M, Lim S, Choi D, Kim S, **Tan AC**, Kang J. (2016). BEST: Next-Generation Biomedical Entity Search Tool for Knowledge Discovery from Biomedical Literature. ***PLoS ONE***.11(10): e0164680. [PMID: 27760149].

117. Wong JP*, Todd JR*, Finetti MA, McCarthy F, Broncel M, Vyse S, Luczynski MT, Crosier S, Ryall KA, Holmes K, Payne LS, Daley F, Wai P, Jenks A, Tanos B, **Tan AC**, Natrajan RC, Williamson D, Huang PH. (2016). Dual targeting of PDGFRα and FGFR1 displays synergistic efficacy in malignant rhabdoid tumours. ***Cell Reports***. 17(5):1265-1275. [PMID: 27783942].

118. 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 of the United States of America***. 113(43): E6669-6678. [PMID: 27791036].

119. 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].

120. 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].

121. Hintzsche JD, Robinson WA, **Tan AC**. (2016). A Survey of Computational Tools to Analyze and Interpret Whole Exome Sequencing Data. ***International Journal of Genomics***. 2016:7983236.

122. Federer C*, Yoo M*, **Tan AC**. (2016). Big Data Mining and Adverse Event Pattern Analysis in Clinical Drug Trials. ***ASSAY and Drug Development Technologies***. 14(10): 557-566. [PMID:27631620]. (*contributed equally). [***Cover Article***]

123. Wuensch KE, **Tan AC**. (2016). Trunk or Branch? Identifying and Targeting Intratumoral Heterogeneity in Hepatocellular Carcinoma using Genomics and Patient Derived Primary Cancer Cells. ***Translational Cancer Research***. 5(Suppl 7): S1383-S1386.

124. **Tan AC**, Vyse S, Huang PH. (2017). Exploiting Receptor Tyrosine Kinase Co-activation for Cancer Therapy. ***Drug Discovery Today***. 22(1): 72-84. [PMID: 27452454].

125. Murakami A, Wang L, Kalhorn S, Schraml P, Rathmell WK, **Tan AC**, Nemenoff R, Stenmark K, Jiang BH, Reyland ME, Heasley L, Hu CJ. (2017). Context-dependent role for chromatin remodeling

component PBRM1/BAF180 in clear cell renal cell carcinoma. **Oncogenesis**. 6: e287.[PMID:28092369].

126. Lee BKB, Tiong KH, Chang JK, Liew CS, Abdul Rahman ZA, **Tan AC**, Khang TF, Cheong SC. (2017). DeSigN: connecting gene expression with therapeutics for drug repurposing and development. **BMC Genomics**. 18(Suppl 1): 934. [PMID: 28198666].

127. 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. (2017). PI3K signaling regulates SOX2 enabling cancer stem cell properties in head and neck cancer. **Journal of the National Cancer Institute**. 109(1): djw189. [PMID:27634934].

128. Turner J*, Couts K*, Sheren J, Saichaemchan S, Ariyawutyakorn W, Avolio I, Cabral E, Glogowska M, Amato C, Robinson S, Hintzsche J, Applegate A, Seelenfreund E, Gonzalez R, Wells K, Bagby S, Tentler J, **Tan AC**, Wisell J, Varella-Garcia M, Robinson WA. (2017). Kinase Gene Fusions in Defined Subsets of Melanoma. **Pigment Cell & Melanoma Research**. 30(1): 53-62. [PMID: 27864876]

129. Wong KM, Micel L, Selby H, **Tan AC**, Pitts TM, Bagby S, Spreafico A, Klauck P[+], Blakemore S, Smith P, McDonald A, Berger A, Tentler J, Eckhardt SG. (2017). Targeting the Protein Ubiquitination Machinery in Melanoma by the NEDD8-Activating Enzyme Inhibitor Pevonedistat (MLN4924). **Investigational New Drugs**. 35(1): 11-25. [PMID:27783255].

130. 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. (2017). 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**. 23(6): 1531-1541. [PMID: 27663586].

131. Smith Jr BJ, Hintzsche JD, Amato CM, **Tan AC**, Wells KR, Applegate AJ, Gonzalez RT, Barr JR, Robinson WA. (2017). Systematic Analysis of Whole Exome Sequencing Determines RET G691S Polymorphism, as Germline Variant in Melanoma. **Marshall Journal of Medicine.** 3(2): Article 10.

132. Brechbuhl HM, Finlay-Schultz J, Yamamoto TM, Gillen AE, Cittelly DM, **Tan AC**, Sams S, Pillai MM, Elias AD, Robinson WA, Sartorius CA, Kabos P. (2017). Fibroblast Subtypes Regulate Responsiveness of Luminal Breast Cancer to Estrogen. **Clinical Cancer Research**. 23(7): 1710-1721. [PMID: 27702820].[**Cover Article**].

133. 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**. 15(4): 382-394. [PMID: 28108622]

134. Harder B, Tian W, La Clair JJ, **Tan AC**, Ooi A, Chapman E, Zhang DD. (2017). Brusatol overcomes chemoresistance through inhibition of protein translation. **Molecular Carcinogenesis**. 56(5): 1493-1500. [PMID: 28019675]

135. Hintzsche JD, Gorden NT, Amato CM Kim J, Wuensch KE, Robinson SE, Applegate AJ, Couts KL, Medina TM, Wells KR, Wisell JA, McCarter MD, Box NF, Shellman YG, Gonzalez RC, Lews 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.** 27(3): 189-199. [[@]Co-corresponding authors.] [PMID: 28296713]

136. 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]

137. Nelson-Taylor SK, Le AT, <u>Yoo M</u>, Schubert L, Mishall KM, Doak A, Varella-Garcia M, **Tan AC**, Doebele RC. (2017). Resistance to RET-inhibition in RET-rearranged NSCLC is mediated by reactivation of RAS/MAPK signaling. *Molecular Cancer Therapeutics*. 16(8):1623-1633. [PMID: 28500237]

138. Ohm AM, **Tan AC**, Heasley LE, Reyland ME. (2017). Co-dependency of PKCδ and K-Ras: Inverse association with cytotoxic drug sensitivity in KRAS mutant lung cancer. *Oncogene*. 36(30):4370-4378. [PMID: 28368426].

139. Donson A, Apps J, Griesinger AM, Amani VA, Witt DA, Anderson RCE, Niazi TN, Grant G, Souweidane M, Johnston JM, Jackson EM, Kleinschmidt-DeMasters BK, Handler MH, **Tan AC**, Gore L, Virasemi A, Gonzalez-Meljem JM, Jacques TS, Martinez-Barbera JP, Foreman NK, Hankinson TC. (2017). Molecular analyses reveal inflammatory mediators in the solid component and cyst fluid of human adamantinomatous craniopharyngioma. *Journal of Neuropathology and Experimental Neurology*. 76(9):779-788. [PMID: 28859336]

140. Zhang C, Liu Z, Bunker E, Ramirez A, Lee S, Peng Y, **Tan AC**, Eckhardt SG, Chapnick DA, Liu X. (2017). Sorafenib Targets the Mitochondrial Electron Transport Chain Complexes and ATP Synthase to Activate the PINK1-Parkin Pathway and Modulate Cellular Drug Response. *Journal of Biological Chemistry*. 292(36): 15105-15120. [PMID: 28673964]

141. Scott AJ, Song EK, Bagby S, Purkey A, McCarter M, Gajdos C, Quackenbush KS, Cross B, Pitts TM, **Tan AC**, Eckhardt SG, Fenton H, Arcaroli J, Messersmith WA. (2017). Evaluation of the efficacy of dasatinib, a Src/Abl inhibitor, in colorectal cancer cell lines and explant mouse model. *PLoS ONE*. 12(11):e0187173. [PMID: 29091939]

142. Yue Z, Zheng Q, Neylon MT, <u>Yoo M</u>, <u>Shin J</u>, Zhao Z, **Tan AC**, Chen JY. (2018). PAGER 2.0: An update to the pathway, annotated-list, and gene-signature electronic repository for Human Network Biology. *Nucleic Acids Research*. 46(D1): D668-D676. [PMID: 29126216]

143. Couts KL, Bemis J, Turner JA, Bagby SM, Murphy D, Christiansen J, <u>Hintzsche JD</u>, Le A, Pitts TM, Wells K, Applegate A, Amato C, Multani P, Chow-Maneval E, Tentler JJ, Shellman YG, Rioth MJ, **Tan AC**, Gonzalez R, Medina T, Doebele RC, Robinson WA. (2018). ALK Inhibitor Response in Melanomas Expressing EML4-ALK Fusions and Alternate ALK Isoforms. *Molecular Cancer Therapeutics*. 17(1); 222-231. [PMID: 29054983] [*Highlights*]

144. Kim S, Park D, Choi Y, Lee K, Kim B, Jeon M, <u>Kim J</u>, **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]

145. Lee K, Kim B, Choi Y, Kim S, Shin W, Lee S, Park S, Kim S, **Tan AC**[@], Kang J[@]. (2018). Deep Learning of Mutation-Gene-Drug Relations from the Literature. *BMC Bioinformatics*. 19:21. [PMID: 29368597] [[@]Co-corresponding authors.]

146. Pilling A, <u>Kim J</u>, 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.

147. <u>Klauck PJ</u>, Bagby SM, Capasso A, Bradshaw-Pierce EL, <u>Selby HM</u>, Spreafico A, Tentler JJ, **Tan AC**, <u>Kim J</u>, 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]

148. <u>Kim J*</u>, <u>Yoo M*</u>, <u>Shin J</u>, <u>Kim H</u>, 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]

149. Hintzsche JD, Yoo M, Kim J, Amato CM, Robinson WA, **Tan AC**. (2018). IMPACT Web Portal: Oncology Database of Integrating Molecular Profiles with Actionable Therapeutics. ***BMC Medical Genomics***. 11(Suppl 2): 26. [PMID: 29697364]

150. Lee BKB, Gan CP, Chang JK, Tan JL, Fadlullah MZ, Abdul Rahman ZA, Prime SS, Gutkind JS, Liew CS, Khang TF, **Tan AC**, Cheong SC. (2018). GENIPAC: A Genomic Information Portal for Head and Neck Cancer Cell Systems. ***Journal of Dental Research***. 97(8):909-916. [PMID: 29512401]

151. Powers R, Goodspeed A, Pielke-Lombardo H, **Tan AC**, Costello J. (2018). GSEA-InContext: Identifying novel and common patterns in expression experiments. ***Bioinformatics***. 34(13):i555-i564. [PMID: 29950010] [***Ian Lawson Von Toch Memorial Award for Outstanding Student Paper Winner, ISMB 2018***]

152. Keysar SB*, Eagles JR*, Miller B, Jackson BC, Chowdhury FN, Reisinger J, Chimed T-S, Le PH, Morton JJ, Somerset HL, Varella-Garcia M, **Tan AC**, Song JI, Bowles DW, Reyland ME, Jimeno A. (2018). Salivary gland cancer patient-derived xenografts enable characterization of cancer stem cells and new gene fusions associated with tumor progression. ***Clinical Cancer Research***. 24(12):2935-2943. [PMID: 29555661]

153. Pozdeyev N, Gay LM, Sokol E, Hartmaier R, Deaver KE, Davis S, French JD, Vanden Borre P, LaBarbera DV, **Tan AC**, Schweppe RE, Fishbain L, Ross JS, Haugan BR, Bowles DW. (2018). Genetic analysis of 779 advanced differentiated and anaplastic thyroid cancers. ***Clinical Cancer Research***. 24(13):3059-3068. [PMID: 29615459] 🏆 Highly Cited Paper

154. Pei S, Minhajuddin M, Adane B, Khan N, Stevens BM, Mack SC, Lai S, Rick JN, Inguva A, Shannon KM, Kim H, **Tan AC**, Myers JR, Ashton JM, Neff T, Pollyea DA, Smith CA, Jordan CT. (2018). AMPK/FIS1-mediated mitophagy is required for self-renewal of human AML stem cells. ***Cell Stem Cell***. 23(1):86-100. [PMID: 29910151]

    o [*Commented by: Schimmer AD. (2018). Mitochondrial shapeshifting impacts AML stemness and differentiation. Cell Stem Cell. 23(1):3-4*]

155. Parrish JK, McCann TS, Sechler M, Sobral LM, Ren WH, Jones KL, **Tan AC**, Jedlicka P. (2018). The Jumonji-domain histone demethylase inhibitor JIB-04 regulates oncogenic programs and increases DNA damage in Ewing Sarcoma, resulting in impaired cell proliferation and survival, and diminished tumor growth. ***Oncotarget***. 9(69): 33110-33123. [PMID: 30237855]

156. 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] [@Co-corresponding authors.] [***Cover Article***]

157. Karam SD, Reddy K, Blatchford PJ, Waxweiler T, DeLouize AM, Oweida A, Somerset H, Marshall C, Young C, Davies KD, Kane M, **Tan AC**, Wang XJ, Jimeno A, Aisner DL, Bowles DW, Raben D. (2018). Final Report of a Phase I Trial of Olaparib with Cetuximab and Radiation for Heavy Smoker Patients with Locally Advanced Head and Neck Cancer. ***Clinical Cancer Research***. 24(20):4949-4959. [PMID: 30084837]

158. Oweida A, Hararah MK, Phan A, Binder D, Bhatia S, Lennon S, Bukkapatnam S, Van Court B, Uyanga N, Darragh L, Kim H, Raben D, **Tan AC**, Heasley L, Clambey E, Nemenoff R, Karam SD. (2018). Resistance to radiotherapy and PD-L1 blockade is mediated by TIM-3 upregulation and regulatory T cell infiltration. ***Clinical Cancer Research***. 24(21): 5368-5380. [PMID: 30042205]

159. 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. [PMID: 30049789]

160. Davis SL, Eckhardt SG, Diamond JR, Messersmith WA, Dasari A, Weekes CD, Lieu CH, Kane M, **Tan AC**, Pitts TM, Leong S. (2018). A Phase I Dose-Escalation Study of Linsitinib (OSI-906), a Small-Molecule Dual Insulin-like Growth Factor-1 Receptor/Insulin Receptor Kinase Inhibitor, in Combination with Irinotecan in Patients with Advanced Cancer. *Oncologist*. 23(12):1409-e140. [PMID: 30139840]

161. Ravindran Menon D, Luo Y, Arcaroli JJ, Liu S, Kutty LK, Osborne DG, Li Y, Samson JM, Bagby S, **Tan AC**, Robinson WA, Messersmith WA, Fujita M. (2018). CDK1 interacts with Sox2 and promotes tumor initiation in human melanoma. *Cancer Research*. 78(23):6561-6574. [PMID: 30297536]

162. Yoo M, Shin J, Kim H, Kim J, Kang J, **Tan AC**. (2019). Exploring the molecular mechanisms of Traditional Chinese Medicine Components using Gene Expression Signatures and Connectivity Map. *Computer Methods and Programs in Biomedicine*. 174:33-40. [PMID: 29650251]

163. Rogers TJ, Christenson JL, Greene LI, O'Neill KI, Williams MM, Gordon MA, Nemkov T, D'Alessandro A, Degala GD, Shin J, **Tan AC**, Cittelly DM, Lambert JR, Richer JK. (2019). Reversal of Triple-negative Breast Cancer EMT by miR-200c Decreases Tryptophan Catabolism and a Program of Immune-Suppression. *Molecular Cancer Research*. 17(1):30-41. [PMID:30213797]

164. Landa I, Pozdeyev N, Korch C, Marlow LA, Smallridge RC, Copland JA, Henderson YC, Lai SY, Clayman GL, Onoda N, **Tan AC**, Garcia-Rendueles MER, Knauf JA, Haugen BR, Fagin JA, Schweppe RE. (2019). Comprehensive Genetic Characterization of Human Thyroid Cancer Cell Lines: A Validated Panel for Preclinical Studies. *Clinical Cancer Research*. 25(10):3141-3151. [PMID: 30737244]

165. Kessler B, Mishall K, Kellett M, Clark E, Pugazhenthi U, Pozdeyev N, Kim J, **Tan AC**, Schweppe R. (2019). 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*. 38(14):2565-2579. [PMID: 30531837]

166. Gan CP, Sam KK, Yee PS, Zainal NS, Lee BKB, Rahman ZAA, Patel V, **Tan AC**, Zain RB, Cheong SC. (2019). IFITM3 knockdown reduces the expression of CCND1 and CDK4 to suppress the growth of oral squamous cell carcinoma. *Cellular Oncology*. 42(4):477-490. [PMID: 30949979]

167. Aguado BA, Schuetze KB, Grim JC, Walker CJ, Cox AC, Ceccato TL, **Tan AC**, Sucharov CC, Leinwand LA, Taylor MRG, McKinsey TA, Anseth KS. (2019). Transcatheter aortic valve replacements alter circulating serum factors to mediate myofibroblast deactivation. *Science Translational Medicine*. 11(509):eaav3233. [PMID: 31511425]

168. Lee BKB, Cheong SC, **Tan AC**. (2019). Expanding the Connectivity Map Concept as the Functional Look-up Table for Systems Biology. *Advances in Molecular Pathology*. 2:201-213.

