Nicholas Tsinoremas, Ph.D.

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I. PERSONAL

Current Academic Rank: Professor
Primary Department: Department of Biochemistry and Molecular Biology
Secondary Appointments: Department of Computer Science
                              Department of Health Informatics
Citizenship: USA

II. HIGHER EDUCATION

University of Leeds, England; PhD in Biochemistry and Molecular Biology, 1991
University of Athens, Greece; BS in Chemistry, 1988

III. EXPERIENCE

University of Miami, Professor, Department Professor of Biochemistry and Molecular Biology, 2020 – Present
Tenured professor participating in curriculum committees, occasionally teach courses in this area, and engage in biochemistry and molecular biology research.

University of Miami, **Vice Provost for Research Computing and Data, 2018 – Present**
Chair the Data Governance Committee for the University of Miami. This committee determines the standardizations, operations, and analytics for all UM data including, but not limited to, health care data, advancement, student admission data and general student life data. Advise the Provost on the Research Computing strategy for the University on recruitment of faculty in Data Science field and developing the computing research infrastructure. Work closely with the CIO to determine the IT services for faculty and students as relates to research and data intense computing.

University of Miami, Founding Director, Institute of Data Science and Computing, 2019 – Present
The University of Miami established the Institute for Data Science and Computing (IDSC) to transform itself into an innovative leader in data science—encompassing research, education, ethics, and service—through cross-disciplinary, industrial, and governmental collaborations, and in interactions with local and global communities. Specifically, the Institute focuses on (1) Empowering researchers from all schools and colleges and from University administration to solve real-world problems with data science; (2) Conducting first-class research in key areas of data science and its application; (3) Infusing data science into instructional programs, (4) Fostering discussion about—and seeking solutions to—the moral and ethical challenges of data use and corresponding computational technologies (5) Increasing interest in and understanding of data science among the general public and (6) Developing governmental and industrial collaborations and consortia through data science to solve critical problems

The Institute is organized around thematic research programs that focus on key areas of societal need such as Atmosphere, Ocean and Earth Science, Data Driven Discovery in Biological Sciences and Health Care, Urban Lab and Smart Cities and around cross-disciplinary research platforms that conduct basic and applied research such as Artificial Intelligence and Machine Learning, Visualization, Data Communication and Information Design, Data Ethics

and Society, and the resources of its Technology Platforms (formerly known as CCS, Center for Computational Science).

As Director, I am responsible for the Institute's success and scientific direction and report to the Provost of the University. I am responsible for the allocation of resources, faculty and staff recruitment, and the negotiations of hardware and software contracts.

University of Miami, Founding Director, Center for Computational Science, 2007 – 2019
The Center for Computational Science (CCS) is a pan-institutional resource providing extraordinary intellectual, hardware, and software resources to the University's research community. CCS is responsible for the design and maintenance of major high advance computer systems that support work in fields such as genomics, computational biology, systems medicine, marine ecosystems, ocean modeling, climate and meteorology, computational economics, big data, smart cities, and social systems informatics to name a few. CCS rapidly emerged as a leading center with a cyber infrastructure that is among the nation's top academic centers and is the leading center in the State of Florida. The Center has a professional software engineering group that collaborates with the research community to provide high level data management and software solutions that enable effective and efficient dissemination of information. Additionally, the Center has several analytical groups that engage in developing state-of-the-art analytic methodologies ranging from bioinformatics and systems medicine approaches to smart and connected cities and health care.

As Director, I am responsible for the Center's success and scientific direction and report to the Provost of the University. I am responsible for the allocation of resources, recruitment, and the negotiations of hardware and software contracts. I serve as key advisor to the Provost for advance computing and disruptive technologies regarding aspects of University businesses for teaching to research to health care.

I also served as a co-PI on a $180 million grant for the State of Florida to develop state of-the-art genomics and translational technologies at the Miller School of Medicine. In this capacity, I recruited more than twenty Bioinformatics faculty and staff along with specialized IT professionals and developed the human and computing infrastructure that enables Genomics and Translational Research at the University of Miami. We currently have over 8 PB of genomics and high throughput data which is growing fast. We anticipate we will reach to over 15 PB in the next two years.

Additionally, I served as a member of Research Cabinet for the Medical School. The Research Cabinet is responsible for providing strategic direction and planning for all research activities across the Medical School and assists the Dean in determining future strategic directions on research investments.

