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Position: Utah Science, Technology, and Research (USTAR) Associate Professor of Bioengineering and Human Genetics, Scientific Computing and Imaging Institute and Huntsman Cancer Institute, University of Utah
Google Scholar: <https://scholar.google.com/citations?user=RKh11ecAAAAI&hl=en>
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Education/Training

Institution	Degree (if applicable)	Completion Date	Field of Study
Stanford University, CA, USA	Postdoctoral Fellowship	1/2004	Genetics
Stanford University, CA, USA	Ph.D.	1/1999	Applied Physics
Tel Aviv University, Israel	B.Sc. <i>magna cum laude</i>	10/1989	Physics

A. Personal Statement

In my research, I develop quantum mechanics-based multi-tensor AI/ML, which, as I prospectively and retrospectively experimentally validated, is uniquely able to discover accurate, precise, clinically actionable, and mechanistically interpretable predictors from small-cohort and noisy, high-dimensional multi-omic data. I am a USTAR associate professor at the Scientific Computing and Imaging Institute¹ and the Huntsman Cancer Institute at the University of Utah, a scientific advisory board member of the NCI-DOE Cancer Moonshot collaboration on predictive oncology, and the CSO and a co-founder of Prism AI Therapeutics, Inc.^{2,3,4} As a genetics postdoctoral fellow at Stanford University, I invented the concept of the “eigengene,” in a top ten most cited *PNAS* paper of the year 2000 and a top 50 most cited *PNAS* paper of all time.^{5,6,7,8} My Ph.D. thesis in applied physics at Stanford University was published by Wiley,^{9,10,11} and is recognized as crucial to gravitational wave detection and quantum computing.^{12,13,14}

I formulate the comparative spectral decompositions, i.e., my multi-tensor^{15,16,17,18} generalizations^{19,20,21,22} of the singular value decomposition, to (i) compare and integrate any data types, of any number and dimensions, and (ii) scale with data sizes. My models (iii) are interpretable in terms of known biology and batch effects and (iv) correctly²³ predict^{24,25,26,27,28} previously unknown mechanisms.^{29,30} My prospective and retrospective validation^{31,32,33,34,35,36} of a genome-wide pattern of DNA copy-number alterations in brain^{37,38,39,40} tumors proved that the models discover predictors of survival and response to treatment that are (v) the most accurate and precise, (vi) clinically actionable in the general population based upon as few as 50–100 patients, and (vii) are consistent across studies and over time. I discovered this, and patterns in, e.g., lung,^{41,42} nerve,^{43,44} ovarian,^{45,46,47,48,49,50} and uterine tumors, in public data. Such alterations were recognized in cancer, yet all other attempts to associate them with outcome failed, establishing that my AI/ML is uniquely suited to personalized medicine.

B. Appointments, Awards and Honors, and Professional Activities

Scientific Appointments

2024– Chief Scientific Officer (CSO) and Co-Founder, Prism AI Therapeutics, Inc.
 2016– Investigator, and Member of the Cancer Control and Population Sciences Program, Huntsman Cancer Institute (HCI), University of Utah
 2010– Utah Science, Technology, and Research (USTAR) Associate Professor, Scientific Computing and Imaging (SCI) Institute and Departments of Bioengineering and Human Genetics, University of Utah
 2010–2016 Adjunct Associate Professor, Department of Mathematics, University of Texas at Austin
 2004–2010 Assistant Professor, Department of Biomedical Engineering, and Fellow, Institute of Cellular and Molecular Biology, University of Texas at Austin
 1998–2004 Postdoctoral Fellow, Department of Genetics, Stanford University
 1991–1998 Graduate Research Assistant, Department of Applied Physics, Stanford University

Military Service

1983–1985 Base Defense Officer, Israeli Air Force; honorably discharged with the rank of First Lieutenant
 1982–1983 Operations Researcher, Israeli Air Force Headquarters

Awards and Honors (see also Research Grants below)