169. Brown P, RELISH Consortium (**Tan AC** et al), Zhou Y. (2019). Large expert-curated database for benchmarking document similarity detection in biomedical literature search. *Database*. 2019: baz085. [PMID: 33326193]

170. Samson JM*, Ravindran Menon D*, Smith DE*, Baird E, Kitano T, Gao D, **Tan AC**[@], Fujita M[@]. (2019). Clinical implications of ALDH1A1 and ALDH1A3 mRNA expression in melanoma subtypes. *Chemico-Biological Interactions*. 314:108822. [PMID: 31580832]. [[@]Co-corresponding authors.]

171. 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. (2019). First-in-class phosphorylated-p68 inhibitor RX-5902 inhibits ß-catenin signaling and demonstrates anti-tumor activity in triple-negative breast cancer. *Molecular Cancer Therapeutics*. 18(11): 1916-1925. [PMID: 31488700].

172. Hinz TK*, Kleczko EK*, Singleton KR, Calhoun J, Marek LA, Kim J, **Tan AC[@]**, Heasley LE[@]. (2019). Functional RNAi Screens Define Distinct Protein Kinase Vulnerabilities in EGFR-Dependent HNSCC Cell Lines. *Molecular Pharmacology*. 96(6): 862-870. [PMID: 31554698] [[@]Co-corresponding authors.]

173. Wilding CP*, Elms ML*, Judson I, **Tan AC**, Jones RL, Huang PH. (2019). The Landscape of Tyrosine Kinase Inhibitors in Sarcoma – looking beyond Pazopanib. *Expert Review of Anticancer Therapy*. 19(11): 971-991. [PMID: 31665941]

174. Jeon M*, Park D*, Lee J, Jeon H, Ko M, Kim S, Choi Y, **Tan AC**, Kang J. (2019). ReSimNet: Drug Response Similarity Prediction using Siamese Neural Networks. *Bioinformatics*. 35(24):5249-5256. [PMID: 31116384]

175. **Tan AC**, Huang PH. (2020). Translational Genomics for Rare Cancers: Challenges and Opportunity. *Seminars in Cancer Biology*. 61:iii-iv. [PMID: 32092353] [*Cover Article*]

176. Nassar KW, **Tan AC**. (2020). The Mutational Landscape of Mucosal Melanoma. *Seminars in Cancer Biology*. 61: 139-148.PMID: 31655118]

177. de la Iglesia JV, Slebos RJC, Martin-Gomez L, Wang X, Teer JK, **Tan AC**, Gerke TA, Aden-Buie G, Van Veen T, Masannat J, Chaudhary R, Song F, Fournier M, Siegel EM, Schabath MB, Wadsworth JT, Caudell JJ, Harrison LB, Wenig B, Conejo-Garcia JR, Hernandez-Prera JC, Chung CH. (2020). Effects of tobacco smoking on the tumor immune microenvironment in head and neck squamous cell carcinoma. *Clinical Cancer Research*. 26(6):1474-1485. [PMID: 31848186]

178. Keysar SB, Gomes N, Miller B, Jackson BC, Le PN, Morton JJ, Reisinger J, Chimed TS, Gomez KE, Nieto C, Frederick B, Pronk GJ, Somerset HL, **Tan AC**, Wang XJ, Raben D, Su TT, Jimeno A. (2020). Inhibiting translation elongation with SVC112 suppresses cancer stem cells and inhibits growth in head and neck squamous carcinoma. *Cancer Research*. 80(5): 1183-1198. [PMID: 31911553]

179. Schreiber AR, Kar A, Goodsped AE, Pozdeyev N, Somerset H, Raeburn CD, **Tan AC**, Leong S, Wierman MW, Kiseljak-Vassiliades K. (2020). Leptomeningeal Metastasis from Adrenocortical Carcinoma: A Case Report. *Journal of the Endocrine Society*. 4(3):bvaa017. [PMID:32154490]

180. Vander Velde R, Yoon N, Marusyk V, Durmaz A, Dhawan A, Miroshnychenko D, Lozano-Peral D, Desai B, Balynska O, Poleszhuk J, Kenian L, Teng M, Abazeed M, Mian O, **Tan AC**, Haura E, Scott J, Marusyk A. (2020). Resistance to Targeted Therapies as a Multifactorial, Gradual Adaptation to Inhibitor Specific Selective Pressures. *Nature Communications*. 11(1):2393. [PMID: 32409712]

181. Mukherjee N, Skees J, Todd KJ, West DA, Lambert KA, Robinson WA, Amato CM, Couts KL, Van Gulick R, MacBeth M, Nassar K, **Tan AC**, Zhai Z, Fujita M, Bagby SM, Dart CR, Lambert JR, Norris DA, Shellman YG. (2020). MCL1 inhibitors S63845/MIK665 plus Navitoclax synergistically kill difficult-to-treat melanoma cells. *Cell Death and Diseases*. 11(6):443. [PMID: 32513939]

182. Geng D, Ciavattone N, Lasola JJ, Shrestha R, Sanchez A, Guo J, Vlk A, Younis R, Wang L, Brown AJ, Zhang Y, Velasco-Gonzalez C, **Tan AC**, Davila E. (2020). Induction of IRAK-M in melanoma induces caspase-3 dependent apoptosis by reducing TRAF6 and calpastatin levels. *Communications Biology*. 3(1):306. [PMID: 32533049]

183. 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, Lopez KL, Gustafson DL, Messersmith WA, Leong S, Eckhardt SG, Pitts TM, Diamond JR. (2020). Preclinical and Dose-Finding Phase 1 Trial Results of Combined Treatment with a TORC1/2 Inhibitor (TAK-228) and Aurora A Kinase Inhibitor (Alisertib) in Solid Tumors. *Clinical Cancer Research*. 26(17):4633-4642. [PMID: 32499299] [ClinicalTrials.gov ID: NCT02719691]

184. Abbott JM, Zhou Q, Esquer H, Pike L, Broneske TP, Rinaldetti S, Abraham AD, Ramirez DA, Lunghofer PJ, Pitts TM, Regan DP, **Tan AC**, Gustafson DL, Messersmith WA, LaBarbera DV. (2020). First-in-Class Inhibitors of Oncogenic CHD1L With Preclinical Activity Against Colorectal Cancer. *Molecular Cancer Therapeutics*. 19(8):1598-1612. [PMID: 32499299]

185. Iwanaga R, Truong BT, Hsu JY, Lambert KA, Vyas R, Orlicky D, Shellman YG, **Tan AC**, Ceol C, Artinger KB. (2020). Loss of prdm1a accelerastes melanoma onset and progression. *Molecular Carcinogenesis*. 59(9):1052-1063. [PMID: 32562448]

186. Amato CM, Hintzsche JD, Wells K, Applegate A, Gorden NT, Vorwald VM, Tobin RP, Nassar K, Shellman YG, Kim J, Medina TM, Rioth 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*. 12(7):1943. [PMID: 32708981]

187. 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*. 15(9):1522-1534. [PMID: 32599072]

188. Chai AWY, Yee PS, Price S, Yee SM, Lee HM, Tiong VK, Gonçalves E, Behan FM, Bateson J, Gilbert J, **Tan AC**, McDermott U, Garnett MJ, Cheong SC. (2020). Genome-wide CRISPR screens of oral squamous cell carcinoma reveal fitness genes in the Hippo pathway. *Elife*. 9:e57761. [PMID: 32990596]

189. Lee WC, Reuben A, Hu X, McGarnahan 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, Witsuba 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 Biology*. 21(1):271. [PMID:33148332]

190. He T, Wildey G, McColl K, Savedelis A, Spainhower K, McColl C, Kresak A, **Tan AC**, Yang M, Abbas A, Dowlati A. (2021). Identification of RUNX1T1 as a potential epigenetic modifier in small cell lung cancer. *Molecular Oncology*. 15(1): 195-209. [PMID: 33084222]

191. Wahdan-Alaswad R, Edgerton SM, Salem H, Kim H, **Tan AC**, Finlay-Schultz J, Wellberg E, Sartorius CA, Jacobsen BM, Haugen BR, Liu B, Thor AD. (2021). Exogenous Thyroid Hormone is Associated with Shortened Survival and Upregulation of High-Risk Gene Expression Profiles in Steroid Receptor Positive Breast Cancers. *Clinical Cancer Research*. 27(2):585-597. [PMID: 33097494].

192. Chaudhary R, Slebos RJC, Song F, McCleary-Sharpe KP, Masannat J, **Tan AC**, Wang X, Amaladas N, Wu W, Hall GE, Conejo-Garcia JR, Hernanez-Prera JC, Chung CH. (2021). Effects of checkpoint kinase 1 inhibition by prexasertib on the tumor immune microenvironment of head and neck squamous cell carcinoma. *Molecular Carcinogenesis*. 60(2): 138-150. [PMID: 33378592]. [*Cover Article*]

193. Morton JJ, Alzofon N, Keysar SB, Chimed T-S, Reisinger J, Perrenoud L, Le PN, Nieto C, Gomez KE, Miller B, Yeager R, Gao D, **Tan AC**, Somerset H, Medina T, Wang XJ, Wang JH, Robinson W, Roop DR, Gonzalez R, Jimeno A. (2021). Studying immunotherapy resistance in a melanoma autologous humanized mouse xenograft. *Molecular Cancer Research*. 19(2):346-357. [PMID: 33087417]

194. Miroshnychenko D, Baratchart E, Ferrall-Fairbanks MC, Velde RV, Laurie MA, Bui MM, **Tan AC**, Altrock PM, Basanta D, Marusyk A. (2021). Spontaneous cell fusions as a mechanism of parasexual recombination in tumour cell populations. *Nature Ecology & Evolution*. 5(3):379-391. [PMID: 33462489] [*Cover Article*]

195. Tengesdal IW, Menon DR, Osborne DG, Neff CP, Powers NE, Gamboni F, Mauro AG, D'Alessandro A, Stefanoni D, Henen MA, Mills TS, De Graaf DM, Azam T, Vogeli B, Palmer BE, Pietras EM, DeGregori J, **Tan AC**, Joosten LAB, Fujita M, Dinarello CA, Marchetti C. (2021). Targeting tumor-derived NLRP3 reduces melanoma progression by limiting MDSCs expansion. ***Proceedings of the National Academy of Sciences USA***. 118(10):e2000915118. [PMID: 33649199]

196. Pollyea DA, Kim HM, Stevens BM, Lee FF, Harris C, Hedin BR, Knapp JR, O'Connor BP, Jordan CT, Pietras EM, **Tan AC**, Alper S. (2020). MDS-associated SF3B1 mutations enhance proinflammatory gene expression in patient blast cells. ***Journal of Leukocyte Biology***. 110(1):197-205. [PMID:33155727]

197. 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]

198. Schubert L, Le A, Estrada-Bernal A, Doak A, Yoo M, Ferrara S, Goodspeed A, Kimose F, Rix U, **Tan AC**, Doebele RC. (2021). Novel human-derived RET fusion NSCLC cell lines have heterogeneous responses to RET inhibitors and differential regulation of downstream signaling. ***Molecular Pharmacology***. 99(6):435-447. [PMID: 33795352]

199. Eschrich SA*, Teer JK*, Reisman P*, Siegel E, Challa C, Lewis P, Fellows K, Malpica E, Carvajal R, Gonzalez G, Cukras S, Montes MB, Aden-Buie G, Avedon M, Manning D, **Tan AC**, Fridley BL, Gerke T, Van Looveren M, Blake A, Greenman J, Rollison D. (2021). Enabling Precision Medicine in Cancer Care through a Molecular Data Warehouse: the Moffitt Experience. ***JCO Clinical Cancer Informatics***. 5:561-569. [PMID: 33989014]

ACCEPTED / IN PRESS / EPUB AHEAD OF PRINT

200. Xie M, Lee K, Lockhart JH, Cukras SD, Carvajal R, Beg AA, Flores ER, Teng M, Chung CH, **Tan AC.** (2021). TIMEx: tumor-immune microenvironment deconvolution web-portal for bulk transcriptomics using pan-cancer scRNA-seq signatures. ***Bioinformatics***. [Epub ahead of print, Apr 26, 2021][PMID: 33901274]

201. Xiong Z, Jeon M, Allaway RJ, Kang J, Park D, Lee J, Jeon H, Ko M, Jiang H, Zheng M, **Tan AC**, Guo X, The Multi-Targeting Drug DREAM Challenge Community, Dang KK, Tropsha A, Hecht C, Das TK, Carlson HA, Abagyan R, Guinney J, Schlessinger A, Cagan R. (2021). Crowdsourced identification of multi-target kinase inhibitors for RET- and TAU-based disease: the Multi-Targeting Drug DREAM Challenge. ***PLoS Computational Biology***. (Preprint available: Feb 17, 2021).