University of Miami, Miller School of Medicine, co-Chair, Precision Medicine Task Force, 2015 – 2018
Helped develop a strategic vision and implementation plan for Precision Medicine for the UM Miller School of Medicine and the UHealth System. The first phase of the plan consisted of providing precision medicine to UHealth patients in a routine clinical setting by integrating molecular profiling tests and EHR data. A business plan was also developed as part of this process and, in 2016, started implementation in two major disease areas besides cancer.

University of Miami, co-Director of Biomedical Informatics, Miami Clinical and Translational Science Institute, 2012 – Present
Responsible for developing the clinical and translation research infrastructure for the Miller School of Medicine. My team is responsible for the design and implementation of University Research Information Data Environment (URIDE) which is based on state of-the-art big data technologies that bring together clinical and discovery (including genomics) data and allow intelligent and rapid querying that integrates both worlds of biomedical research.

University of Miami, Interim Director of Bioinformatics and Biostatistics, Sylvester Comprehensive Cancer Center (SCCC), 2009 – 2012
Re-organized the clinical informatics and biostatistics groups. Established and recruited a bioinformatics group as well as the permanent Director for the group. Member of the leadership committee of SCCC and special advisor to the Director for all informatics, a role that I still hold.

University of Miami, Professor, Department of Health Informatics, 2010 – Present
Participate in the curriculum committees, occasionally teach courses in this area, and engage in health care analytics research using big data.

University of Miami, Professor, Department of Computer Science, 2008 – Present
Participate in research in bioinformatics, and computational genomics. Main areas of focus methodologies and algorithms understanding the dark matter of the Human Genome.

University of Miami, Professor, Department of Medicine, 2007 – Present
Engage in active research in systems medicine, big data, and translational research. Research projects include with non-coding RNA, with specialty in cancer and neurodegenerative diseases. Systems Medicine and big data approaches to identify disease biomarkers and best networks for targeted drug development

The Scripps Research Institute, Senior Director and Head, Department of Informatics, 2004 – 2007
Recruited personnel and managed the Informatics and Information Technology (IT) Departments at Scripps Florida. The Informatics Department had eighteen members and was responsible for providing expertise in all informatics-related and IT areas, ranging from chemo-informatics and high-through-put screening to computational biology and algorithm development, and high-performance computing. My group consisted of world-class bioinformatics scientists, computer scientists, and scientific software engineers. The Department focused on five main areas: Scientific Computing/High Performance Computing, Scientific Software Engineering, Computational Genomics, Cheminformatics, and Statistical Sciences/Data Mining.

Planned and consulted with the COO and President of The Scripps Research Institute the Informatics and IT budgets, building design, and personnel for the present facilities. I was responsible for the planning and execution of the IT budget for the new Scripps Florida campus that consisted of three buildings and nearly 400,000 square feet. The IT component was responsible for all network, client services, security, high performance computing, telephony, and media for the research facility.

One of the main goals of my research focused on identifying key intervention points for drug discovery in the areas of inflammation and autoimmune diseases like lupus. We were combining approaches to human and mouse genetics and genomics (gene expression and Proteomics) to prioritize genes and reconstruct disease networks. More specifically we were using Whole Genome Association studies to identify causative genes in human lupus and were complementing these studies with an in-silico approach using the mouse lupus model.

Director of Informatics and co-investigator on two ~$10MM Roadmap NIH grant for Molecular Screening of Small Molecule Libraries (MLSCN (The Scripps Research Institute and Columbia University). My group is responsible for the automation, database design and operation, and analysis of screening and chemical compound data, as well as developing tools for lead optimization and predictive modeling.

Developed various collaborations with companies, like IBM, SUN Microsystems MDL and SAS, and academic institutions (e.g. Columbia University, University of Florida, University of Miami) to pursue sponsored research in computational biology, clinical genomics bioinformatics, and cheminformatics. With the academic institutions I partnered with faculty to develop grant proposals for large-scale program grants.

Merck and Co., Senior Director, Genomic Discovery and Computational Genomics and Informatics, 2002 – 2004
During my first year, I led a multidisciplinary project called the Drug Target Annotation Program (DTAP). The objective of this project was to discover and annotate all genes in the human genome using a combination a computational and gene expression strategies. The most interesting genes were validated and patents are being filed. My immediate group of bioinformatics scientists and analysts were directly responsible for developing the database infrastructure and analysis tools and methodologies where the integration and analysis of the different data types takes place. My group, using the microarrays developed for DTAP, was also responsible for generating a Merck proprietary Gene Expression Atlas of all known and predicted genes. This resource is now available to all MRL scientists worldwide.