2025 *25th Advances in Genome Biology and Technology (AGBT) General Meeting* (Marco Island, FL), Plenary Lecture, “Multi-Tensor AI/ML Uniquely Able to Identify Actionable and Mechanistically Interpretable Predictors from Small-Cohort and Noisy High-Dimensional Multi-Omic Clinical Data;” <https://youtu.be/bqH-2UCkPdg>

- 2020 *Amazon Web Services (AWS) Education Research Webinar, "Multi-Tensor Decompositions for Personalized Cancer Diagnostics, Prognostics, and Therapeutics;"* <https://youtu.be/s4ezu0OHKAs>
- 2018 *14th International Conference on Latent Variable Analysis and Signal Separation (LVA ICA 2018) (Guildford, United Kingdom), Plenary Lecture*
- 2018 *2018 Society for Industrial and Applied Mathematics (SIAM) Conference on Applied Linear Algebra (SIAM-ALA18) (Hong Kong, China), Plenary Lecture, "Comparative Spectral Decompositions for Personalized Cancer Diagnostics and Prognostics"*
- 2014 *American Association of Physicists in Medicine (AAPM) Science Council Session Winner (SCSW) Lecture Award, "Singular Value Decomposition Identifies Transcript Length Distribution Functions from DNA Microarray Data and Reveals Evolutionary Forces Globally Affecting Glioblastoma Multiforme Metabolism"*
- 2014 *Bloomberg L.P. Distinguished Speaker Lectures, "Discovery of Principles of Nature from Matrix and Tensor Modeling of Large-Scale (Molecular Biological) Data," and "(Physics-Inspired) Mathematical Vocabulary for Discovery from Data"*
- 2006 *6th International Conference on Independent Component Analysis and Blind Source Separation (ICA 2006) (Charleston, SC), Plenary Lecture, "Uncovering the Molecular Biological Principles That Govern Cellular Systems with Blind Source Separation Models"*
- 2005 *International Linear Algebra Society (ILAS) Linear Algebra and Its Applications (LAA) Lecture, "Genomic Signal Processing: From Matrix Algebra to Genetic Networks"*
- 1998 *American Physical Society (APS), Outstanding Doctoral Thesis Research in Atomic, Molecular, or Optical Physics (DAMOP) Award Finalist, "Impossibility of Determining the Quantum Wavefunction of a Single System and Fundamental Limit to External Force Detection"*
- 1997 *5th International Conference on Squeezed States and Uncertainty Relations (FICUSSUR 1997) (Balatonfüred, Hungary), Plenary Lecture*