202. Nassar KW, Hintzsche JD, Bagby SM, Espinoza V, Langouët-Astrié C, Amato CM, Chimed TS, Fujita M, Robinson W, **Tan AC**[@], Schweppe RE[@]. (2021). Targeting CDK4/6 represents a therapeutic vulnerability in acquired BRAF/MEK inhibitor resistant melanoma. ***Molecular Cancer Therapeutics***. (Epub ahead of print, Aug 10, 2021). [PMID: 34376578] [[@]Co-corresponding authors.]

203. Lee K*, Lockhart JH*, Xie M, Chaudhary R, Slebos RJ, Flores ER, Chung CH, **Tan AC**. (2021). Deep Learning of Histopathology Images at the Single Cell Level. ***Frontiers in Artificial Intelligence***. (Accepted Aug 27, 2021)

D. PUBLISHED PEER REVIEWED ABSTRACTS (SELECTED)

1. Gilbert D, Viksna J, **Tan AC**, Wernisch L. (2001). Clustering proteins by fold patterns. In the *Conference Program of the International Conference on Intelligent Systems for Molecular Biology (ISMB 2001)*, Copenhagen, Denmark.

2. **Tan AC**, Gilbert D. (2002). Hierarchical Machine Learning for Characterising Protein Families. In *Currents in Computational Molecular Biology, RECOMB 2002*, L. Florea, B. Walenz, S. Hannenhali (editors), p.176-177. Washington DC.

3. **Tan AC**, Gilbert D. (2002). Hierarchical Machine Learning for Characterising Protein Families. In the *Conference Program of the International Conference on Intelligent Systems for Molecular Biology (ISMB 2002)*, p.76. Edmonton, Canada.

4. **Tan AC**, Gilbert D. (2002). Hierarchical Machine Learning and Knowledge Discovery in Characterising Protein Families. In the *Proceedings of the European Conference on Computational Biology (ECCB) 2002 in conjunction with German Conference on Bioinformatics (GCB) 2002*, Saarbrucken, Germany. T. Lengauer, H.-P. Lenhof, R. Christmann (editors), p.162. Saarbrucken, Germany

5. Al-Shahib A, **Tan AC**, Gilbert D. (2003). A rule-based approach for generating phylogenetic relationships between bacteria from the prediction of protein functional classes from sequence. Poster presented in the *Young Bioinformaticians Forum (YBF 2003)*. Oxford, United Kingdom.

6. **Tan AC**, Gilbert D, Deville Y. (2003). Multi-class protein fold classification using an integrative machine learning approach. In the *Conference Program of the International Conference on Intelligent Systems for Molecular Biology (ISMB 2003)*, p.67. Brisbane, Australia.

7. **Tan AC**, Al-Shahib A, Gilbert D, Deville Y. (2003). Learning sets of positive rules of amino acid properties to classify protein functional classes. In the *Proceedings of the European Conference on Computational Biology (ECCB) 2003 in conjunction with JOBIM 2003*, Paris, France. C. Christophe, H.-P. Lenhof and M.-F. Sagot (editors), pp.241-242. ISBN: 2-7261-1257. Paris, France.

8. Al-Shahib A, **Tan AC**, Gilbert D. (2003). A rule-based approach for generating phylogenetic relationships between bacterial protein functional classes from taxonomical and sequence information. In the *Proceedings of the European Conference on Computational Biology (ECCB) in conjunction with JOBIM 2003*, Paris, France. C. Christophe, H.-P. Lenhof and M.-F. Sagot (editors), pp.237-238. ISBN: 2-7261-1257. Paris, France.

9. Lennon AM, Stuart D, **Tan AC**, Sheahan KS, O'Donoghue DP, Brown B. (2003). Ovarian and colon cell lines can be differentiated using SELDI-MS protein profiling. *Presented in the Irish Society of Gastroenterology Winter Meeting 2003*, Dublin, Ireland.

10. Lennon AM, Stuart D, **Tan AC**, Fox E, Sheahan KS, Hyland JM, O'Donoghue DP, Brown B. (2003). SELDI-MS protein profiling can differentiate tumour from normal colorectal tissue. *Presented in the Irish Society of Gastroenterology Winter Meeting 2003*, Dublin, Ireland.

11. Al-Shahib A, **Tan AC**, Gilbert D. (2003). A rule-based approach for generating phylogenetic relationships between bacteria from the prediction of protein functional classes from sequence. *Presented in the MGMS Young Modellers' Forum in Conjunction with the Royal Society of Chemistry Molecular Modeling Group*. London, United Kingdom.

12. Lennon AM, Stuart D, **Tan AC**, Sheahan KS, O'Donoghue DP, Brown B. (2004). Ovarian and colon cell lines can be differentiated using SELDI-MS protein profiling. *GUT* 53 (Suppl. 3): a67 (Abstract 261). *Presented in the 2004 Annual Meeting of the British Society of Gastroenterology*, Scottish Exhibition and Conference Centre, Glasgow, United Kingdom.

13. Lennon AM, Stuart D, **Tan AC**, Fox E, Sheahan KS, Hyland JM, O'Donoghue DP, Brown B. (2004). SELDI-MS protein profiling can differentiate tumour from normal colorectal tissue. *GUT* 53 (Suppl. 3): a68 (Abstract 265). *Presented in the 2004 Annual Meeting of the British Society of Gastroenterology*, Scottish Exhibition and Conference Centre, Glasgow, United Kingdom.

14. Lennon AM, **Tan AC**, Gleeson F, Brannigan A, Lennon JR, O'Sullivan J, White A, Keegan D, Mulcahy H, Hyland JM, Sheahan K, O'Donoghue DP, Brown R. (2005). Proteomics: A new tool for screening for colon cancer? *GUT* 54 (Suppl. 2): a20 (Abstract 072). *Presented in the 2005 Annual Meeting of the British Society of Gastroenterology*, International Convention Centre, Birmingham, United Kingdom.

15. **Tan AC**, Naiman DQ, Winslow RL, Geman, D. (2005). Simple decision rules for classifying human cancers from gene expression profiles. *Presented in International Conference on Intelligent Systems for Molecular Biology (ISMB 2005)*, Detroit, MI.

16. Xu L, **Tan AC**, Naiman DQ, Geman D, Winslow RL. (2005). Robust prostate cancer marker genes emerge from direct integration of inter-study microarray data. *Presented in International Conference on Intelligent Systems for Molecular Biology (ISMB 2005)*, Detroit, MI.

17. Jimeno A, **Tan AC**, Coffa J, NV Rajeshkumar, Kulesza P, Rubio-Viqueira B, Wheelhouse J, Diosdado B, Messersmith WA, Iacobuzio-Donahue C, Maitra A, Varella-Garcia M, Hirsch FR, Meijer GA, Hidalgo M. (2007). Coordinated over-expression of genes in the EGFR pathway predicts sensitivity to EGFR inhibition in pancreatic cancer. *Presented in AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics*, San Francisco, CA.

18. Jimeno A, Wheelhouse J, Chan F, Chan A, Solomon A, **Tan AC**, NV Rajeshkumar, Hidalgo M. (2008). A gene expression-based approach to devise combinations with gemcitabine (GEM) in pancreatic cancer (PC) identifies polo-like kinase 1 (Plk1) as a rational target. *Presented in 99th American Association for Cancer Research Annual Meeting 2008*, San Diego, CA. (Mini-symposium).

19. **Tan AC**, Jimeno A, Rubio-Viqueira B, Hidalgo M. (2008). Identifying gemcitabine signature in pancreatic cancer for personalized medicine. *Presented in the 99th American Association for Cancer Research Annual Meeting 2008*, San Diego, CA.

20. Rudek MA, Khan Y, Goldsweig H, Donehower RC, Jimeno A, Shah P, **Tan AC**, Linden S, Hidalgo M, Laheru DA. (2008). Integrated development of S-Trans,Trans-Farnesylthiosalicyclic Acid (FTS,Salisarib) in pancreatic cancer. *Presented in American Society of Clinical Oncology Annual Meeting 2008*, Chicago, IL.

21. **Tan AC**, Jimeno A, Rubio-Viqueira B, Hidalgo M. (2008). NCI-60 Gene Set Connectivity Map (GS-CMAP): connecting pathway-based gene expression profiles for therapeutic efficacy determination. *Presented in American Society of Clinical Oncology Annual Meeting 2008*, Chicago, IL.

22. Villarroel MC, **Tan AC**, Garrido-Laguna I, Rubio-Viqueira B, NV RajeshKumar, Jimeno A, Hidalgo M. (2008). Developing a novel method for predicting tumor responses to drug combination based on pathway expression signatures. *Presented in the 3rd American Association for Cancer Research Molecular Diagnostics Meeting*, Philadelphia, PA.

23. Garrido-Laguna I, **Tan AC**, Villarroel MC, NV Rajeshkumar, Rubio-Viqueira B, Gray L, Hidalgo M. (2008). Activity of the T-type calcium channel antagonist Mibefradil in pancreatic cancer xenografts. *Presented in the 3rd American Association for Cancer Research Molecular Diagnostics Meeting*, Philadelphia, PA.

24. NV Rajeshkumar, **Tan AC**, Wheelhouse J, Jimeno A, Messersmith WA, Green TP, Hidalgo, M. (2008). Prediction and in vivo validation of AZD0530 sensitivity by gene expression profiling in human pancreatic tumor xenografts. *Presented in the 20th EORTC-NCI-AACR Symposium on Molecular Targets and Cancer Therapeutics*, Geneva, Switzerland.

25. **Tan AC**, Anderson R, Frederick B, Raben D, Jimeno A. (2009). Pathway-based comparison approach for the identification of responders to the mitotic modulator ON 01910.Na in head and neck cancer (HNC). *Presented in the 100th American Association for Cancer Research Annual Meeting 2009*, Denver, CO.

26. Garrido-Laguna I, **Tan AC**, Villarroel MC, Angenendt M, Pastori W, NV Rajeshkumar, Jimeno A, Ciomei M, Rubio-Viqueira B, Hidalgo M. (2009). Activity of PHA-848125 in pancreatic cancer xenografts is related to downregulation of S6 via p53 pathway. *Presented in the 100th American Association for Cancer Research Annual Meeting 2009*, Denver, CO.

27. Villarroel MC, **Tan AC**, Garrido-Laguna I, Rubio-Viqueira B, De Oliveira E, NV RajeshKumar, Jimeno A, Hidalgo M. (2009). Orthotopic cancer models are better predictors of clinical response than s.c.

models. *Presented in the* 100th *American Association for Cancer Research Annual Meeting 2009*, Denver, CO.

28. Kono SA, **Tan AC**, Bunn PA, Davies A, Doebele RC, Oton AB, Hirsch FR, Varalle-Garcia M, Franklin W, Camidge DR. (2009). Increased EGFR gene copy number is variably associated with both EGFR and KRAS mutation (Mt) status and influences Progression Free Survival (PFS) to first line chemotherapy in EGFR/KRAS wildtype (WT) patients. *Presented in the 2009 EORTC-NCI-ASCO Annual Meeting on Molecular Markers in Cancer*, Brussels, Belgium.

29. Chen C-S, **Tan AC**, Kim KS, Zhu, H. (2009). Fabrication of an E. coli Proteome Chip and its Application on Surveying Infant to Adult Human Immune Response to Commensal Microorganisms. *Presented in the 10th International Conference on Systems Biology (ICSB 2009)*, Stanford, CA.

30. Kim J[+], Henry C, DeGregori J, **Tan AC.** (2009). Genome-wide survey of age-related gene expression patterns relative to binding sites for the global regulator of chromatin CTCF. *Presented in the 12*[th] *International Microarray Gene Expression Databases (MGED) Meeting*, Phoenix, AZ.

31. Tentler JJ, Nallapareddy S, **Tan AC**, Spreafico A, Flanigan SA, Pitts TM, Eckhradt SG. (2009). Members of the noncanonical WNT pathway confer resistance to the MEK 1/2 inhibitor AZD6244 in colorectal cancer cell lines. *Presented in the 2009 AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics*, Boston, MA.

32. Pitts TM, **Tan AC**, Kulikowski GK, Tentler JJ, Flanigan SA, Leong S, Brown A, Coldren CD, Varella-Garcia M, Hirsch FR, Eckhardt SG. (2009). Development and valiation of an integrated genomic classifier to predict sensitivity to the IGF-1R/IR tyrosine kinase inhibitor, OSI-906, in colorectal cancer. *Presented in the 2009 AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics*, Boston, MA.

33. Spreafico A, **Tan AC**, Tentler JJ, Nallapareddy S, Pitts TM, Eckhardt SG. (2009). MicroRNA expression patterns as potential biomarkers of responsiveness to the MEK 1/2 inhibitor, AZD6244, in colorectal cancer cell lines. *Presented in the 2009 AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics*, Boston, MA.

34. Flaginan SA, Pitts TM, Kulikowski GN, **Tan AC**, Nallapareddy S, Tentler JJ, Eckhardt SG, Leong S. (2009). Rational combination of the IGF-1R/IR tyrosine kinase inhibitor (TKI), OSI-906, with the MEK inhibitor, U0126, results in synergistic and apoptotic effects in human colorectal cancer (CRC) cell lines. *Presented in the 2009 AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics*, Boston, MA.

35. Kulikowski GN, Pitts TM, **Tan AC**, Tentler JJ, Britt BC, Britt BW, Murray BW, Carley W, Smeal T, Guo C, Eckhardt SG. (2009). Characterization of in vitro activity and predictive biomarkers of the novel p21-activated kinase 4 (PAK4) inhibitor, PF-3758309, in colorectal cancer cell lines. *Presented in the 2009 AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics*, Boston, MA.

36. **Tan AC**, Tentler JJ, Ryugazova N, Kachaeva MI, Pitts TM, Eckhardt SG. (2009). Identification of candidate microRNAs that correlate with sensitivity of the IGF-1R/IR inhibitor, OSI-906, in colorectal cancer (CRC) cell lines. *Presented in the 2009 AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics*, Boston, MA.

37. Xiong Y, Li Z, **Tan AC**, Bemis J, Xie X, Bunting KD, Chen J, Bemis L, Tse W. (2009). The AML prognostic marker, AF1q, is directly regulated by MiR-29b. *Presented in the 51*[st] *American Society of Hematology Annual Meeting,* New Orleans, LA.

38. Nallapareddy S, Arcaroli JJ, Touban B, **Tan AC**, Foster NR, Erlichman C, Wright JJ, Picus J, Hidalgo M, Messersmith WA. (2010). A phase II trial of saracatinib (AZD0530), an oral Src inhibitor, in previously treated metastatic pancreatic cancer. *Presented in the 2010 Gastrointestinal Cancers Symposium,* Orlando, FL.

39. Repine JJ, **Tan AC,** Beehler CJ, Crader K, Elkins ND, Vina J, Wilson P, Queensland K, Wischmeyer P, Eaton J, Repine JE. (2010). Unique rat strain survives breathing pure oxygen, exercises and lives longer: possible role for heat-shock proteins and reduced inflammation. *Journal of Investigative Medicine* 58(1): 233. Meeting Abstract: 454.