After the first year, I re-directed and focused the DTAP program to better define and study in great detail the alternative splice patterns of the Merck drug target genes. Using a combination of microarray technology, bioinformatic approaches, and development of new methods, a large part of my group was responsible for discovering and validating novel alternative splice forms of high value drug target genes. Numerous collaborations have been established with the Merck therapeutic franchises around this program. The most interesting alternative splice forms are being patented aggressively. Some of this work has also generated multiple manuscripts for publication that are in the preparation stage.

A smaller part of my group was involved in collaboration with the Research Genetics group, where we study human and mouse forward genetics and the genetics of gene expression for discovery and prioritization of new drug target genes. My group provided the database infrastructure, bioinformatics and computational analysis of the genetics and micro array data.

During my time at Merck, I recruited and organized a team of eleven scientists and analysts to operate in a multidisciplinary and metrics-based organization. I have also established significant collaboration with the therapeutic teams around specific projects of high interest to Merck.

I have served as a member of the informatics committee that evaluated external bioinformatics and genomics products and determines the overall informatics strategy for Merck.

Consulted with the VP of Informatics concerning the strategic development of tools and projects that would have an impact in MRL worldwide.

DoubleTwist Inc., Vice President, Genomics and Data Mining Tools, 2001 – 2002
Developed product strategy for all five of DoubleTwist's Genomics and Data Mining products in 2000-2001. I managed a group of bioinformatics scientists which grew to sixteen people over two years; this group was organized into three separate areas of expertise. The Associate Director of On-line Products, Associate Director of Data Mining Tools and Senior Scientist for Human Genomics reported directly to me.

My group was responsible for providing the scientific leadership of the company as we defined the scientific foundation for DoubleTwist's products.

Responsible for the strategic positioning of DoubleTwist products and direction through critical assessment of market trends and emerging technologies.

Consulted with the CEO and COO concerning all DoubleTwist's strategic business partnerships, including potential mergers and acquisitions.

DoubleTwist Inc., Director, Research, 1999 – 2001
Texas A&M University, Research Scientist, Department of Biology, 1992 – 1997
Worked on a project funded by the NSF and the Human Frontiers Program. Using unicellular organisms as a model system, this project studied the molecular aspects of the circadian clock and, more specifically, how photoreceptors were able to entrain the biological clock. I was also involved in a project studying the circadian clock in chick CNS, more specifically, understanding the molecular mechanism by which melatonin receptor(s) are able to entrain the circadian clock.

University of Leeds and SERC Fellowship, Institut Pasteur, Paris, France, Research Fellow, Département de Physiologie Microbienne, 1989 – 1991
While I was conducting research for my Ph.D., I had the opportunity to visit and work at the Institut Pasteur, Paris. This project, funded by the University of Leeds and the Institut Pasteur, focused on isolating and studying the gene of a phosphoprotein which is differently phosphorylated according to the light quality in photosynthetic blue-green algae.

IV. PUBLICATIONS

Research Informatics and the COVID-19 Pandemic: Challenges, Innovations, Lessons Learned, and Recommendations. Bookman, Richard & Cimino, James & Harle, Christopher & Kost, Rhonda & Mooney, Sean & Pfaff, Emily & Rojevsky, Svetlana & Tobin, Jonathan & Wilcox, Adam & Tsinoremas, Nick. (2021). Research Informatics and the COVID-19 Pandemic: Challenges, Innovations, Lessons Learned, and Recommendations. Journal of Clinical and Translational Science. 5. 1-40. 10.1017/cts.2021.26.

Pitfalls, Perils, and Potential for Real-world Evidence to combat COVID-19 under the Stimulus. Medscape (submitted) Skapik J and Tsinoremas, NF.

Response to the COVID-19 Pandemic: Contributions from the Medical Device Ecosystem. Pandemic Response and Emergency Preparedness Task Force (PREPT). Tsinoremas, NF; co-Chair of PREPT. 2021.

Network assessment of demethylation treatment in melanoma: Differential transcriptome-methylome and antigen profile signatures. Jiang Z, Cinti C, Taranta M, Mattioli E, Schena E, Singh S, Khurana R, Lattanzi G, Tsinoremas NF, Capobianco E. PLoS One. 2018 Nov 28;13(11):e0206686. doi: 10.1371/journal.pone.0206686. eCollection 2018.

