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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
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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

I am a USTAR associate professor of bioengineering and human genetics at the Scientific Computing and Imaging Institute and the Huntsman Cancer Institute at the University of Utah,¹ a scientific advisory board member of the NCI-DOE Cancer Moonshot collaboration on predictive oncology, the principal investigator of the American Institute of Mathematics Quantum Research Community (AIM Q), and the CSO and a co-founder of Prism AI Therapeutics.² My \$3.4M NCI Physical Sciences in Oncology project³ partially supported my developing quantum mechanics-based multitensor AI/ML and solving the 75-year-old problem of correctly predicting—glioblastoma patients' survival, gene targets, and drug responses—from their genomes.⁴ As a genetics postdoctoral fellow at Stanford University, I invented the "eigengene" in a top 50 most cited *PNAS* paper of all time.⁵ My Ph.D. thesis in applied physics, also at Stanford, was published by Wiley⁶ and is recognized as crucial to quantum computing.⁷

I have mathematically proven that my AI/ML overcomes the challenges of real-world "skinny," noisy, and high-dimensional data.⁸ I have computationally shown that the algorithms, known as comparative spectral decompositions, are uniquely able to discover accurate, precise, actionable, and mechanistically interpretable predictors, applicable to the general population, from the multiomes of as few as 18 patients.⁹ I have experimentally demonstrated that the predictors consistently validate across laboratories and sometimes across indications, in federated and imbalanced studies and over time, and outperform all other indicators where they exist.¹⁰

Most Relevant Publications

Books

1. **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).

Journal Papers

2. **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).
3. 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

4. **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," *AACR Annual Meeting* (2025); [doi: 10.1158/1538-7445.AM2025-CT227](https://doi.org/10.1158/1538-7445.AM2025-CT227)
5. **O. Alter**, D. B. Oberman, D. Shabtai, J. W. Tsai and A. Zviran, "Discovery from Single-Cell RNA Sequencing Profiles of 18 CPTAC Glioblastoma Patients and Validation in Bulk Profiles of 138 TCGA Patients and Two Human-Derived Cell Lines of a Whole-Transcriptome Predictor of Overall Survival and Drug Targets by Using Quantum Mechanics-Based AI/ML," *ASCO Annual Meeting* (2026).

6. **O. Alter**, S. P. Ponnappalli, M. Coppola, A. C. Gushue, T. O. House, P. L. Miron, K. L. S. Miskimen, K. A. Waite, S. Pollock, D. Bogumil, E. P. Kiernan, H. Yang, J. Bowen, G. A. Nakouzi, D. Lipson, J. S. Barnholtz-Sloan, A. E. Sloan, T. R. Hodges, A. Zviran and J. W. Tsai, “Quantum Mechanics-Based Multi-Tensor AI/ML Correctly Predicts—Patients’ Overall Survival, Gene Targets, and Drug Responses—from Their Glioblastoma Tumors’ Whole Genomes,” *ASCO Annual Meeting* (2026).

Completed Projects Highlighted

	Project	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; 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				
3.	R01 HG-004302	O. Alter	NIH/NHGRI	8/23/2007–5/31/2015	\$1,768,525
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				

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

- 2026– NSF/American Institute of Mathematics (AIM) Quantum Research Community Project Grant, “AIM Q;” <https://alterlab.org/aim-q/>
 2025 Society for Industrial and Applied Mathematics (SIAM), Mathematics and Statistics Month Honors; <https://siam.org/publications/siam-news/articles/siam-celebrates-mathematics-and-statistics-awareness-month-2025/#Alter>
 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-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 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;” <https://aapm.org/org/history/SCSessionWinners.asp>
 2014 *Bloomberg L.P. Distinguished Speaker Lectures* (New York, NY), “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;” <https://ilasic.org/laa-lecturers/>
- 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 (ICSSUR 1997)* (Balatonfüred, Hungary), Plenary Lecture, “Impossibility of Determining the Quantum Wavefunction of a Single System and Fundamental Limit to External Force Detection”

Professional Activities

- 12/2025– State of Utah, Quantum Initiative Roundtable, University of Utah Representative
- 2/2024– University of Utah, Scientific Computing and Imaging (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”
- 2025–2027 ILAS, *Joint Mathematics Meetings (JMM)* Invited Speaker Selection Committee Member
- 11/2025 State of Utah, Pro Human AI Initiative Visioning Workshop, Invited Participant
- 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/vy8UZftSXXI>
- 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, 7/2021, 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; Virtual; 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 NIH/NCI, *Decade of the PS-ON at the NCI Virtual Symposium*, Co-Chair, Co-Organizer, and Invited Speaker; <https://youtu.be/5LKYwVby9Rc>
- 6/2020 *ACR Annual Meeting*, Education Session Co-Chair, Co-Organizer, and Invited Speaker, “AI/ML 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>
- 10/2018 *2018 Biomedical Engineering Society (BMES) Annual Meeting* (Atlanta, GA), Speaker and Panelist, “Physical Sciences in Oncology”
- 8/2018 *European Association for Signal Processing (EURASIP) Summer School on Tensors in Medicine* (Leuven, Belgium), Invited Speaker
- 9/2013 *2013 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;”
<https://genome.gov/11006874/vision-acknowledgements>

C. Contributions to Science

C.1. Mathematically proven that the algorithms, known as comparative spectral decompositions, (i) always converge to a model, (ii) which is almost always unique, (iii) where its computation is by definition lossless.

Journal Papers

1. **O. Alter**, P. O. Brown and D. Botstein, "Singular Value Decomposition for Genome-Wide Expression Data Processing and Modeling," *PNAS* **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).
2. **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)
3. 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* **104**, 18371 (2007); [doi: 10.1073/pnas.0709146104](https://doi.org/10.1073/pnas.0709146104)
4. 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," *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
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
5. 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

6. **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>
7. 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. Computationally demonstrated the discovery of accurate, precise, actionable, and mechanistically interpretable predictors, applicable to the general population, from the multiomes of as few as 18 patients.

Journal Papers

1. **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)
2. **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)
3. 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).
4. 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)
5. 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

6. **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

7. **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

8. **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. Experimentally demonstrated validation across laboratories and sometimes across indications, in federated and imbalanced studies and over time.

Journal Papers

1. 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)
2. 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)
3. 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).

Technical Reports

4. 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)
5. **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," *ASCO Annual Meeting* (2024); [doi: 10.1200/JCO.2024.42.16_suppl.e14028](https://doi.org/10.1200/JCO.2024.42.16_suppl.e14028)
6. **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," *AACR Annual Meeting* (2025); [doi: 10.1158/1538-7445.AM2025-3686](https://doi.org/10.1158/1538-7445.AM2025-3686)

C.4. Discovered, validated, and interpreted multiomic predictors, in cancer and other diseases, by using open-source data, establishing that the AI/ML is uniquely suited to personalized medicine.

Journal Papers

1. 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

2. **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," *ASCO Annual Meeting* (2024); [doi: 10.1200/JCO.2024.42.16_suppl.10043](https://doi.org/10.1200/JCO.2024.42.16_suppl.10043)
3. **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," *AACR Annual Meeting* (2025); [doi: 10.1158/1538-7445.AM2025-3687](https://doi.org/10.1158/1538-7445.AM2025-3687)

Patents

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