

**Name:** Alter, Orly | <https://alterlab.org/> | **Citizenship:** Israel and U.S.  
**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>  
**LinkedIn Profile:** <https://linkedin.com/in/orly-alter>  
**ORCiD Works:** <https://orcid.org/0000-0002-0418-1078>

## 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

I develop quantum mechanics-based multi-tensor AI/ML,<sup>1</sup> which, as I experimentally validated, is uniquely able to discover accurate, precise, clinically actionable, and mechanistically interpretable predictors from small-cohort, noisy, and multi-dimensional, multi-omic data.<sup>2</sup> I am a USTAR associate professor at the Scientific Computing and Imaging Institute<sup>3</sup> and the Huntsman Cancer Institute at the University of Utah, a scientific advisory board member of the NCI-DOE Cancer Moonshot collaboration, and the CSO and a co-founder of Prism AI Therapeutics, Inc.<sup>4</sup> As a genetics postdoctoral fellow at Stanford University, I invented the concept of the “eigengene” in a top 50 most cited *PNAS* paper of all time.<sup>5,6,7</sup> My Ph.D. thesis in applied physics, also at Stanford, was published by Wiley<sup>8,9,10</sup> and is recognized as crucial to gravitational wave detection and quantum computing.<sup>11,12</sup>

I proved that my multi-tensor algorithms,<sup>13,14</sup> known as comparative spectral decompositions,<sup>15,16,17</sup> (i) always converge, and (ii) almost always into a mathematically unique model, from any data types, of any number and dimensions. I showed that my models (iii) comprehensively remove batch effects and capture known biology, and (iv) correctly predict previously unknown mechanisms.<sup>18,19</sup> My clinical trial validation of a pattern of DNA copy-number alterations in brain tumors solved the 70 year-old problem of correctly predicting a patient’s response and survival from their genome,<sup>20,21,22</sup> and demonstrated that my predictors are (v) the most accurate and precise, (vi) clinically actionable in the general population based upon as few as 19<sup>23</sup> patients, and (vii) consistent across federated studies and over time. Recent experiments additionally demonstrated that the models (viii) correctly predict drug targets to sensitize a tumor to treatment.<sup>24</sup> I discovered and validated multi-omic predictors, in cancer<sup>25</sup> and other diseases, in public data, 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 | Society for Industrial and Applied Mathematics (SIAM) Mathematics and Statistics Month Honoree; <a href="https://siam.org/publications/siam-news/articles/siam-celebrates-mathematics-and-statistics-awareness-month-2025/#Alter">https://siam.org/publications/siam-news/articles/siam-celebrates-mathematics-and-statistics-awareness-month-2025/#Alter</a> |
|------|---|

- 2025 25th *Advances in Genome Biology and Technology (AGBT) General Meeting* (Marco Island, FL), Opening Session 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-2UCkPdQ>
- 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 *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*
- 1997 5th *International Conference on Squeezed States and Uncertainty Relations (FICUSSUR 1997)* (Balatonfüred, Hungary), Plenary Lecture

### Professional Activities

- 1/2025– ILAS, *Joint Mathematics Meetings (JMM)* Invited 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
- 3/2025 *SIAM Conference on Computational Science and Engineering (CSE25)* (Fort Worth, TX), Organizing Committee Member, Panel Moderator, and Invited Speaker
- 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*
- 9/2013 *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"*
- 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 proved that my multi-tensor algorithms, known as comparative spectral decompositions, (i) always converge, and (ii) almost always into a mathematically unique model, from any data types, of any number and dimensions.

#### 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 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](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](https://alterlab.org/in_the_news/Pavlou_Pathologist_2015_Feature.pdf)  
Feature: "Ovarian Cancer: Increasing Accuracy of Diagnosis, Prognosis," *USA Today* **144**, 8 (2016); [https://alterlab.org/in\\_the\\_news/Alter\\_USA\\_Today\\_2016\\_Feature.pdf](https://alterlab.org/in_the_news/Alter_USA_Today_2016_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) comprehensively remove batch effects and capture known biology, 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 clinical trial validation of a pattern of DNA copy-number alterations in brain tumors solved the 70 year-old problem of correctly predicting a patient's response and survival from their genome, and demonstrated that my predictors are (v) the most accurate and precise, (vi) clinically actionable in the general population based upon as few as 19 patients, and (vii) consistent across federated studies and over time. Recent experiments additionally demonstrated that the models (viii) correctly predict drug targets to sensitize a tumor to treatment.

#### 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**, "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)
- f. **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)
- g. **O. Alter**, M. Coppola, T. O. House and J. W. Tsai, "Multi-Tensor AI/ML Uniquely Able to Identify Mechanistically Interpretable and Actionable Predictors from Small-Cohort and Noisy High-Dimensional Multi-Omic Clinical Data," *2025 AACR Annual Meeting* (Chicago, IL). AACR (2025); <https://abstractsonline.com/pp8/#!/20273/presentation/5675>
- h. **O. Alter**, J.-I. Park, P. Guan, A. Zviran and L. N. Harris, "Quantum Mechanics-Based Multi-Tensor AI/ML Discovery of a Whole-Transcriptome Predictor of Response and Survival in Patients Treated with Dabrafenib and Trametinib in the Tumor-Agnostic Small-Cohort NCI-MATCH Subprotocol H with Validation in Three Tumor Types in TCGA," *2025 AACR Annual Meeting* (Chicago, IL). AACR (2025); <https://abstractsonline.com/pp8/#!/20273/presentation/10544>

C.4. I discovered and validated multi-omic predictors, in cancer and other diseases, in public data, 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**, 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)
- c. **O. Alter**, D. B. Oberman and A. Zviran, "Multi-Tensor AI/ML Discovery and Validation of Whole-Transcriptome Predictors of Survival in Response to Immunotherapy from Multi-Omic Clinical Data," *2025 AACR Annual Meeting* (Chicago, IL). AACR (2025); <https://abstractsonline.com/pp8/#!/20273/presentation/5676>

### Patents

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

C.5. My Ph.D. thesis in applied physics 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., *Physical Review D* **67**, 082001 (2003).

### D. Research Grants

|  | Grant              | PI              | Sponsor   | Period              | Total/Share |
|--|--------------------|-----------------|-----------|---------------------|-------------|
| 1.   | U01 CA-202144      | <b>O. Alter</b> | NIH/NCI   | 9/23/2015–8/31/2023 | \$3,395,986 |
| NIH/NCI Physical Sciences in Oncology U01 Project; <a href="https://app.dimensions.ai/details/grant/grant.4455012">https://app.dimensions.ai/details/grant/grant.4455012</a> |                    |                 |           |                     |             |
| 2.   | CAREER DMS-0847173 | <b>O. Alter</b> | NSF/DMS   | 8/1/2009 –7/31/2015 | \$400,053   |
| NSF/Division of Mathematical Sciences (DMS) Faculty Early Career Development (CAREER) Award  |                    |                 |           |                     |             |
| 3.   | R01 HG-004302      | <b>O. Alter</b> | NIH/NHGRI | 8/23/2007–5/31/2015 | \$1,768,525 |
| 4.   | K01 HG-000038      | <b>O. Alter</b> | 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 | <b>O. Alter</b> | DOE/Sloan | 9/1/1999 –8/31/2003 | \$100,000   |
| DOE/Alfred P. Sloan Foundation Postdoctoral Fellowship in Computational Molecular Biology  |                    |                 |           |                     |             |