Simulated Microgravity Impairs Cardiac Autonomic Neurogenesis from Neural Crest Cells. Hatzistergos KE, Jiang Z, Valasaki K, Takeuchi LM, Balkan W, Atluri P, Saur D, Seidler B, Tsinoremas N, DiFede DL, Hare JM. Stem Cells Dev. 2018 Jun 15;27(12):819-830. doi: 10.1089/scd.2017.0265. Epub 2018 Mar 20.

Ensemble Modeling Approach Targeting Heterogeneous RNA-Seq data: Application to Melanoma Pseudogenes. Capobianco E, Valdes C, Sarti S, Jiang Z, Poliseno L, Tsinoremas NF. Nature Sci Rep. 2017 Dec 11;7(1):17344. doi: 10.1038/s41598-017-17337-7.

Induction of endogenous retro elements as a potential mechanism for mouse-specific drug-induced carcinogenicity. Coskran TM, Jiang Z, Klaunig JE, Mager DL, Obert L, Robertson A, Tsinoremas N, Wang Z, Gosink M. PLoS One. 2017 May 4;12(5):e0176768. doi: 0.1371/journal.pone.0176768. eCollection 2017. PMID: 28472135

The landscape of BRAF transcript and protein variants in human cancer. Marranci A , Jiang Z, Vitiello M, Guzzolino E, Comelli L, Sarti S, Lubrano S, Franchin C, Echevarría-Vargas I, Tuccoli A, Mercatanti A, Evangelista M, Sportoletti P, Cozza G, Luzi E, Capobianco E, Villanueva J, Arrigoni G, Signore G, Rocchiccioli S, Pitto L, Tsinoremas N, Poliseno L. Mol Cancer. 2017 Apr 28;16(1):85. doi: 10.1186/s12943-017-0645-4.

Abstract P6-08-05: Genome-wide identification of transcripts regulated by estrogen in MCF-7 cells using BrU-seq. Sun J, Capobianco E, Tsinoremas N, Lippman M. Cancer Research 77(4 Supplement): P6-08-05-P6-08-05 · February 2017 DOI: 10.1158/1538-7445.SABCS16-P6-08-05

Emerging Putative Associations between Non-Coding RNAs and Protein-Coding Genes in Neuropathic Pain: Added Value from Reusing Microarray Data. Raju HB, Tsinoremas NF, Capobianco E. 2016 Front Neurol. 2016 Oct 18;7:168.

Non-coding RNAs profiling in head and neck cancers. D Salyakina and NF Tsinoremas 2016 NPJ Genomic Medicine 1 15004

Identification of BRAF 3'UTR Isoforms in Melanoma. Marranci A, Tuccoli A, Vitiello M, Mercoledi E, Sarti S, Lubrano S, Evangelista M, Fogli A, Valdes C, Russo F, Dal Monte M, Adelaide Caligo M, Pellegrini M, Capobianco E, Tsinoremas N, Poliseno L. J Invest Dermatol. 2015 Feb 16. doi: 10.1038/jid.2015.47.

Integrative analysis of cancer imaging readouts by networks. Dominietto M., Tsinoremas N., Capobianco E. Mol Oncol. 2015 Jan;9(1):1-16. doi:10.1016/ j.molonc.2014.08.013. Epub 2014 Sep 10.

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V. PROFESSIONAL

Ongoing Funded Research

PI-CD33-PCOR
Task Force for Global Health, Inc   10/01/2020 – 07/31/2022
COVID-19 Electronic Health Data Initiative $150,500
Role: PI
The COVID-19 electronic healthcare data initiative project will demonstrate PCORnet sites ability to collect information on COVID data through the implementation of a nationally distributed data infrastructure. The collection of these COVID-19 data will help to answer critical questions to assist in the emergency response to the COVID-19 pandemic.

UL1TR002736 (Sacco)   06/28/2018 – 05/31/2023
NIH $17,957,590
Miami Clinical and Translation Science Institute
Role: Biomedical Core Director
This project is part of a national consortium of research institutions working to transform clinical and translational research and helping accelerate laboratory discoveries into treatments for patients.

1OT2OD032581-01 (Core PI: Carlisle, NADPH)   09/17/2021 – 09/16/2022
NIH $800,000
A COMPUTATIONAL ECOSYSTEM TO SUPPORT ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING HEALTH DISPARITIES RESEARCH. Building a Consortium to Deliver Standards, Technology, Tools, and Data to Support Collaborative Interdisciplinary Health Disparities Research – Infrastructure Core
Subaward PI
The Infrastructure Core has a goal to engage HBCUs and MSIs in an effort to gauge their interest, capabilities, and capacity to apply artificial intelligence and machine learning-based approaches to data analysis.