Professional Activities

- 3/2025 *SIAM Conference on Computational Science and Engineering (CSE25) (Fort Worth, TX), Organizing Committee Member*
- 1/2025– *ILAS, Joint Mathematics Meetings (JMM) Speaker Selection Committee Member*
- 2/2024– *University of Utah, SCI Institute, Associate Director*
- 2/2023– *NIH/NCI-DOE Cancer Moonshot Collaboration, Scientific Advisory Board Member, "Innovative Methodologies and New Data for Predictive Oncology Model Evaluation (IMPROVE) Project"*
- 11/2024, 11/2023, 11/2022, 11/2020
Supercomputing (SC) NCI Computational Approaches for Cancer Workshop (CAFCW) (Atlanta, GA; Denver, CO; Dallas, TX; Virtual), Workshop Organizing Committee Member
- 9/2024 *2024 BrainStorm Summit: End Childhood Cancer (Washington, DC), Invited Speaker*
- 1/2024 *Precision Medicine World Conference (PMWC) 2024 (Santa Clara, CA), Invited Speaker;*
<https://youtu.be/vy8UZftSXKI>
- 1–12/2023, 1–12/2019
NIH/NCI Physical Sciences in Oncology Network (PS-ON), Steering Committee Co-Chair
- 9/2015–12/2023
NIH/NCI PS-ON, Steering Committee Member
- 11/2023 *NIH/NCI Cancer Systems Biology Consortium (CSBC) and PS-ON Joint Meeting (Bethesda, MD), Co-Chair, Co-Organizer, and Invited Speaker*
- 7/2023, 6/2022, 6/2017, 6/2016, 6/2015, 6/2014
International High-Performance Computing (HPC) Summer School on HPC Challenges in Computational Sciences (Atlanta, GA; Athens, Greece; Boulder, CO; Ljubljana, Slovenia; Toronto, Canada; Budapest, Hungary), Mentor and Invited Speaker
- 2/2023 *3rd Gordon Research Conference on the Physics of Cancer (Galveston, TX), Invited Speaker*
- 11/2021 *26th Annual Meeting of the Society for Neuro-Oncology (SNO) (Boston, MA), Invited Speaker, "How High-Dimensional Multi-Tensor Machine Learning Is Being Used to Improve the Prognosis, Diagnosis, and Treatment of Gliomas;"* <https://youtu.be/oMfYXLZfrmo>
- 9/2020 *Decade of the PS-ON at the NCI Virtual Symposium, Co-Chair, Co-Organizer, and Invited Speaker;*
<https://youtu.be/5LKywVby9Rc>
- 6/2020 *2020 American Association for Cancer Research (AACR) Virtual Annual Meeting II, Education Session Co-Chair, Co-Organizer, and Invited Speaker, "Artificial Intelligence and Machine Learning from Research to the Cancer Clinic;"* <https://youtu.be/rxEbMnL8iGc>
- 1/2020 *Linear Algebra and Optimization Seminar, Stanford University Institute for Computational and Mathematical Engineering (ICME) (Stanford, CA), Invited Speaker;* <https://youtu.be/opiYfUKDJ2U>

- 8/2018 *European Association for Signal Processing (EURASIP) Summer School on Tensors in Medicine* (Leuven, Belgium), Invited Speaker
- 9/2014 *5th Association for Computing Machinery (ACM) Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB)* (Newport Beach, CA), Panel Co-Chair, Co-Organizer, and Participant
- 9/2013 *2013 Biomedical Engineering Society (BMES) Annual Meeting* (Atlanta, GA), Track Chair, Organizer, and Invited Speaker, "Bioinformatics, Computational and Systems Biology"
- 2/2009 NSF, Workshop Participant, "Future Directions in Tensor-Based Computation and Modeling"
- 2/2008 *SXSVD (South by SVD): Gene H. Golub's World Day Celebration* (Austin, TX), Chair and Organizer
- 1/2008 NIH/National Human Genome Research Institute (NHGRI), Planning Meeting Participant, "The Cancer Genome Atlas (TCGA) Data Portal"
- 8/2006 NSF, Workshop Participant, "Petascale Computing in the Biosciences"
- 12/2001 NIH/NHGRI, Planning Meeting Participant, "A Vision for the Future of Genomics Research"

C. Contributions to Science

C.1. I invented the concept of the "eigengene." I formulate the comparative spectral decompositions, i.e., my multi-tensor generalizations of the singular value decomposition, to (i) compare and integrate any data types, of any number and dimensions, and (ii) scale with data sizes.