40. Varella-Garcia M, Flacco A, Cho Y.G, **Tan A.C,** Kono S, Franklin W, Cappuzzo F, Doebele R, Camidge DR. (2010). Lack of intra-tumoral heterogeneity in lung adenocarcinoma supports gene fusions involving ALK as early clonal events. *Presented in the 101st American Association for Cancer Research Annual Meeting 2010*, Washington, DC.

41. Phang TL, Kim H, Kim J[+], Gao D, Tong T, Selby H^{+}, **Tan AC**. (2010). An Analysis Workflow for Loss-of-function RNA Interference Whol-Genome Screening using the Next Generation Sequencing Technology. *Presented* in the 53rd Annual Meeting Thomas L. Petty Aspen Lung Conference, Aspen, CO.

42. Kim J[+], Kim H, Gao D, Gregory M, Selby H^{+}, Tong T, Phang TL, DeGregori J, **Tan AC**. (2010). Computational Analysis of Genome-wide Synthetic Lethal Screen with a tyrosine kinase inhibitor in Leukemia cell using BiNGS!SL-seq. *Presented in the 18th Annual Meeting of the International Society for Computational Biology (ISCB) (ISMB 2010)*, Boston, MA.

43. Kim H, Kim J[+], Phang TL, Gao D, Tong T, Selby H^{+}, Zhang Q, Wang XJ, Bentley D, **Tan AC.** (2010). A Case Study for Genome-wide Smad4 Binding Sites Using BiNGS!ChIP-seq. *Presented in the 18th Annual Meeting of the International Society for Computational Biology (ISCB) (ISMB 2010)*, Boston, MA.

44. Gao D, Kim J[+], Kim H, Selby H^{+}, Phang TL, **Tan AC**, Tong T. (2010). Comparative Statistical Analysis on Identifying Differentially Expressed Reads in Next Generation Sequencing Data. *Presented in the 18th Annual Meeting of the International Society for Computational Biology (ISCB) (ISMB 2010)*, Boston, MA.

45. Phang TL, Kim H, Kim J[+], Gao D, Tong T, Selby H^{+}, **Tan AC**. (2010). BiNGS!SL-Seq: A Computational Analysis Workflow for Whole-Genome RNA Interference Screening Using the Next Generation Sequencing Technology. *Presented in the 18th Annual Meeting of the International Society for Computational Biology (ISCB) (ISMB 2010)*, Boston, MA.

46. Selby HM[+], Kim J[+], Tentler JJ, Diamond JR, Pitts TM, Leong S, Jimeno A, Messersmith WA, Eckhardt SG, **Tan AC**. (2010). A Systems Biology Strategy to Accelerate the Development of Predictive Biomarkers for Novel Anti-cancer Agents. *Presented in the 18th Annual Meeting of the International Society for Computational Biology (ISCB) (ISMB 2010)*, Boston, MA.

47. Jones LK, **Tan AC**, Zou F, Kheifets A, Rybnikov K, Berry D. (2010). Confident Predictability: A Statistical Tool for Identifying Patients for which a Machine Learning Algorithm provides a Reliable. *Presented in the 18th Annual Meeting of the International Society for Computational Biology (ISCB) (ISMB 2010)*, Boston, MA.

48. Fretwell DL, Knox AJ, Xu M, Wierman ME, Lillehei KO, Kleinschmidt-DeMasters BK, **Tan AC**, Kerr JM. (2010). MicroRNA-200c Is Downregulated in Sparsely-Granulated Growth Hormone Pituitary Tumors and Regulates ZEB1 Expression in GH-Derived Cells. *Endocrine Reviews, Supplement 1, June 2010, 31[3]: S287. Presented in The Endocrine Society 92nd Annual Meeting (ENDO 2010),* San Diego, CA.

49. Powell RW, Messersmith WA, Garcia M, **Tan AC**, Touban B, Pitts TM, Dasari A, Arcaroli JJ. (2010). The combination of PF03084014 (a γ-secretase inhibitor) and Irinotecan reduces ALDH+ tumor-initiating cells and recurrence in tumors with elevated notch pathway. Presented in the AACR Special Conference: Colorectal Cancer: Biology to Therapy, Philadelphia, PA.

50. Keysar S, Anderson R, Takimoto S, **Tan AC**, Deyneko I, McGovern K, Ross RW, Song J, Jimeno A. (2010). Combined hedgehog and epidermal growth factor receptor (EGFR) inhibition in a direct patient tumor model (DPTM) of head and neck squamous cell cancer (HNSCC). *Journal Clinical Oncology 28:15s, 2010 (suppl; abstr 5558). Presented in the 2010 American Society of Clinical Oncology Annual Meeting*. Chicago, IL.

51. Spreafico A, Tentler JJ, **Tan AC**, Pitts TM, Kachaeva MI, Selby HM[+], Eckhardt SG. (2011). Evaluation of antiproliferative and apoptotic effects of the rational combination of the MEK1/2 inhibitor selumetinib (AZD6244) and inhibitors of the hedgehog pathway in colorectal cancer (CRC) cell lines. *Journal Clinical Oncology* 29: 2011 (suppl 4; abstr 422). *Presented in the 2011 Gastrointestinal Cancers Symposium*. San Francisco, CA.

52. Im E, Pitts TM, Kulikowski G, **Tan AC**, Tentler JJ, Murray B, Carley W, Smeal T, Guo C, Eckhardt SG. (2011). Contribution of the epithelial-mesenchymal (EMT) phenotype to the sensitivity of colorectal cancer cell lines to the p21-activated kinase inhibitor, PF-3758309. *Journal Clinical Oncology*: 2011 (suppl 4; abstr 438). *Presented in the 2011 Gastrointestinal Cancers Symposium*. San Francisco, CA.

53. Powell RW, **Tan AC**, Varella-Garcia M, Touban B, Dasari A, Puls L, Pitts TM, Kulikowski G, Quackenbush K, Messersmith WA, Arcaroli JJ. (2011). Biomarkers of sensitivity to PF-03084014, a γ-secretase Inhibitor, in a preclinical model of colorectal cancer. *Presented in the 102nd American Association for Cancer Research Annual Meeting 2011*, Orlando, FL.

54. Dasari A, Powell RW, Puls L, Quackenbush K, **Tan AC**, Messersmith WA, Boylan J, Arcaroli JJ. (2011). Biomarkers for sensitivity to gamma secretase inhibitors in mouse models of pancreatic adenocarcinoma. *Presented in the 102nd American Association for Cancer Research Annual Meeting 2011*, Orlando, FL.

55. Eckhardt SG, Messersmith WA, Pitts TM, Tentler JJ, Leong S, Arcaroli JJ, **Tan AC** (2011). Development and Integration of Predictive Biomarkers in Early Clinical Trials of Novel Agents for Colorectal Cancer. In: *Proceedings of the National Cancer Institute Translational Science Meeting 2011, Abstract 61*. Washington, DC.

56. Micel LN, Selby HM[+], Tentler JJ, Brunkow KL, **Tan AC**, Pitts TM, Eckhardt SG (2011). Antitumor efficacy of the investigational MEK inhibitor, TAK-733, against melanoma cell lines and human-derived tumor explant models. In: *Proceedings of the 2011 AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics; 2011 Nov 12-16; San Francisco, CA. Philadelphia (PA): AACR; Mol Cancer Ther 2011;10(11 Suppl): Abstract C182*. San Francisco, CA.

57. Tentler JJ, Micel LN, Selby HM[+], **Tan AC**, Brunkow KL, Pitts TM, Blakemore S, Smith PG, Eckhardt SG. (2011). Molecular determinants of response to the investigational small molecule inhibitor of Nedd8-activating enzyme (NAE), MLN4924, in melanoma cell lines and patient-derived tumor explant models. In: *Proceedings of the 2011 AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics; 2011 Nov 12-16; San Francisco, CA. Philadelphia (PA): AACR; Mol Cancer Ther 2011;10(11 Suppl): Abstract B178*. San Francisco, CA.

58. McPhillips KL, Pitts TM, Im EK, Spreafico A, **Tan AC**, Tentler JJ, Arcaroli JJ, Pierce EL, Murray BW, Eckhardt SG (2011). Synergistic anti-proliferative effects of the P21-activated kinase (PAK) inhibitor, PF-03758309 and standard of care agents in colorectal cancer models. In: *Proceedings of the 2011 AACR-NCI-EORTC International Conference on Molecular Targets and Cancer Therapeutics; 2011 Nov 12-16; San Francisco, CA. Philadelphia (PA): AACR; Mol Cancer Ther 2011;10(11 Suppl): Abstract B245*. San Francisco, CA.

59. Kim J[+], Cano C[+], **Tan AC.** (2011). PathCMap: Development of pathway signature system for identifying druggable partners of synthetic lethal genes in cancer. *Presented in the 9th Annual Rocky Mountain Bioinformatics Conference*, Aspen/Snowmass, CO.

60. Astling DP[+], Chan T[+], Kim J[+], **Tan AC.** (2011). Opportunities and Challenges Associated with Computational RNAseq Data Analysis. *Presented in the 9th Annual Rocky Mountain Bioinformatics Conference*, Aspen/Snowmass, CO.

61. Porter CC, Kim J[+], Fosmire S, Gearheart CM[+], van Linden A, Zaberezhnyy V, Gao D, **Tan AC**, DeGregori J. (2011). 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.

62. Micel L, Selby H, Tentler J, Brunkow K, Tan AC, Pitts T, Eckhardt SG. (2012). Antitumor efficacy of the investigational MEK inhibitor, TAK-733, against melanoma cell lines and human-derived tumor explant models. Presented in the (Pediatric Blood & Cancer, 2012; 58(7):1077).

63. Pilling AB, Le AT, **Tan AC**, Kim J[+], Singleton KR, Heasley LE, Helfrich B, DeGregori J, Doebele RC. (2012). 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.

64. Bradshaw-Pierce EL, Pitts TM, McPhillips K, Gustafson DL, **Tan AC**, Nguyen L, West M, Fisher T, Murray BW, Eckhardt SG. (2012). Tumor P-glycoprotein Correlates with Efficacy of PF-03758309 Against In Vitro and In Vivo models of Colorectal Cancer. *Presented in the American Association for Cancer Research Special Conference on Molecularly Targeted Therapies: Mechanisms of Drug Resistance*, San Francisco, CA.

65. **Tan AC**, Britt BW[+], Astling DP[+], Leong S, Lieu C, Tentler JJ, Pitts TM, Arcaroli JJ, Messersmith WA, Eckhardt SG. (2012). Validation of Preclinical Colorectal Cancer Models Against TCGA Data for Pathway Analysis and Predictive Biomarker Discovery. *Presented in the EORTC-NCI-AACR Symposium on Molecular Targets and Cancer Therapeutics*, Dublin, Ireland. *(European Journal of Cancer, 2012; 48(Suppl 6):50-51)*.

66. Pitts TM, McPhillips KL, Selby HM[+], Spreafico A, Bagby SM, Britt BC, **Tan AC**, Tentler JJ, Ecsedy JA, Eckhardt SG. (2012). In Vitro and in Vivo Antitumor Activity of the Investigational Aurora a Selective Kinase Inhibitor MLN8237 Alone and in Combination with Standard Agents Against CRC Models. *Presented in the EORTC-NCI-AACR Symposium on Molecular Targets and Cancer Therapeutics*, Dublin, Ireland. *(European Journal of Cancer, 2012; 48(Suppl 6):78)*.

67. Tentler JJ, Bagby SM, **Tan AC**, Pitts TM, Selby HM[+], McPhillips KL, Eckhardt SG, Leong S. (2012). Molecular Markers of Sensitivity to the Aurora and Angiogenic Kinase Inhibitor ENMD-2076 in Human Colorectal Cancer (CRC) Models. *Presented in the EORTC-NCI-AACR Symposium on Molecular Targets and Cancer Therapeutics*, Dublin, Ireland. *(European Journal of Cancer, 2012; 48(Suppl 6):78)*.

68. Lieu CH, Tentler JJ, **Tan AC**, Pitts TM, Spreafico A, Selby HM[+], McPhillips KL, Bagby SM, Eckhardt SG. (2012). TAK-733, an Investigational Novel MEK Inhibitor, Suppresses Colorectal Cancer (CRC) Tumor Growth in Biomarker Positive Patient-derived Human Tumor Explants. *Presented in the EORTC-NCI-AACR Symposium on Molecular Targets and Cancer Therapeutics*, Dublin, Ireland. *(European Journal of Cancer, 2012; 48(Suppl 6):119-120)*.

69. Pitts TM, McPhillips KL, Selby HM[+], Spreafico A, Bagby SM, Britt BC, Tentler JJ, **Tan AC**, Kuida K, Eckhardt SG. (2012). Antitumor Activity of the Polo-like Kinase (PLK) Inhibitor, TAK-960, Alone and in Combination with Standard Agents Against KRAS WT and MT Colorectal Cancer (CRC) Models. *Presented in the EORTC-NCI-AACR Symposium on Molecular Targets and Cancer Therapeutics*, Dublin, Ireland. *(European Journal of Cancer, 2012; 48(Suppl 6):50-51)*.

70. Spreafico A, Klauck PJ[+], Tentler JJ, Pitts TM, **Tan AC**, Kim J[+], Gregory MA, McManus MC, Arcaroli JJ. (2012). Targeting the MAP Kinase and Wnt Signaling Pathways in Preclinical Models of Colorectal Cancer. *Presented in the EORTC-NCI-AACR Symposium on Molecular Targets and Cancer Therapeutics*, Dublin, Ireland. *(European Journal of Cancer, 2012; 48(Suppl 6):150)*.

71. Gregory MA, **Tan AC**, Kim J[+], DeGregori J. (2012). RNAi Screen Identifies ATM-directed Metabolic Pathway as Synthetic Lethal with FLT3 Inhibition in AML. *Presented in the EORTC-NCI-AACR Symposium on Molecular Targets and Cancer Therapeutics*, Dublin, Ireland. *(European Journal of Cancer, 2012; 48(Suppl 6):50-51)*.

72. Diamond JR, **Tan AC**, Pitts TM, van Bokhoven A, Aisner D, Elias AD, Borges VF, Miller KD, Eckhardt SG, Tentler JJ. (2013). A Phase II Clinical Trial of ENMD-2076 in Metastatic Triple-Negative Breast Cancer: Translating a p53-based Biomarker grom Bench to Bedside. *Presented in the 11th*

International Congress on Targeted Anticancer Therapies (TAT 2013), Paris, France. *(Annals of Oncology, 2013; 24(suppl_1):i36).*

73. Wang CA, Jedlicka P, Zaberezhnyy V, **Tan AC**, Ford H. (2013). Novel functions of the homeoprotein SIX2 in mediating anchorage independence and metastasis in breast cancer. *Presented in the AACR 104th Annual Meeting 2013,* Washington, DC. (*Cancer Research, 2013; 73(8 Supplement): 2705*).