OT2HL161847-01 (Kaushal, Weill Cornell Medicine)   11/08/2021 – 11/07/2022
NIH $210,700
Adult PCORnet-PASC Response to the Proposed Revised Milestones for the PASC EHR/ORWD Teams (RECOVER)
Subaward PI
The PCORnet RECOVER EHR Consortium aims to be a highly participative collaboration, engaging the expertise and interest of participating systems as well as data.

Funded Research Performed

75F40119C10164   11/13/2020 – 09/29/2021
FDA Implementation of SHIELD-Harmonized Lab Data Standards. $83,350
Deloitte
Role: Subaward PI
This project focuses on implementing infrastructure that directly addresses laboratory data interoperability failures at their root by harmonizing how laboratory data Informatics standards are practically applied within healthcare institutions through a sole authoritative source.

UM 2020-2234   4/1/2020 – 7/31/2020
University of Miami COVID-19 Rapid Response Grant $29,975
Developing a COVID-19 early detection, tracking and re-porting system
Role: PI
The goal of this project was to utilize state-of-the-art machine learning techniques to leverage the metadata embedded in social media data for predictive analytics and create a hyper-local geographic early detection system.

1U54MD010722 (Cox, N; Lima, M; Weiss, R; Wilkins, C)   04/01/2016 – 3/31/2021
NIH $131,504
Center for Excellence in Precision Medicine and Population Health
Role: Investigator
The proposed Vanderbilt-Miami-Meharry Center of Excellence in Precision Medicine and Population Health will bring together institutions and faculty with substantial expertise in precision medicine and health disparities research among African Americans and Latinos/Hispanics

CDRN1501-26692 (Shenkman, E)   10/01/2015 – 10/31/2018
PCORI $8,175,731
One Florida Clinical Research Consortium
Role: Subaward Principal Investigator
This consortium is a statewide partnership among the University of Florida, University of Miami, Florida State University, health care systems, health plans, providers, and patients; it also includes 22 hospitals, 914 clinical practices, and 4,100 physicians. The funding award will create a clinical data research network that is part of a larger collaborative initiative called the National Patient-Centered Clinical Research Network, or PCORnet.

1UL1TR000460 (Sacco, R)   07/01/2011 – 05/31/2018
NIH $20,382,279
Miami Clinical and Translation Science Institute
Role: Biomedical Informatics Core Director
This project is part of a national consortium of research institutions working to transform clinical and translational research and helping accelerate laboratory discoveries into treatments for patients.

UG3/UH3 (Züchner, Pericak-Vance, Carrasquillo)   08/26/2017 – 06/30/2018
NIH $3,849,511
"The South-East Enrollment Center (SEEC)"
Role: Collaborator
This project allows the University of Miami (UM) to join the NIH All of Us Research program, a growing precision medicine initiative, which aims to ensure that the benefits of personalized medicine are available to all. UM will join four major academic healthcare centers to create the SouthEast Enrollment Center consortium. UM will be able to contribute members of South Florida's impressively diverse populations to program enrollment, with a goal of 10,000 enrollees by the end of the first year.

1620695 (Bottum)   07/01/2016 – 06/30/2017
NSF $748,490
RCN: Advancing Research and Education Through a National Network of Campus Research Computing Infrastructures – The CaRC Consortium
Role: Co-Principal Investigator
The goal of the Campus Research Computing (CaRC) Infrastructures Consortium is to provide a national forum for the exchange and dissemination of best practices, expertise, and technologies, enabling the advancement of campus-based research computing activities.

DMS-1410 771 (Clarke, J)   08/01/2013 – 07/31/2016
NSF $81,307
ATD: Statistical Ensembles for the Identification of Bacterial Genomes
Role: Subcontract Principal Investigator

M1401631 (Tsinoremas, N)   03/21/2014 – 09/21/2015
Pfizer $19,565
Sequence Analysis to Evaluate Retro-Element Medicated Non-Genotoxic Carcinogenicity in Rodents
Role: Principal Investigator

NIDA 1ROIDA06227-16ª (Mash, DC)   03/01/2011 – 02/28/2014
Carbon-14 Birth Dating of Neurons in Addiction $1,278,090
Role: Collaborator

1RO1(Mash, DC)   06/01/2011 – 05/31/2014
NIH $378,675
CNS Mechanism in Cocaine-Related Sudden Death
Role: Collaborator