Journal Papers

- a. **O. Alter**, P. O. Brown and D. Botstein, "Singular Value Decomposition for Genome-Wide Expression Data Processing and Modeling," *Proceedings of the National Academy of Sciences (PNAS) USA* 97, 10101 (2000); [doi: 10.1073/pnas.97.18.10101](https://doi.org/10.1073/pnas.97.18.10101)
Feature: National Research Council, *Mathematics and 21st Century Biology*. National Academies Press (2005).
[Mention](#): Top ten most cited *PNAS* paper of the year 2000 and top 50 most cited *PNAS* paper of all time, *Google Scholar* (April 12, 2024).
- b. **O. Alter**, P. O. Brown and D. Botstein, "Generalized Singular Value Decomposition for Comparative Analysis of Genome-Scale Expression Datasets of Two Different Organisms," *PNAS* 100, 3351 (2003); [doi: 10.1073/pnas.0530258100](https://doi.org/10.1073/pnas.0530258100)
Feature: J. Wixon and J. Ashurst, *Comparative and Functional Genomics* 4, 509 (2003).
Feature: M. E. Kilmer and C. D. Moravitz Martin, "Decomposing a Tensor," *SIAM News* 37 (2004).
- c. **O. Alter** and G. H. Golub, "Reconstructing the Pathways of a Cellular System from Genome-Scale Signals by Using Matrix and Tensor Computations," *PNAS* 102, 17559 (2005); [doi: 10.1073/pnas.0509033102](https://doi.org/10.1073/pnas.0509033102)
- d. L. Omberg, G. H. Golub and **O. Alter**, "A Tensor Higher-Order Singular Value Decomposition for Integrative Analysis of DNA Microarray Data from Different Studies," *PNAS USA* 104, 18371 (2007); [doi: 10.1073/pnas.0709146104](https://doi.org/10.1073/pnas.0709146104)
- e. P. Sankaranarayanan,* T. E. Schomay,* K. A. Aiello and **O. Alter**, "Tensor GSVD of Patient- and Platform-Matched Tumor and Normal DNA Copy-Number Profiles Uncovers Chromosome Arm-Wide Patterns of Tumor-Exclusive Platform-Consistent Alterations Encoding for Cell Transformation and Predicting Ovarian Cancer Survival," *Public Library of Science (PLoS) One* 10, e0121396 (2015); [doi: 10.1371/journal.pone.0121396](https://doi.org/10.1371/journal.pone.0121396)
Press Release: J. Kiefer, "New Method Increases Accuracy of Ovarian Cancer Prognosis and Diagnosis," *American Association for the Advancement of Science (AAAS) EurekAlert!* (2015); <https://eurekalert.org/news-releases/866753>
Feature: R. Atkins, "Calculating Cancer Cures," *National Academy of Engineering (NAE) Innovation Podcast and Radio Series* (2015); https://alterlab.org/in_the_news/Atkins_NAE_WTOP_Radio_2015_Feature.mp3
Feature: F. Pavlou, "Big Data, Hidden Knowledge," *The Pathologist* (2015); https://alterlab.org/in_the_news/Pavlou_Pathologist_2015_Feature.pdf
- f. S. P. Ponnappalli, M. A. Saunders, C. F. Van Loan and **O. Alter**, "A Higher-Order Generalized Singular Value Decomposition for Comparison of Global mRNA Expression from Multiple Organisms," *PLoS One* 6, e28072 (2011); [doi: 10.1371/journal.pone.0028072](https://doi.org/10.1371/journal.pone.0028072)
Mention: Among the top 10% most cited *PLoS One* articles as of 2017, *PLoS One* (2017).

Technical Reports

- g. **O. Alter**, P. O. Brown and D. Botstein, "Singular Value Decomposition for Gene Expression Data Processing and Modeling," *After the Genome V* (Jackson Hole, WY). DOE Office of Science (1999); <https://osti.gov/servlets/purl/803995>
- h. S. P. Ponnappalli, G. H. Golub and **O. Alter**, "A Novel Higher-Order Generalized Singular Value Decomposition for Comparative Analysis of Multiple Genome-Scale Datasets," *Stanford University and Yahoo! Research Workshop on Algorithms for Modern Massive Datasets (MMDS)* (Stanford, CA, 2006).

C.2. My models (iii) are interpretable in terms of known biology and batch effects and (iv) correctly predict previously unknown mechanisms.