74. Schlegel J, Sambade M, Sather S, Moschos S, **Tan AC**, Winges A, DeRyckere D, Carson CC, Trembath DG, Tentler JJ, Eckhardt SG, Kuan PF, Hamilton RL, Duncan LM, Miller CR, Nikolaishvili-Feinberg N, Midkiff BR, Wang X, Liu J, Zhang W, Yang C, Frye SV, Earp HS, Shields J, Graham DK. (2013). Mer receptor tyrosine kinase is a novel therapeutic target in melanoma. *Presented in the AACR 104th Annual Meeting 2013,* Washington, DC. (*Cancer Research, 2013; 73(8 Supplement): 3037*).

75. Wang CA, Jedlicka P, **Tan AC**, Pham C, Zaberezhnyy V, Ford H. (2013). The Six2 homeoprotein mediates breast cancer metastasis via repressing E-cadherin. *Presented in the AACR Special Conference on Advances in Breast Cancer Research: Genetics, Biology, and Clinical Applications,* San Diego, CA. (*Molecular Cancer Research, 2013; 11(10 Supplement): PR04*).

76. Ionkina AA, Tentler JJ, Newton TP, Brunkow KL, Johnson JS, **Tan AC**, Pitts TM, Eckhardt SG, Diamond JR. (2013). The role of p53 family tumor suppressors in mediating response to the Aurora and angiogenic kinase inhibitor ENMD-2076 in triple-negative breast cancer. *Presented in the AACR-NCI-EORTC International Conference: Molecular Targets and Cancer Therapeutics*, Boston, MA. (*Molecular Cancer Therapeutics, 2013; 12(11 Supplement); A286*).

77. Dimberg LY, Cabrera J, Menke C, Kim J[+], Porter CC, **Tan AC**, Behbakht K, Thorburn A, Ford HL. (2013). Use of a genome-wide loss-of-function screen to identify novel mechanisms of resistance to TRAIL induced apoptosis. *Presented in the AACR-NCI-EORTC International Conference: Molecular Targets and Cancer Therapeutics*, Boston, MA. (*Molecular Cancer Therapeutics, 2013; 12(11 Supplement); B115*).

78. Diamond JR, Tan AC, Ionkina AA, Newton TP, Pitts TM, Eckhardt SG, Tentler JJ. (2013). The role of p53 family tumor suppressors in mediating response to aurora kinase inhibition in triple-negative breast cancer. *Presented in the San Antonio Breast Cancer Symposium*, San Antonio, TX. (*Cancer Research, 2013; 73(24 Supplement);P2-09-06*).

79. Golan T, Eckhardt SG, Stossel C, Atias D, Wang G[+], Pitts TM, Aisner D, Weekes CD, Berger R, **Tan AC**. (2014). RNA-seq and KRAS mutational status in ascitic pancreatic cancer cells: Novel results and distinct subsets. *Presented in the 50th ASCO Annual Meeting,* Chicago, IL. (*Journal of Clinical Oncology, 2014; 32(15_suppl):e15214*).

80. Beadnell TC, Mishall KM, Zhou Q, Strait AA, Corpuz ML, Kim J[+], Wang G[+], **Tan AC**, Schweppe RE. (2014). Elucidating Mechanisms of Resistance to Src Inhibition in Thyroid Cancer. *Presented in the Endocrine Society's 96th Annual Meeting and Expo*, Chicago, IL. (*Endocrine Reviews, 2014; 35(4 Supplement): OR39-5*).

81. Wong K, **Tan AC**, Pitts T, Klauck P[+], Earp S, Frye S, Wang X, Graham DK, Eckhardt SG. (2014). MER as a novel therapeutic target in colorectal cancer. *Presented in the 6th EORTC – NCI – AACR Symposium on Molecular Targets and Cancer Therapeutics*, Barcelona, Spain. (*European Journal of Cancer, 2014; 50(Suppl 6):120-121*).

82. **Tan AC**, Kim J[+], Yoo M[+], Kang J. (2014). K-Map: Connecting Kinases with Therapeutics for Drug Repurposing and Development. *Presented in the 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Boston, MA.

83. Wang G[+], **Tan AC**, Jimeno A. (2014). Human Tumor Model-based Databank Shared Resources. *Presented in the 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Boston, MA.

84. Pozdeyev N, Zhou Q, Pike LA, Tan AC, Morrison JA, Schweppe RE, Haugen BR. (2015). Thyroid Cancer Cell Lines Gene Expression Analysis. *Presented in the Endocrine Society's 97th Annual Meeting and Expo*, San Diego, CA. (*Endocrine Reviews, 2015; 36(4 Supplement): LBF-002*).

85. Pitts TM, Kim J+, **Tan AC**, You YN, Eng C, Eckhardt SG, Lieu CH. (2015). Emerging transcriptional landscape and putative therapeutic strategies in young patients with metastatic colorectal cancer (CRC). *Presented in the 51st ASCO Annual Meeting,* Chicago, IL. (*Journal of Clinical Oncology, 2015; 33(15_suppl):e14627*).

86. Fadlullah MZH, Chiang IKN, Dionne KR, Yee PS, Gan CP, Sam KK, Molinolo A, Tiong V, Ng A, Hamid S, Martin D, Lim KP, Kallarakkal G, Mustafa WMW, Abraham MT, Zain RB, Rahman ZAA, Patel V, Gutkind JS, **Tan AC**, Cheong SC. (2015). Molecular Profiling of Oral Squamous Cell Carcinoma Model Reveals Clinically Relevant Genetic Signatures for the Identification of Novel Therapies. *Presented in the 5th World Congress of the International Academy of Oral Oncology (IAOO)*, Sao Paulo, Brazil. (*Head & Neck, 2015; 37: E59*).

87. Helfrich B, Kim J+, Gao D, Chan D, **Tan AC**, Bunn Jr PA. (2015). The Aurora Kinase B Inhibitor AZD1152-HQPA Inhibitor in Small Cell Lung Cancer (SCLC). *Presented in the 16th World Conference on Lung Cancer (WCLC)*, Denver, CO. (*Journal of Thoracic Oncology, 2015;10(9):S363*).

88. Nelson S, Schubert L, Le AT, Ryall KA+, Kako S, **Tan AC**, Varella-Garcia M, Doebele RC. (2015). Adaptor Re-Programming and Acquired Resistance in RET-Fusion Positive NSCLC. *Presented in the 16th World Conference on Lung Cancer (WCLC)*, Denver, CO. (*Journal of Thoracic Oncology, 2015;10(9):S296*).

89. Nakachi I, Stearman RS, Edwards M, Franklin WA, Rice JL, **Tan AC**, Kim J+, Yoo M+, Fujisawa A, Betsuyaku T, Soejima K, Miller YE, Geraci MW. (2015). Subtraction of Allelic Fractions (Delta-theta): A Sensitive Metric to Detect Chromosomal Alterations in Heterogeneous Premalignant Specimens. *Presented in the IASLC 16th World Conference on Lung Cancer (WCLC)*, Denver, CO. (*Journal of Thoracic Oncology, 2015;10(9):S347*).

90. Kim J+, Foster D, Mishra R, Kern J, **Tan AC**, Finigan JH. (2015). Kinome RNAi Screens Identify Essential Genes and Therapeutics In'Driver Negative'Non-Small Cell Lung Cancer. *Presented in the 16th World Conference on Lung Cancer (WCLC)*, Denver, CO. (*Journal of Thoracic Oncology, 2015;10(9):S593*).

91. Ionkina AA, Eckhardt SG, Pitts TM, Sartorius C, Kabos P, Kim J+, **Tan AC**, Tentler JJ, Diamond JR. (2015). Senescence as a mechanism of resistance to the Aurora kinase and angiokinase inhibitor, ENMD-2076, in p53 mutated triple-negative breast cancer (TNBC) models. *Presented in the AACR-NCI-EORTC International Conference: Molecular Targets and Cancer Therapeutics*, Boston, MA. (*Molecular Cancer Therapeutics, 2015; 14(12 Supplement 2):C34*).

92. Gregory MA, D'Alessandro A, Alvarez-Calderon F, Kim J+, Nemkov T, **Tan AC**, Hansen KC, DeGregori J. (2015). ATM/G6PD-dependent metabolic pathways promote mitochondrial redox homeostasis and resistance to FLT3 inhibition in acute myeloid leukemia. *Presented in the AACR-NCI-EORTC International Conference: Molecular Targets and Cancer Therapeutics*, Boston, MA. (*Molecular Cancer Therapeutics, 2015; 14(12 Supplement 2):C78*).

93. Lieu CH, Pitts TM, Kim J+, **Tan AC**, Messersmith WA, You YN, Eng C, Eckhardt SG. (2016). Emerging transcriptional landscape and putative therapeutic targets in young patients with metastatic colorectal cancer (CRC). *Presented in the ASCO Gastrointestinal Cancer Sympoisum,* San Francisco, CA. (*Journal of Clinical Oncology, 2016; 34(4_suppl):605*).

94. Lieu CH, Golemis E, Kim J+, Serebriiskii I, Bailey M, **Tan AC**, Pitts TM, Eng C, Ennis R, Eckhardt SG, Frampton GM, Meyer JE. (2016). Emerging genomic landscape and therapeutic targets in young patients with colorectal cancer (CRC). *Presented in the 52nd ASCO Annual Meeting,* Chicago, IL. (*Journal of Clinical Oncology, 2016; 34(15_suppl):3589*).

95. Cavalli G, Koenders M, Kim J[+], **Tan AC**, Garlanda C, Mantovani A, Dagna L, Joosten L, Dinarello C. (2016). *Presented in the Annual European Congress of Rheumatology (EULAR 2016)*, London, UK. (*Annals of the Rheumatic Diseases, 2016; 75(Suppl 2):426*).

96. Capasso A, Lang J, Pitts TM, Davis SL, Lieu CH, Bagby SM, **Tan AC**, Tentler JJ, Slansky JE, Pelanda R, Eckhardt SG. (2016). Characterizing the immune context of responses to immunotherapy in humanized patient derived xenograft models of CRC. *Presented in the AACR Special Conference: Patient-Derived Cancer Models: Present and Future Applications from Basic Science to the Clinic,* New Orleans, LA. (*Clinical Cancer Research, 2016; 22(16 Supplement):PR03*).

97. Eckhardt SG, Pitts T, **Tan AC**, Bagby S, Arcaroli J, Capasso A, Wong K, Klauck P, Messersmith W, Davis SL, Lieu C, Leong S, Diamond J, Tentler J. (2016). Challenges, opportunities, and lessons learned in the bench-to-bedside translation of xenopatient studies. *Presented in the AACR Special Conference: Patient-Derived Cancer Models: Present and Future Applications from Basic Science to the Clinic,* New Orleans, LA. (*Clinical Cancer Research, 2016; 22(16 Supplement): IA20*).

98. Helfrich B, Scarborough H, Heasley L, Ryall K^{+}, **Tan AC**, DeGregori J, Bunn PA. (2017). Rational Combinations to Improve Outcome for EGFR-TKIs in NSCLCs with EGFR Mutations. *Presented in the IASLC 17th World Conference on Lung Cancer (WCLC)*, Yokohama, Japan. (*Journal of Thoracic Oncology, 2017;12(1): S1242*).

99. Henry CJ, 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. (2017). Blunting age-associated chronic inflammation preserves hematopoiesis and immunity and reduces leukemogenesis. *Presented in the Immunology 2017 Meeting*, Washington, DC. (J*. Immunology, 2017; 198 (1 Suppl) 60.8*).

100. Lee K, Kim B, Kim S, Choi Y, Shin W, Lee S, Park S, Kim S, **Tan AC**, Kang J. (2017). Deep Learning of Mutation-Gene-Drug Relations from the Literature for Precision Medicine*. Presented in the 25th Conference on Intelligent Systems for Molecular Biology (ISMB) and the 16th European Conference on Computational Biology (ECCB)*, Prague, Czech Republic.

101. Lee S, Kim D, Kim S, Lee K, Choi J, Kim S, Jeon M, Lim S, Choi D, **Tan AC**, Kang J. (2017). BEST: Next-Generation Biomedical Entity Search Tool for Knowledge Discovery from Biomedical Literature. *Presented in the 25th Conference on Intelligent Systems for Molecular Biology (ISMB) and the 16th European Conference on Computational Biology (ECCB)*, Prague, Czech Republic.

102. Summer I[+], Yoo M[+], Shin J[+], **Tan AC**. (2017). Predicting Adverse Events Associated with Kinase Inhibitors from Clinical Drug Trials. *Presented in the 15th Rocky Mountain Bioinformatics Conference*, Snowmass/Aspen, CO.

103. Hintzsche J[+], Yoo M[+], Kim J[+], Amato C, Robinson W, **Tan AC**. (2017). IMPACT Web Portal: An Oncology Database Integrating Molecular Profiles with Actionable Therapeutics from Next Generation Sequencing Data. *Presented in the 15th Rocky Mountain Bioinformatics Conference*, Snowmass/Aspen, CO.

104. Kim J[+], Suda K, Murakami I, Rozeboom L, Rivard CJ, Mitsudomi T, Hirsch FR, **Tan AC**. (2017). Tracing the Innate Genetic Evolution and Spatial Heterogeneity in Treatment Naïve Lung Cancer Lesions. *Presented in the 15th Rocky Mountain Bioinformatics Conference*, Snowmass/Aspen, CO.

105. Kim H^{+}, Wuensch K^{+}, Hintzsche J[+], Kim J[+], **Tan AC**. (2017). SALSA: Systematic Alternative Splicing Analysis Pipeline for Detecting Cryptic 3' Splice Site Usage in SF3B1 Mutant Cancer RNA-seq. *Presented in the 15th Rocky Mountain Bioinformatics Conference*, Snowmass/Aspen, CO.

106. Lee B, Gan CP, Rahman ZAA, Khang TF, **Tan AC**, Cheong SC. (2017). DeSigN: Exploiting Gene Expression Signatures to Identify Potential Therapeutic Agents. *Presented in the 15th Rocky Mountain Bioinformatics Conference*, Snowmass/Aspen, CO.

107.   Powers R, Pielke-Lombardo H, **Tan AC**, Costello J. (2017). A rank-based hypergeometric test to extend GSEA for discerning specific effects of small molecule treatment. *Presented in the 15th Rocky Mountain Bioinformatics Conference*, Snowmass/Aspen, CO.

108.   Robertson KM, Gustafson AL, Tentler JJ, Bagby SM, Capasso A, Klauck PJ, Pitts TM, Kim J[+], **Tan AC**, Su TT, Eckhardt SG. (2017). Exploiting translation inhibition: antitumor efficacy of SVC112 in preclinical models of colorectal cancer. *Presented in the AACR-NCI-EORTC International Conference: Molecular Targets and Cancer Therapeutics*, Philadelphia, PA. (*Molecular Cancer Therapeutics, 2018;17(1 Supplement): B051*).