NIH W81XWH0710151 (Burnstein)   07/11/2009 – 04/30/2011
"Vav3 oncogene potentiation of androgen $1,924,311
receptor signaling in prostate cancer"
Role: Investigator

NGA/MLSCN 1 U54 MH074404-01   03/01/2005 – 02/28/2011
"Scripps Research Institute Molecular Screening Center" $10,400,0000
This study is focused on high throughput chemical approaches integrated with state-of-the art post-genome
sequence, cell, molecular, and in vivo biology to provide a rapid and facile mechanism for enhancing the process of
biomedical science and the discovery of proof-of-concept molecules.
PI: Hugh Rosen, PhD
Role: Co-PI

MLSCN 1 U54 HG003914-01   07/01/06-6/30/08
"Molecular Library Screening Centers $9,000,000
Network Center at Columbia University"
This study is focused on high throughput screening using phenotypic assays at the cellular and subcellular levels to
identify bioactive compounds.
PI: James Rothman, MD
Role: Investigator – Director of Informatics/Cheminformatics

Dyadic SFP 1640
"Annotation of the Chrysoporium
lucknowense ("C1") genome"
This study is focused on obtaining and annotating the genomic DNA sequence of C1, a proprietary fungal organism.
Role: Principal Investigator

Professional Organizations

2005 - 2010	Scientific Advisory Board, NextBio Inc, acquired by Illumina
2006 - 2009	College of Engineering and Computer Science Executive Advisory Council, Florida Atlantic University
2006 - 2010	Biotechnology Advisory Committee, Miami Dade College
2006 - 2008	Board Member, Palm Beach County Library System
2009 -	Board Member, Southeastern Universities Research Association
2009 -	Advisory Board, Hussman Institute for Human Genomics, University of Miami
2010 - 2015	Editorial Board Member, Journal of Clinical Bioinformatics
2010 -	Board Member, (Vice Chair 2013-2015) (Secretary of the Board (2015 – Present) Sunshine State Research Computing Alliance (SSERCA)
2014 -	Editorial Board Member, Journal of Investigative Genomics
2014 -	Editorial Board Member, Journal of Clinical And Experimental Genetics

2017 -	Innovation Board of Coral Gables, special advisor to the Mayor of Coral Gables

2017 -	Scientific Advisory Board Sivotec Analytics and Sivotec Bioinformatics

Other Professional Activities

2015 -	Special panel reviewer for CTSA awards, NCATS. I was a member of the CTSA review in all review panels with the exception of two due to conflict of interest. CTSA awards are very large and prestigious institutional awards for Academic Medical Centers and their partners with the sole purpose to accelerate clinical and translational research.

2002 -	Reviewers for numerous journals, including, Science, Nature, Nature Communications, Nature Scientific reports, Frontiers series, Genome Medicine.

Invention Disclosures and Patents

Christopher Armour, John Castle, Phillip Garrett-Engele, Z. Kan, Patrick Loerch, and Nicholas Tsinoremas. Alternative Spliced Isoforms of Nuclear Factor Kappa-B Subunit 1 (NFKB1)

Christopher Armour, John Castle, Phillip Garrett-Engele, Z. Kan, Patrick Loerch, and Nicholas Tsinoremas. Atlernative Spliced Isoform of Mitotic Centromere-Associated Kinesin (MCAK)

Christopher Armour, John Castle, Phillip Garrett-Engele, Z. Kan, Patrick Loerch, and Nicholas Tsinoremas Alternative Spliced Isoforms of Sodium Channel, Voltage gated, Type III, Alpha (SCN8A)

Christopher Armour, John Castle, Phillip Garrett-Engele, Z. Kan, Christopher Raymond, and Nicholas Tsinoremas. Alternatively Splice Isoforms of Human ERBB2

Christopher Armour, John Castle, Phillip Garrett-Engele, Z. Kan, Patrick Loerch, and Nicholas Tsinoremas. Alternatively Spliced Isoforms of Human MCAK (KNSL6)

Christopher Armour, John Castle, Phillip Garrett-Engele, Z. Kan, Patrick Loerch, and Nicholas Tsinoremas. Alternatively Spliced Isoforms of Human SCN8A

Christopher Armour, John Castle, Phillip Garrett-Engele, Z. Kan, Patrick Loerch, and Nicholas Tsinoremas . Alternatively Spliced Isoforms of Centromer Protein E (CENPE)

Nicholas Tsinoremas, Al Darzins, and Charles Squires. The isolation of *Rhodococcus* strain I19 mutants capable of utilizing TMD370 DRM as a sole source of sulfur.