Journal Papers

- a. **O. Alter** and G. H. Golub, "Integrative Analysis of Genome-Scale Data by Using Pseudoinverse Projection Predicts Novel Correlation between DNA Replication and RNA Transcription," *PNAS* **101**, 16577 (2004); [doi: 10.1073/pnas.0406767101](https://doi.org/10.1073/pnas.0406767101)
- b. **O. Alter** and G. H. Golub, "Singular Value Decomposition of Genome-Scale mRNA Lengths Distribution Reveals Asymmetry in RNA Gel Electrophoresis Band Broadening," *PNAS* **103**, 11828 (2006); [doi: 10.1073/pnas.0604756103](https://doi.org/10.1073/pnas.0604756103)
- c. L. Omberg, J. R. Meyerson, K. Kobayashi, L. S. Drury, J. F. X. Diffley and **O. Alter**, "Global Effects of DNA Replication and DNA Replication Origin Activity on Eukaryotic Gene Expression," *Molecular Systems Biology (MSB)* **5**, 312 (2009); [doi: 10.1038/msb.2009.70](https://doi.org/10.1038/msb.2009.70)
Press Release: B. Rische, "Mathematical Modeling Correctly Predicts Previously Unknown Biological Mechanism of Regulation," *AAAS EurekAlert!* (2009); <https://eurekalert.org/news-releases/815594>
Recommendation: M. Méchali, *Faculty Opinions* recommendation 1728974 (2010).
- d. C. Muralidhara, A. M. Gross, R. R. Gutell and **O. Alter**, "Tensor Decomposition Reveals Concurrent Evolutionary Convergences and Divergences and Correlations with Structural Motifs in Ribosomal RNA," *PLoS One* **6**, e18768 (2011); [doi: 10.1371/journal.pone.0018768](https://doi.org/10.1371/journal.pone.0018768)
- e. N. M. Bertagnolli, J. A. Drake, J. M. Tennessen and **O. Alter**, "SVD Identifies Transcript Length Distribution Functions from DNA Microarray Data and Reveals Evolutionary Forces Globally Affecting GBM Metabolism," *PLoS One* **8**, e78913 (2013); [doi: 10.1371/journal.pone.0078913](https://doi.org/10.1371/journal.pone.0078913)

Commentaries

- f. **O. Alter**, "Discovery of Principles of Nature from Mathematical Modeling of DNA Microarray Data," *PNAS* **103**, 16063 (2006); [doi: 10.1073/pnas.0607650103](https://doi.org/10.1073/pnas.0607650103)

Book Chapters

- g. **O. Alter**, "Genomic Signal Processing: From Matrix Algebra to Genetic Networks." In: M. J. Korenberg, editor, *Microarray Data Analysis: Methods and Applications*. Springer Nature, Methods in Molecular Biology (MIMB), vol. 377, 17 (2007); [doi: 10.1007/978-1-59745-390-5_2](https://doi.org/10.1007/978-1-59745-390-5_2)

Technical Reports

- h. **O. Alter**, G. H. Golub, P. O. Brown and D. Botstein, "Novel Genome-Scale Correlation between DNA Replication and RNA Transcription During the Cell Cycle in Yeast is Predicted by Data-Driven Models." In: M. P. Deutscher et al., editors, *Miami Nature Biotechnology Winter Symposium: Cell Cycle, Chromosomes and Cancer* (Miami Beach, FL). University of Miami School of Medicine, vol. 15 (2004).

C.3. My prospective and retrospective validation of a genome-wide pattern of DNA copy-number alterations in brain tumors proved that the models discover predictors of survival and response to treatment that are (v) the most accurate and precise, (vi) clinically actionable in the general population based upon as few as 50–100 patients, and (vii) are consistent across studies and over time.