109.   Diamond JR, Orth JD, Ionkina A, Dailey K, Pitts TM, Capasso A, Marcus JM, Burke RT, Davis SL, Kim J[+], **Tan AC**, Eckhardt SG, Tenter JJ. (2017). Rational combination of mTOR and Aurora kinase A inhibition in preclinical models of triple-negative breast cancer. *Presented in the AACR-NCI-EORTC International Conference: Molecular Targets and Cancer Therapeutics*, Philadelphia, PA. (*Molecular Cancer Therapeutics, 2018;17(1 Supplement): B175*).

110.   Tentler JJ, Frank JG, Kim DJ, George C, Lee YB, Ely B, **Tan AC**, Kim J[+], Pitts TM, Capasso A, Dailey KL, Eckhardt SG, Diamond JR. (2017). Preclinical studies of RX-5902, a beta-catenin modulator in triple negative breast cancer. *Presented in the 2017 San Antonio Breast Cancer Symposium*, San Antonio, TX. (*Cancer Research, 2018; 78(4 Suppl):Abstract nr P5-21-16*).

111.   Hintzsche JD[+], Gorden NT, Amato CM, Kim J[+], Wunesch K^{+}, Couts K, Medina T, Wells K, **Tan AC**, Robinson W. (2017). Whole exome sequencing identifies recurrent R625 mutations in novel drug target and driver, SF3B1 in the largest cohort to date of mucosal melanoma. *Presented in the XXIII triennial International Pigment Cell Conference (IPCC)*, Denver, CO. (*Pigment Cell & Melanoma Research, 2017; 30:e63.*).

112.   Baird E, Ravindran Menon D, **Tan AC**, Fujita M. (2018). Distinct prognostic values of ALDH isoenzymes in human melanoma. *Presented in the International Investigative Dermatology (IID) 2018 Meeting*, Orlando, FL. (*Journal of Investigative Dermatology, 2018; 5(Suppl 5): S101*).

E. SOFTWARE AND COMPUTATIONAL RESOURCES

Machine Learning

1.   **k-TSP classifier**. The *k-TSP* (*k-T*op disjoint *S*coring *P*airs) algorithm is a novel machine learning method that seeks to discriminate disease classes by finding pairs of genes (or proteins or miRNAs) whose expression levels typically invert from one class to the other (e.g. Cancer versus Normal). [REF: **Tan AC**, Naiman DQ, Xu L, Winslow RL, Geman D. (2005). ***Bioinformatics***]

Next-Generation Sequencing Data Analysis Pipelines

(Functional genomics, Synthetic lethality screens, Essential gene screens, RNA-seq, Whole-Exome Seq)

2.   **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. [REF: Kim J[+], **Tan AC**. (2012). ***Methods Mol Biol***]

3.   **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. [REF: Hintzsche J[+], Kim J[+], Yadav Y, Amato C, Robinson SE, Seelenfreund E, Shellman Y, Wisell J, Applegate A, McCarter M, Box N, Tentler J, De S, Robinson WA, **Tan AC**. (2016). ***JAMIA.***]

Chemical Systems Biology, Computational Drug Repurposing & Repositioning

4. **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. [REF: Kim J[*+], Yoo M[*+], Kang J, **Tan AC**. (2013). *Human Genomics*; Kim J[*+] et al (2014). *Bioinformatics*]

5. **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. [REF: Yoo M[+], Shin J[+], Kim J[+], Ryall KA[+], Lee K, Lee S, Jeon M, Kang J, **Tan AC**. (2015). *Bioinformatics*]

6. **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/. [REF: Ryall KA[+], Shin J[+], Yoo M[+], Hinz TK, Kim J[+], Kang J, Heasley LE, **Tan AC**. (2015). *Bioinformatics*]

7. **QAPC.** Quantitative Analysis of Pharmacogenomics in Cancer (QAPC) integrates high-throughput drug screening data from multiple data sources (CCLE, GDSC and CTRP) using adjusted AUC. The QAPC portal provides interface for querying these data sources in a unified format, to explore and download the summarized data. QAPC can be accessible at http://tanlab.ucdenver.edu/QAPC. [REF: Pozdeyev N, Yoo M[+], Mackie R, Schweppe RE, **Tan AC**[@], Haugen BR[@]. (2016). *Oncotarget*].

8. **DeSigN.** Differentially Expressed Gene Signatures - Inhibitors (DeSigN) platform is a web-based bioinformatics tool for associating gene signatures with drug response phenotype based on IC50 data, with the aim of identifying novel drugs that have good potential to be repurposed for cancer therapy. DeSigN can be accessible at http://design.cancerresearch.my. [REF: Lee BKB, Tiong KH, Chang JK, Liew CS, Abdul Rahman ZA, **Tan AC**, Khang TF, Cheong SC. (2017). *BMC Genomics*].

9. **IMPACT Web Portal.** IMPACT Web Portal contains a total of 776 drugs connected to 1326 target genes and 435 target variants, fusion, and copy number alterations. The online IMPACT Web Portal allows users to search for various genetic alterations and connects them to three levels of actionable therapeutics. The results are categorized into 3 levels: Level 1 contains approved drugs separated into two groups; Level 1A contains approved drugs with variant specific information while Level 1B contains approved drugs with gene level information. Level 2 contains drugs currently in oncology clinical trials. Level 3 provides pharmacogenetic associations between approved drugs and genes. IMPACT Web Portal can be accessible at http://tanlab.ucdenver.edu/IMPACT. [REF: Hintzsche JD[+], Yoo M[+], Kim J[+], Amato CM, Robinson WA, **Tan AC**. (2018). *BMC Medical Genomics*]

10. **TCM Hub.** Traditional Chinese Medicine Drug Repurposing Hub (TCM Hub) – a connectivity map resource to facilitate the elucidation of TCM MoA for drug repurposing research. TCM Hub can be accessible at: http://tanlab.ucdenver.edu/TCMHub. [REF: Yoo M[+], Shin J[+], Kim H^{+}, Kim J[+], Kang J, **Tan AC**. (2018). *Computer Methods and Programs in Biomedicine*.]

Network Discovery and Visualization

11. **BEReX**. BEReX is a new biomedical knowledge integration, search, and exploration tool. BEReX integrates eight popular databases (STRING, DrugBank, KEGG, PhamGKB, BioGRID, GO, HPRD, and MSigDB) and delineates an integrated network by combining the information available from these databases. Users can search the integrated network by entering keywords and BEReX returns a sub-

network matching the keywords. The resulting graph can be explored interactively. BEReX is implemented as a stand-alone Java application and can be downloaded at: http://infos.korea.ac.kr/berex. [REF: Jeon M, Lee S, Lee K, **Tan AC**, Kang J. (2013). *Bioinformatics*]

12. **COSSY**. COntext-Specific Subnetwork discoverY. COSSY is an algorithm to discover important subnetworks differentiating between two phenotypes (context). It automatically finds differentially expressed subnetworks of closely interacting molecules from molecular interaction networks (such as KEGG or STRING) using gene expression profiles. This is the first non-greedy approach of its kind. COSSY works for any interaction network regardless of the network topology. It can also be used as a highly accurate classification platform. COSSY has been implemented in R and can be downloaded at: http://infos.korea.ac.kr/cossy. [REF: Saha A, **Tan AC**, Kang J. (2014). *PLoS ONE*]

13. **iCOSSY.** iCOSSY is an online gene expression analytical tool that implements the novel pathway-based COntext-specific Subnetwork discoverY (COSSY) algorithm. Users can upload their gene expression datasets, and discover important subnetworks of closely interacting molecules to differentiate between two phenotypes (context). They can also interactively visualize the resulting subnetworks. iCOSSY is a web server that finds subnetworks that are differentially expressed in two phenotypes. Users can visualize the subnetworks to understand the biology of the difference. iCOSSY is available at http://icossy.korea.ac.kr. [REF: Saha A, Jeon M, **Tan AC**, Kang J. (2015). *PLoS ONE.*]

Knowledge Discovery, Biomedical Text Mining

14. **BRONCO.** Biomedical entity Relation ONcology COrpus (BRONCO) is a new corpus that contains more than 400 variants and their relations with genes, diseases, drugs and cell lines in the context of cancer and anti-tumor drug screening research. The variants and their relations were manually extracted from 108 full-text articles. BRONCO can be utilized to evaluate and train new methods used for extracting biomedical entity relations from full-text publications, and thus be a valuable resource to the biomedical text mining research community. BRONCO is available at: http://infos.korea.ac.kr/bronco. [REF: Lee K, Lee S, Park S, Kim S, Kim S, Choi K, **Tan AC**[@], Kang J[@]. (2016). *DATABASE.*]

15. **BEST.** Next-generation biomedical entity search tool (BEST) directly returns relevant entities rather than a list of documents to the user's query. BEST uses a dictionary-based approach to extract biomedical entities from texts, and indexes the entities along with the source texts. BEST finds an entity relevant to a query based primarily on the number of co-occurrences between the query terms and the entity in the literature. Besides the co-occurrence, the ranking function of BEST takes into account other various metrics including the authority of journals, the recency of articles, and the term frequency-inverse document frequency (TF-IDF) weighting. BEST is freely accessible at http://best.korea.ac.kr. [REF: Lee S, Kim D, Lee K, Choi J, Kim S, Jeon M, Lim S, Choi D, Kim S, **Tan AC**, Kang J. (2016). *PLoS ONE.*]

16. **HiPub**. HiPub is a seamless Chrome browser plug-in that automatically recognizes, annotates and translates biomedical entities from texts to networks for knowledge discovery. HiPub is available at: http://hipub.korea.ac.kr. [REF: Lee K, Shin W, Kim B, Lee S, Choi Y, Kim S, Jeon M, **Tan AC**[@], Kang J[@]. (2016). *Bioinformatics.*]

17. **VarDrugPub.** VarDrugPub is a database developed by extracting mutation-gene-drug relations that were extracted from all the PubMed abstracts using deep learning approach. VarDrugPub is available at: http://vardrugpub.korea.ac.kr. [REF: Lee K, Kim B, Choi Y, Kim S, Shin W, Lee S, Park S, Kim S, **Tan AC**[@], Kang J[@]. (2018). *BMC Bioinformatics*.]
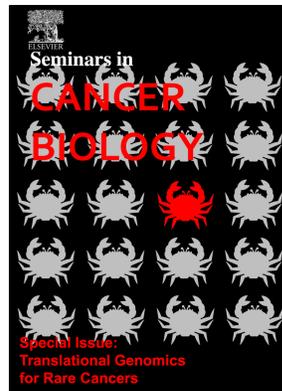
F. BOOK AND JOURNAL COVERS
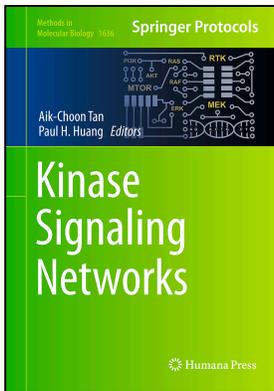
(Tan & Huang, 2017)*
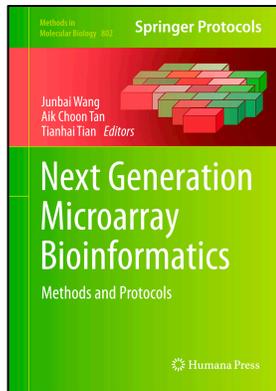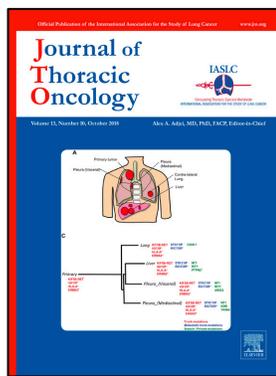
(Wang, Tan & Tian, 2012)*

(Tan & Huang, 2020)*
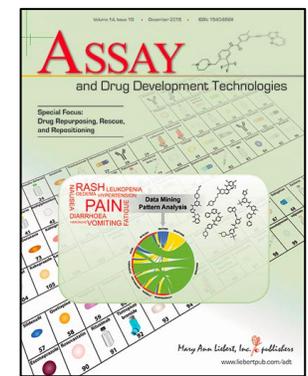
(Miroshnychenko et al, 2021)
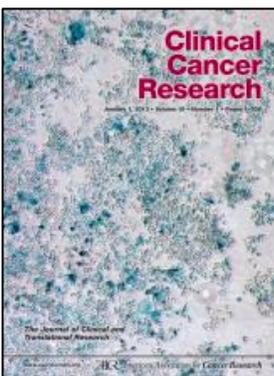
(Chaudhary et al, 2021)

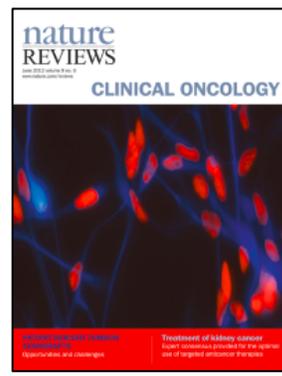(Suda et al, 2018)
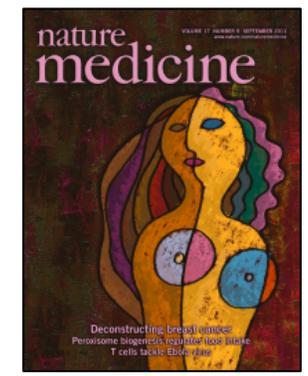
(Brechbuhl et al, 2017)

(Federer et al, 2016)*

(Diamond et al, 2013)

(Giles et al, 2012)

(Tentler et al, 2012)

(Lyons et al, 2011)

*Covers designed by **AC Tan**.

G. MEDIA AND PUBLIC AWARENESS

1. Research profile highlighted in the University of Colorado Cancer Center Magazine: C3: Collaborating to Conquer Cancer (Winter 2014), Aurora, CO. http://www.coloradocancerblogs.org/treatment-cancer-sitting-dusty-shelf/

2. Research profile highlighted in the University of Colorado Cancer Center tri-annual Newsletter: _C3: Collaborating to Conquer Cancer_. (Fall 2010), Aurora, CO. http://www.coloradocancerblogs.org/c3-mag/exposing-cancers-roadmap

3. Research and scholarships highlighted in the University of Colorado Cancer Center News:

    a. _C3: Collaborating to Conquer Cancer (Spring 2011)_ – _Creating Uncontaminated Thyroid Cancer Cell Lines_ – a report on our American Recovery and Reinvestment Act (ARRA) grant.

    b. 4/5/2011 – "_Colorado will continue as a lung cancer leader for years to come_" by Dr. York Miller.

    c. 6/7/2011 – "_We're in the middle of a cancer revolution_" by Dr. Wells Messersmith.

    d. 10/5/2011 – "_Three new grants will help CU Cancer Center investigators plug cancer's escape routes_" by Mr. Garth Sundem.

    e. 12/19/2012 – "_Healthy lifestyle during menopause may decrease breast cancer risk later on_" by Mr. Garth Sundem.

    f. 5/21/2014 – "_Drug-Target Database Lets Researchers Match Old Drugs to New Uses_" by Mr. Garth Sundem.

    g. 7/28/2015 – "_New tool uses 'drug spillover' to match cancer patients with treatments_" by Mr. Garth Sundem.

    h. 3/29/2016 – "_New data tool mines whole exome sequencing to match cancer with best drug_" by Mr. Garth Sundem.

    i. 8/3/2016 – "_New text-mining tool lets researchers visualize gene, protein, drug and disease connections_" by Mr. Garth Sundem.

    j. 3/15/2017 – "_New driver, target in advanced mucosal melanoma_" by Mr. Garth Sundem.