Journal Papers

- a. C. H. Lee,* B. O. Alpert,* P. Sankaranarayanan and **O. Alter**, "GSVD Comparison of Patient-Matched Normal and Tumor aCGH Profiles Reveals Global Copy-Number Alterations Predicting Glioblastoma Multiforme Survival," *PLoS One* **7**, e30098 (2012); [doi: 10.1371/journal.pone.0030098](https://doi.org/10.1371/journal.pone.0030098)
- b. K. A. Aiello and **O. Alter**, "Platform-Independent Genome-Wide Pattern of DNA Copy-Number Alterations Predicting Astrocytoma Survival and Response to Treatment Revealed by the GSVD Formulated as a Comparative Spectral Decomposition," *PLoS One* **11**, e0164546 (2016); [doi: 10.1371/journal.pone.0164546](https://doi.org/10.1371/journal.pone.0164546)
- c. K. A. Aiello, S. P. Ponnappalli and **O. Alter**, "Mathematically Universal and Biologically Consistent Astrocytoma Genotype Encodes for Transformation and Predicts Survival Phenotype," *Applied Physics Letters Bioengineering (APL Bioeng)* **2**, Special Topic: Bioengineering of Cancer invited article 031909 (2018); [doi: 10.1063/1.5037882](https://doi.org/10.1063/1.5037882)
Feature: A. J. Engler and D. E. Discher, "Rationally Engineered Advances in Cancer Research," *APL Bioeng* **2**, Special Topic: Bioengineering of Cancer preface 031601 (2018).
Mention: Among the top 10 most downloaded *APL Bioeng* articles as of 2019, *APL Bioeng* (2019).
- d. S. P. Ponnappalli, et int., **O. Alter**, "Retrospective Clinical Trial Experimentally Validates Glioblastoma Genome-Wide Pattern of DNA Copy-Number Alterations Predictor of Survival," *APL Bioeng* **4**, 026106 (2020); [doi: 10.1063/1.5142559](https://doi.org/10.1063/1.5142559)
Press Release: J. Kiefer, "Genome-Wide Pattern Found in Tumors from Brain Cancer Patients Predicts Life Expectancy," *AAAS EurekAlert!* (2020); <https://eurekalert.org/news-releases/477030>
Mention: Among the most shared *APL Bioeng* research as of 2021, *APL Bioeng* (2021).

Technical Reports

- e. S. P. Ponnappalli, et int., **O. Alter**, "Prospective and Clinical Prediction in a Retrospective Trial That Experimentally Validated an AI/ML-Derived Whole-Genome Predictor as the Most Accurate and Precise Predictor of Survival and Response to Treatment in Glioblastoma," *AACR Special Conference in Cancer Research: Brain Cancer* (Minneapolis, MN). AACR (2024); [doi: 10.1158/1538-7445.BRAIN23-A031](https://doi.org/10.1158/1538-7445.BRAIN23-A031)
- f. S. P. Ponnappalli, et int., **O. Alter**, "AI/ML-Derived Whole-Genome Predictor Prospectively and Clinically Predicts Survival and Response to Treatment in Brain Cancer," *SC23 9th NCI CAFCW* (Denver, CO). ACM (2023); [doi: 10.1145/3624062.3624078](https://doi.org/10.1145/3624062.3624078)
- g. **O. Alter**, S. P. Ponnappalli, J. W. Tsai, P. Miron, K. L. S. Miskimen, K. A. Waite, N. Sosonkina, S. E. Coppens, A. C. Bryan, E. P. Kiernan, H. Yang, J. Bowen, G. A. Nakouzi, J. S. Barnholtz-Sloan, A. E. Sloan and T. R. Hodges, "Prospective Validation from a Retrospective Trial That Validated an AI/ML-Derived Whole-Genome Biomarker as the Most Accurate and Precise Predictor of Survival and Response to Treatment in Glioblastoma," *2024 American Society of Clinical Oncology (ASCO) Annual Meeting* (Chicago, IL). ASCO (2024); [doi: 10.1200/JCO.2024.42.16_suppl.e14028](https://doi.org/10.1200/JCO.2024.42.16_suppl.e14028)

C.4. I discovered this, and patterns in, e.g., lung, nerve, ovarian, and uterine tumors, in public data. Such alterations were recognized in cancer, yet all other attempts to associate them with outcome failed, establishing that my AI/ML is uniquely suited to personalized medicine.