4. Research and scholarships highlighted in the Media

    a. 4/4/2016 – "_Researchers Develop Whole-Exome Sequencing Pipeline to ID Variants, Match Patients to Drugs_" by Elizabeth Newbern, GenomeWeb.

5. Interviewed by the Colorado Clinical and Translational Sciences Institute (CCTSI) Translational Informatics Education Support (TIES) Podcast Episode #14. Aurora, CO. [9/12/2012] [Link to podcast] [Link to transcript]

11. BIOINFORMATICS RESEARCH TRANSLATED INTO CLINICAL TRIALS

1. ClinicalTrials.gov ID: NCT01869218
Feasibility Study of Genomic Sequencing to Find Potential Targets for Personalized Therapy in Patients With Advanced Malignancies. (PI: Elaine Lam).

2. ClinicalTrials.gov ID: NCT02188264
Phase I/IB Study of the Combination of Selumetinib (AZD6244) and Cyclosporin A (CsA) in Patients with Advanced Solid Tumors with an Expansion Cohort in Metastatic KRAS Mutant Colorectal Cancer. (PI: Christopher Lieu).

Laboratory Discovery (BiNGS! applications):
- 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*. 9(15):4149-4162.
- Krishnamurthy A et al. (2018). *Phase Ib Results of the Rational Combination of Selumetinib and Cyclosporin A in Advanced Solid Tumors with an Expansion Cohort in Metastatic Colorectal Cancer*. Cancer Research. [Epub ahead of print, July 24, 2018] [PMID: 30042150]

3. ClinicalTrials.gov ID: NCT01639248
A Phase II Study of the Aurora and Angiogenic Kinase Inhibitor ENMD-2076 in Previously Treated Locally Advanced and Metastatic Triple-Negative Breast Cancer. (PI: Jennifer R. Diamond).

Laboratory Discovery (k-TSP applications):
- Diamond JR, Eckhardt SG, Tan AC, Newton TP, Selby HM, Brunkow KL, Kachaeva MI, Varella-Garcia M, Pitts TM, Bray MR, Fletcher GC, Tentler JJ. (2013). **Predictive Biomarkers of Sensitivity to the Aurora and Angiogenic Kinase Inhibitor ENMD-2076 in Preclinical Breast Cancer Models**. *Clinical Cancer Research*. 19(1): 19:291-303.
- Diamond JR et al. (2018). **A phase II clinical trial of the Aurora and angiogenic kinase inhibitor ENMD-2076 for previously treated, advanced, or metastatic triple-negative breast cancer**. *Breast Cancer Res*. 20(1):82.

4. ClinicalTrials.gov ID: NCT01016860
A Phase I/IB Study of OSI-906 and Irinotecan in Patients With Advanced Cancer With Expanded Cohorts of Patients With Colorectal Cancer Stratified by the OSI-906 Integrated Classifier. (PI: Stephen Leong).

Laboratory Discovery (k-TSP applications):
- Pitts TM*, Tan AC*, Kulikowski GN, Tentler JJ, Brown AM, Flanigan SA, Leong S, Coldren CD, Hirsch FR, Varella-Garcia M, Korch C, Eckhardt SG. (2010). **Development of an integrated genomic classifier for a novel agent in colorectal cancer: approach to individualized therapy in early development**. *Clinical Cancer Research*. 16(12):3193-3204.
- Flanigan SA, Pitts TM, Eckhardt SG, Tentler JJ, Tan AC, Thorburn A, Leong S. (2010) **The insulin-like growth factor I receptor/insulin receptor tyrosine kinase inhibitor PQIP exhibits enhanced antitumor effects in combination with chemotherapy against colorectal cancer models**. *Clinical Cancer Research*. 16(22):5436-5446.
- Davis SL, Eckhardt SG, Diamond JR, Messersmith WA, Dasari A, Weekes CD, Lieu CH, Kane M, **Tan AC**, Pitts TM, Leong S. (2018). **A Phase I Dose-Escalation Study of Linsitinib (OSI-906), a Small-Molecule Dual Insulin-like Growth Factor-1 Receptor/Insulin Receptor Kinase Inhibitor, in Combination with Irinotecan in Patients with Advanced Cancer**. *Oncologist*. [Epub ahead of print, Aug 23, 2018]. [PMID: 30139840]

5. ClinicalTrials.gov ID: NCT00735917
A Phase II Trial of AZD0530 in Previously Treated Metastatic Pancreatic Cancer. (PI: Wells A. Messersmith).

Laboratory Discovery (k-TSP applications):
- Rajeshkumar NV*, Tan AC*, De Oliveira E, Womack C, Wombwell H, Morgan S, Warren MV, Walker J, Green TP, Jimeno A, Messersmith WA, Hidalgo M. (2009) **Antitumor effects and biomarkers of activity of AZD0530, a Src inhibitor, in pancreatic cancer**. *Clinical Cancer Research*. 15(12):4138-4146.
- Arcaroli JJ, Touban BM, Tan AC, Varella-Garcia M, Powell RW, Eckhardt SG, Elvin P, Gao D, Messersmith WA. (2010) **Gene array and fluorescence in situ hybridization biomarkers of activity of saracatinib (AZD0530), a Src inhibitor, in a preclinical model of colorectal cancer**. *Clinical Cancer Research*. 16(16):4165-4177.
- Arcaroli J, Quackenbush K, Dasari A, Powell R, McManus M, Tan AC, Foster NR, Picus J, Wright J, Nallapareddy S, Erlichman C, Hidalgo M, Messersmith WA. (2012). **Biomarker-Driven Trial in Metastatic Pancreas Cancer: Feasibility in a Multi-Center Study of Saracatinib, an Oral Src Inhibitor, in Previously Treated Pancreatic Cancer**. *Cancer Medicine*. 1(2):207-217.

12. GRANTS AND RESEARCH SUPPORT

A. CURRENT RESEARCH GRANTS AND SUPPORTS

NIH/NIDCR R01 DE030508 (Tan/Chung) 09/01/2021 – 08/31/2024
Decoding tobacco-related oral cancer ecosystem by integrative approach
The goal of this proposal is to comprehensively evaluate the tobacco-related effects on the oral cancer ecosystem through integrated multi-omics approaches, identify novel therapeutic agents leveraging the oral cancer-specific TIME, and develop an oral cancer specific web portal to advance the field in tobacco-related cancer research.
Role: Principal Investigator

Florida Biomedical Research Program-JEK 21K04 (Chung/Tan) 05/06/2021 – 04/30/2026
Effects of hypoxia in tumor immune microenvironment in tobacco-related head and neck squamous cell carcinoma (HNSCC)
The goal of this project is to determine the effects of hypoxia in tumor immune microenvironment and biomarkers that modulate the combination of cabozantinib and pembrolizumab in HNSCC.
Role: Co-Principal Investigator

ORIEN NOVA Award (Tarhini) 05/03/2021 – 05/02/2023
Predictors of Immunotherapeutic Benefits in Patients with Advanced Malignancies Treated with Immune Checkpoint Inhibitors
The goal of this project is to identify predictors of immunotherapies in the ORIEN AVATAR cohort utilizing clinical and genomic data across multiple tumor types.
Role: Co-Investigator

NIH/NCI P30 CA076292 (Cleveland) 02/01/2019 – 01/31/2022
Cancer Center Support Grant – Biostatistics and Bioinformatics Shared Resource
The goal of this development grant is to provide biostatistics and bioinformatics support to the Moffitt Cancer Center Investigators.
Role: Associate Scientific Director

Bristol Myers Squibb (Boyle/Beg) 12/23/2019 – 12/22/2021
Use of Tumor Samples from Rapid Tissue Donation to Explore Inflammation, Mechanisms
of I-O Resistance, and Tumor Neoantigen Landscape.
The goal of this project is to perform data analysis of RTD lung cancer cases treated with immunotherapy.
Role: Co-Investigator

Bristol Myers Squibb/Providence Health System (Chung) 09/01/2020 – 09/20/2022
Evaluation of MHC class I methylation as a mechanism of checkpoint inhibitor resistance
in head and neck squamous cell carcinoma (HNSCC)
The goal of this project is to identify methylation markers of MHC class I in immunotherapy response to HNSCC.
Role: Co-Investigator

B. COMPLETED RESEARCH GRANTS AND SUPPORTS

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: Principal Investigator
Amount: Total $ 570,863

DOD W81XWH-11-1-0526 (Eckhardt) 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: Co-Principal Investigator
Amount: Total $ 505,438

Cancer League of Colorado AWD#163421-AT 2016 (Tan/Eckhardt) 07/01/2016 – 06/30/2017
Exploiting Patient Derived Cancer Models for Novel Immunotherapy Regimens
The goal of this project is to develop new algorithms to detect mutation signatures that could predict response to immunotherapy.
Role: Principal Investigator
Amount: $60,000

Cancer League of Colorado (Tan/Finigan) 07/01/2014 – 06/30/2015
Kinome Essential Screen for Discovery of Novel Targets in Small Cell Lung Cancer
The goal of this proposal is to perform kinome essential screen on a panel of small cell lung cancer cell lines to identify therapeutic targets.
Role: Principal Investigator
Amount: Total $ 60,000

Cancer League of Colorado (Tan/Lam) 07/01/2013 – 06/30/2014
Genomic Sequencing-based Predictive Biomarker Development for Targeted Anti-Cancer Therapies
The goal of this proposal is to develop predictive biomarkers for targeted therapies in cancer based on genomic sequencing of cancer patients.
Role: Principal Investigator
Amount: Total $ 60,000

The Michael J. Fox Foundation for Parkinson's Research (Tan/Khoo) 04/01/2010 – 03/31/2011
Circulating microRNAs as Biomarkers for Early Detection of Parkinson's Disease
The major goal of this project is to develop circulating miRNA signatures for predicting PD patients.
Role: Principal Investigator
Amount: Total $ 74,901

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: Principal Investigator
Amount: Total $ 50,000

Colorado CTSI UL1 RR025780 CO-Pilot Award (Tan) 01/01/2010 – 12/31/2011
Developing Circulating MicroRNA Signature to Guide Targeted Therapies in Cancer Treatment
The major goal of this project is to develop predictive circulating miRNA signatures for guiding patient selection in targeted therapies cancer treatment.
Role: Principal Investigator
Amount: Total $ 20,000

The Michael J. Fox Foundation for Parkinson's Research (Tan/Khoo) 10/01/2012 – 09/30/2013
Circulating microRNAs: a new paradigm for Parkinson's disease biomarker discovery

The goal of this proposal is to identify and validate circulating miRNAs as diagnostic biomarkers for Parkinson's disease in MJFF DATATOP samples.
Role: Principal Investigator
Amount: Total $ 99,779

NIH/NCI P50 CA058187 Pilot Project (Tan/Kim/Heasley)   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
Amount: Total: $50,000

NIH/NCI P50 CA58187 (Bunn)   05/01/2014 - 04/30/2019
Lung SPORE Project 2: Improving outcomes from EGFR specific TKIs using rational combinations
The goal of this project is to define signal pathways that can be inhibited in combination with EGFR in EGFR mutant lung cancers to yield synergistic tumor growth inhibition
Role: Co-Investigator
Amount: $273,099 per year (Total: $1,365,495)

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: Co-Director
Amount: $250,697 per year (Total: $1,253,485)

NIH DP7 OD018422 (Wefes)   09/20/2013 – 08/31/2018
Innovative Biomedical Graduate Training for Workforce Readiness
The goal of this project is to develop new courses to train the next generation of biomedical scientists in academia and industries.
Role: Co-Investigator
Amount: $235,468 per year (Total: $1,177,340)

NIH/NCI P30 CA046934 (Theodorescu)   02/01/2017 – 01/31/2022
Cancer Center Support Grant – Bioinformatics Core
The goal of this development grant is to provide bioinformatics support to the University of Colorado Cancer Center Investigator.
Role: Core Director
Amount: $100,000

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
Amount: $237,381 per year (Total: $414,813)

VA BX001994 (Heasley)   10/01/2013 – 09/30/2017
An FGFR1 oncogene driver pathway in head and neck cancer.
This 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: Collaborator

Amount: $200,000 per year (Total: $1,000,000)

DOD W81XWH-17-1-0344 (Heasley, PI, Tan, Co-PI)   08/01/2017 – 07/31/2019
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.
Role: Co-Principal Investigator
Amount: $200,000 per year (Total: $400,000)

DOD W81XWH-18-1-0172 (Jedlicka)   07/15/2018 – 07/14/2020
Identification of Novel Epigenetic Modifiers of Metastasis Progression in Ewing Sarcoma
The goal of this project is to execute and perform preliminarily validation of an *in vivo* shRNA screen for novel epigenetic modifiers controlling metastasis of Ewing Sarcoma.
Role: Co-Investigator
Amount: $200,000 per year (Total: $400,000)

NIH/NIDDK R01DK119394-01 (Pietras)   11/1/2018 – 10/31/2023
Impact of IL-1 signaling on hematopoietic stem cell function and emergence of clonal hematopoiesis
The goal of this project is to identify mechanisms by which chronic IL-1 suppresses blood production by HSC via a PU.1 gene program, and how HSC bearing oncogenic mutations circumvent these effects to preferentially expand in the bone marrow.
Role: Co-Investigator
Amount: $250,000 per year

NIH/NCI R01 CA152303 (Messersmith)   07/02/2010 – 05/31/2015
Biomarker-driven Src inhibitor studies in colorectal cancer patients
The goal of this project is to develop and validate predictive classifier for Src inhibitor, AZD0530, in colorectal cancer patients.
Role: Co-Investigator
Amount: Total: $1,490,635

NIH/NCI R01 CA149456 (Jimeno)   08/09/2010 – 05/31/2015
Hedgehog signaling in head and neck cancer stem cells, and its role in resistance to EGFR inhibitors
The goal of this project is to employ novel mouse models to identify genetic determinants of hedgehog signaling in head and neck cancer stem cells and their roles in resistance to EGFR inhibitors.
Role: Co-Investigator
Amount: Total: $2,103,750

NIH/NHLBI R01 HL104070 (Pillai)   04/08/2011 – 01/31/2016
Role of microRNAs in regulation of the marrow microenvironment
The goal of this application is to employ a systems-biology approach based on HITS-CLIP to define the role of miRNAs in the hematopoietic Marrow Microenvironment (ME).
Role: Collaborator
Amount: Total: $1,803,850

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: Co-Investigator
Amount: Total: $1,590,415

NIH/NCI R01 CA138482 (Anderson)   09/15/2011 – 07/31/2014
GLUT1 Required for Tumor Growth and the Warburg Effect?
The overall goal of this proposal is to determine whether glucose transported into tumor cells via hexose transporters represents the major metabolic event that supports altered tumor metabolism in vivo.
Role: Co-Investigator
Amount: Total: $545,487