Journal Papers

- a. M. W. Bradley, K. A. Aiello, S. P. Ponnappalli,* H. A. Hanson* and **O. Alter**, "GSVD- and Tensor GSVD-Uncovered Patterns of DNA Copy-Number Alterations Predict Adenocarcinomas Survival in General and in Response to Platinum," *APL Bioeng* **3**, 036104 (2019); [doi: 10.1063/1.5099268](https://doi.org/10.1063/1.5099268)

Technical Reports

- b. **O. Alter**, "DNA Copy-Number Alterations in Primary Ovarian Serous Cystadenocarcinoma Encoding for Cell Transformation and Predicting Survival and Response to Platinum Therapy Throughout the Course of the Disease," *AACR Special Conference on Advances in Ovarian Cancer Research: Exploiting Vulnerabilities* (Orlando, FL). AACR (2016); [doi: 10.1158/1557-3265.OVCA15-A60](https://doi.org/10.1158/1557-3265.OVCA15-A60)
- c. **O. Alter**, E. Newman, S. P. Ponnappalli and J. W. Tsai, "AI/ML-Derived Mechanistically Interpretable Whole-Genome Biomarkers of Patient Survival in Pre-Treatment Primary Neuroblastoma Tumors and Whole Blood," *2024 ASCO Annual Meeting* (Chicago, IL). ASCO (2024); [doi: 10.1200/JCO.2024.42.16_suppl.10043](https://doi.org/10.1200/JCO.2024.42.16_suppl.10043)

Issued Patents

- d. **O. Alter**, "Genetic Alterations in Glioma," *United States Patent* US 10202643 B2 (2019).
- e. **O. Alter**, "Genetic Alterations in Glioblastoma," *European Patent* EP 2773777 A4 (2020).

C.5. My Ph.D. thesis in applied physics at Stanford University was published by Wiley, and is recognized as crucial to gravitational wave detection and quantum computing.

Books

- a. **O. Alter** and Y. Yamamoto, *Quantum Measurement of a Single System*. Wiley (2001); [doi: 10.1002/9783527617128](https://doi.org/10.1002/9783527617128)

Citation: K. S. Thorne et al., "Noise in Gravitational-Wave Detectors and Other Classical-Force Measurements is Not Influenced by Test-Mass Quantization," *Physical Review D* **67**, 082001 (2003).

D. Research Grants

Grant	PI	Sponsor	Period	Total/Share
1. U01 CA-202144	O. Alter	NIH/NCI	9/23/2015–8/31/2023	\$3,395,986
NIH/NCI Physical Sciences in Oncology U01 Project, "Multi-Tensor Decompositions for Personalized Cancer Diagnostics and Prognostics;" https://app.dimensions.ai/details/grant/grant.4455012				
2. CAREER DMS-0847173	O. Alter	NSF/DMS	8/1/2009 –7/31/2015	\$400,053
NSF/Division of Mathematical Sciences (DMS) Faculty Early Career Development (CAREER) Award, "Integrative and Comparative Tensor Algebra Models of DNA Microarray Data from Different Studies of the Cell Cycle;" https://app.dimensions.ai/details/grant/grant.3096148				
3. R01 HG-004302	O. Alter	NIH/NHGRI	8/23/2007–5/31/2015	\$1,768,525
NIH/NHGRI R01 Project, "Tensor Computations for Modeling Large-Scale Molecular Biological Data – from Discovery of Patterns to Discovery of Principles of Nature"				
4. K01 HG-000038	O. Alter	NIH/NHGRI	4/1/2000 –3/31/2005	\$527,367
NIH/NHGRI K01 Individual Mentored Research Scientist Award in Genomic Research and Analysis				
5. DOE FG03-99ER62836	O. Alter	DOE/Sloan	9/1/1999 –8/31/2003	\$100,000
DOE/Alfred P. Sloan Foundation Postdoctoral Fellowship in Computational Molecular Biology				