NIH/NIAID R01 AI097493 (Obaro)   08/17/2012 – 07/31/2016
Global Genomic and Proteomic Profiling of African Children with Typhoid Fever
The goals of this proposal are to identify diagnostic biomarkers for Typhoid fever from genomics and proteomics profiles of African children.
Role: Co-Investigator
Amount: Total: $1,768,524

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: Co-Investigator
Amount: Total: $1,586,545

NIH/NCI R01 CA095277 (Ford)   01/01/2003 – 12/31/2017
Role of SIX1 and the MIR106B 25 Cluster I EMT and Tumor Progression
The goal of this project is to study the role of SIX1 and miR-106b-25 cluster in regulating EMT and tumor progression.
Role: Co-Investigator
Amount: $240,925 per year (Total: $1,204,625)

NIH/NCI R21 CA187354 (Cramer)   04/06/2015 – 03/31/2017
CHD1 and TAK1 Synthetic Lethality in Prostate Cancer
The goals of this proposal is to determine synthetic lethality genes/pathways in CHD1 and TAK1 co-mutations of prostate cancer.
Role: Collaborator
Amount: Total: ~$400,000

NIH/NCI R21 CA194662 (Malkoski)   04/01/2015 – 03/31/2017
Targeting Defective DNA Pathways in SMAD4 Deficient Lung Cancer
The goals of this proposal is to test the hypothesis that the defective DNA repair phenotype of Smad4-deficient NSCLC can be therapeutically exploited if the DNA repair genes critical for survival of Smad4-deficient lung cancer cells are identified and targeted.
Role: Collaborator
Amount: Total: ~$400,000

NIH/NCI P30 CA046934   (Theodorescu)   02/01/2014 – 01/31/2017
Cancer Center Support Grant – Dev Core
The goal of this development grant is to implement a comprehensive genomics database for patient-derived xenografts generated by the University of Colorado Cancer Center Investigator to facilitate collaboration.
Role: Co-Investigator
Amount: $56,650 per year (Total: $169,950)

NIH/NCI R01 CA190170 (Thorburn)   07/01/2015 – 06/30/2020

Therapeutic Targeting of Autophagy-Dependent Cancer
The goal of this proposal is to identify autophagy-dependent breast cancer using functional genomics approaches, and to identify therapeutic targets for this cohort of cancer
Role: Co-Investigator
Amount: $395,393 per year (Total: $1,976,965)

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
Amount: $230,227 per year (Total: $1,151,135)

NIH/NCI UM1 CA186688 (Meric-Bernstam/Eckhardt/Yao)   03/14/2014 – 02/28/2017
Southwest Early Clinical Trials Consortium
The Southwest Early Clinical Trials (SECT) Consortium is strategically and geographically placed to lead, collaborate on and execute phase I clinical trials in the NCI Experimental Therapeutics-Clinical Trials Network in broad patient populations, including in several underserved regions.
Role: Co-Investigator
Amount: $337,941 per year (Total: $1,689,705)

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: Co-Investigator
Amount: Total: $450,000

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
Amount: Total: $486,000

NIH/NCI R21 CA164617 (Diamond)   07/01/2012 – 06/30/2014
The Development of Novel Individualized Therapy for Metastatic Triple Negative Breast Cancer
This proposal aims to complete a single-arm, dual institution, two-stage phase II clinical trial of ENMD-2076 in patients with advanced or metastatic, previously treated TNBC. A secondary aim of this study is to explore genomic biomarkers predictive of clinical response to ENMD-2076 in this patient population.
Role: Co-Investigator
Amount: Total: $430,074

NIH/NIDCR R56 DE023245 (Reyland/Jimeno)   09/26/2012 – 08/31/2013
Functional Charaterization of Salivary Gland Cancers and Development of Patient-Derived Tumor Xenograft Models
The goals of this proposal are to generate patient derived salivary gland tumor xenografts and systematic characterize these models with multiple "omics" data.
Role: Co-Investigator
Amount: Total: $244,715

NIH/NCI RC1 CA147371 (Haugen)   09/30/2009 – 08/31/2012
A Validated Resource of Thyroid Cancer Cell Lines for Pathway Discovery
The major goal of this project is to generate and characterize new thyroid cancer cell lines.

Role: Co-Investigator
Amount: Total: $999,914

NIH/NHLBI P20 HL101435 (Lowes)   04/01/2010 – 03/31/2012
Using Molecular Pathology to Predict Response in Heart Failure
This project aims to integrate different high-throughput data for the development of a predictive classifier for heart failure.
Role: Co-Investigator
Amount: Total: $1,500,948

NIH/NCI P50 CA058187 Pilot Project (DeGregori)   11/01/2010 – 10/31/2011
Development of novel high-throughput approaches to validate and screen for genes and pathways whose inhibition potentiates gefitinib efficacy for NSCLC
The goal of this project is to validate the SLuG hits in vivo.
Role: Co-Investigator
Amount: Total: $22,933

NIH/NCI P50 CA058187 Pilot Project (Heasley)   11/01/2011 – 10/31/2012
Functional Genomics Screening for Novel Protein Kinase Drivers in Lung Cancer Cell Lines
This project seeks to discover novel protein kinases that serve as oncogene drivers in lung cancer cell lines.
Role: Co-Investigator
Amount: Total: $50,000

University of Colorado Boulder Innovative Seed Grant Program (Su) 06/01/2012 – 05/31/2013
The Genetic Basis for Sensitivity to Translation Inhibition in Human Cancer Cells
The goal of this proposal is to understand why some cancer cells are sensitive to a drug that inhibits protein synthesis while others are not using both experimental and computational approaches.
Role: Co-Investigator
Amount: Total: $49,512

Colorado Neuroscience Center Neuroscience Innovation Award (Yu) 06/01/2012 – 05/31/2013
Bioinformatics Approach to Identify Antigens in Multiple Sclerosis
The goal of this proposal is to identify antigens in multiple sclerosis using computational and experimental approaches.
Role: Co-Investigator
Amount: Total: $30,000

Cancer League of Colorado (Shen)   07/01/2012 – 06/30/2013
Dissection of the perforin pathway in cancer immunotherapy
The goal of this proposal is to dissect the perforin pathway in cancer using computational and experimental approaches.
Role: Co-Investigator
Amount: Total: $30,000

C. MENTORING AND TRAINING GRANTS

MENTOR
Cancer League of Colorado (Hintzsche)   07/01/2018 – 06/30/2019
Patient-centric Multi-omics Approach to Identifying Actionable Therapeutics in Cancer
The overall goal of this project is to develop and implement IMPACT-cBioportal as that focuses on patients with genetically similar tumors and use it to predict new therapeutic options.
Role: Mentor
Amount: Total: $30,000

NIH/NCI T32 CA190216 (Wuensch)   08/01/2017 – 07/31/2018
Cancer Biology Training Program for Graduate Student.
Role: Mentor
Amount: $23,000 per year.

Cancer League of Colorado (Kim)   07/01/2017 – 06/30/2018
Systematic Alternative Splicing Analysis for Transcriptomic MIsregulation in Cancer
The overall goal of this project is to develop novel computational methods to systematic determine and evaluate alternative splicing from cancer RNA-seq.
Role: Mentor
Amount: Total: $30,000

NIH Ruth L. Kirschstein NRSA T32 CA174648 (Jackson)   05/01/2015 – 04/30/2017
A Novel Systematic Analysis of ALDH Isozyme Specificity in Head and Neck Squamous Cell Carcinoma
Role: Mentor
Amount: Total: ~$100,000

NIH Ruth L. Kirschstein NRSA T32 CA174648 (Ryall)   07/01/2013 – 09/30/2016
Systems analysis of EGFR-inhibitor induced kinome reprogramming in non-small cell lung cancer.
Role: Mentor
Amount: Total: ~$100,000

Cancer League of Colorado (Ryall)   07/01/2015 – 06/30/2016
Systems analysis of EGFR-inhibitor induced kinome reprogramming and EMT in non-small cell lung cancer
The overall goal of this project is to employ systems biology approaches to understand kinome reprogramming and EMT in non-small cell lung cancer induced by EGFR inhibitors.
Role: Mentor
Amount: Total: $30,000

Cancer League of Colorado (Hintzsche)   07/01/2015 – 06/30/2016
Identifying molecular targets in melanoma resistant to BRAF/MEK combination therapy
The overall goal of this project is to identify acquired resistance mechanisms in BRAF/MEK combination treatment using next-generation sequencing analysis.
Role: Mentor
Amount: Total: $30,000

Cancer League of Colorado (Astling)   07/01/2012 – 06/30/2013
Development of a robust classifier for predicting multiple drug classes and molecular targets for tumor subtypes
The goal of this project is to develop a robust classification algorithm that can predict the sensitivity of a tumor to multiple classes of drugs from gene expression data.
Role: Mentor
Amount: Total: $30,000

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: Mentor
Amount: Total: $30,000

Colorado CTSI UL1RR025780 CO-Pilot Award (Salstrom)   01/01/2013 – 12/31/2013

Identifying novel therapeutic targets for high risk FLT3-mutated Acute Myeloid Leukemia
This proposal seeks to perform a kinome shRNA screens to identify rational combination for FLT3-mutated acute myeloid leukemia.
Role: Co-Mentor
Amount: Total $30,000

MENTORING COMMITTEE
NIH/NCI K23 CA190849 (Lieu)   07/08/2015 – 06/30/2018
The Development of Novel Targeted Therapy for KRAS Mutant Colorectal Cancer
The overall goal of this proposal is to develop novel and effective therapy for KRAS mutant colorectal cancer, with special emphasis in younger-onset CRC.
Role: Co-Mentor
Amount: Total $ 170,640 per year

NIH/NCI K23 CA172691 (Diamond)   07/01/2013 – 06/30/2018
The Development of Novel Individualized Therapy for Triple-Negative Breast Cancer
The overall goal of this proposal is to develop novel and effective therapy for advanced TNBC, including the investigation of unique biomarker selection strategies which represents a major area of unmet need in human cancer care.
Role: Co-Mentor
Amount: Total $ 171,720 per year

TRAINING GRANT THAT I PARTICIPATED
NIH/NCI T32 CA174648 (Wang/Bunn)   07/01/2013 – 06/30/2018
Training in Translational Research of Lung, Head and Neck Cancer
Training specifically devoted to lung, head and neck cancer research will greatly enhance progress toward establishing new treatments and therapies for these cancers.
Role: Participating Faculty Mentor
Amount: $223,764 per year.

NIH/NCI T32 CA190216 (Reyland/Cramer)   07/07/2016 – 06/30/2021
Cancer Biology Training specifically focused on translational applications of basic research.
Role: Participating Faculty Mentor
Amount: $227,499 per year.

D. PHARMACEUTICAL GRANTS & CONTRACTS

AstraZeneca (Eckhardt)   12/01/2012 – 11/30/2013
Rational Combination of AZD6244 and AZD1366 in Colorectal Cancer Cell Lines and Human Colorectal Tumor Explants
The goal of this project is to assess the rational combinations of AZD6244 and AZD1366 in CRC.
Role: Co-Investigator
Amount: Total $ 126,890

Millennium/Takeda (Eckhardt)   05/01/2011 – 05/31/2013
Combination of MLN8237 and TAK960 with standard of care in KRAS wildtype and mutant colorectal cancer models
The goal of this project is to perform combination studies using MLN8237 and TAK960 with standard of care (SOC) in KRAS wildtype and mutant CRC explants and o identify pathways involved in responsiveness to MLN8237 and TAK960 that may lead to rational combinations.
Role: Co-Investigator
Amount: Total $ 413,279

Millennium/Takeda (Eckhardt)   09/01/2011 – 10/31/2012
Comprehensive Rational Combination of TAK-899, TAK-733, MLN8237, MLN2480/TAK632 in Colorectal
Cancer Cell Lines and Human Colorectal Tumor Explant Models
The goal of this project is to assess several rational combinations of several novel agents in CRC with a
specific focus on determining induction of cell death and potent synergy, within the context of a molecularly-
defined subset in CRC.
Role: Co-Investigator
Amount: Total $ 538,638

Millennium/Takeda (Eckhardt)   08/03/2010 – 05/14/2012
Preclinical Development of Predictive Biomarkers for the Ubiquitin Ligase Inhibitor, MLN4924, in
Melanoma Models
The overall goal of this project is to develop predictive biomarkers for MLN4924 using melanoma cell lines
and human tumor xenografts.
Role: Co-Investigator
Amount: Total $ 264,901

Millennium/Takeda (Eckhardt)   03/01/2010 – 03/31/2012
Preclinical Development of Predictive Biomarkers for the MEK Inhibitor, TAK-733, in Melanoma Models
The overall goal of this project is to develop predictive biomarkers for TAK-733 using melanoma cell lines
and human tumor xenografts.
Role: Co-Investigator
Amount: Total $ 328,844

Roche (Messersmith)   01/01/2011 – 12/31/2011
Evaluation of RO4929097 (γ-secretase inhibitor) Pancreatic Cancer Models
The major goal of this project is to identify biomarkers for γ-secretase inhibitor in pancreatic cancer.
Role: Co-Investigator
Amount: Total $ 150,000

Pfizer (Messersmith)   01/01/2011 – 12/31/2011
Evaluation of PF-03084014 as a Single Agent and in combination with Irinotecan in a Preclinical Model of
Colorectal Cancer
The major goal of this project is to identify biomarkers for Notch inhibitor in colorectal cancer.
Role: Co-Investigator
Amount: Total $ 37,800

Pfizer (Eckhardt)   09/01/2009 – 04/30/2011
Comprehensive Biomarker and Rational Combination Strategy PF-3758309 in Colorectal Cancer
The major goal of this project is to identify biomarkers for combining PAK4 inhibitor with other targeted
agents in colorectal cancer.
Role: Co-Investigator
Amount: Total $ 292,496

Eli Lilly (Doebele/Camidge)   01/01/2011 – 12/31/2011
Overcoming primary and acquired resistance to ALK inhibition
The major goal of this project is to identify resistance biomarkers for ALK inhibitor in non small cell lung
cancer.
Role: Co-Investigator
Amount: Total $ 105,896

Pfizer (Doebele)   01/01/2011 – 12/31/2011

Synthetic Lethal in Crizotinib (SLIC): An unbiased genome-wide shRNA screen to identify genes that synergize with crizotinib to induce cell death in ALK+ NSCLC
The major goal of this project is to identify genes that synergize with crizotinib to induce cell death in ALK+ NSCLC.
Role: Co-Investigator
Amount: Total $ 95,462

AstraZeneca (Eckhardt)   04/01/2009 – 03/31/2010
Comprehensive Biomarker and Rational Combination Development for the MEK Kinase Inhibitor, AZD6244, in Colorectal Cancer
The major goal of this project is to discover comprehensive biomarkers for MEK inhibitor in colorectal cancer in vitro and in vivo preclinical systems.
Role: Co-Investigator
Amount: Total $ 150,000

13. REFERENCES

Available Upon Request.