# BIOGRAPHICAL SKETCH

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NAME: Good, Zinaida

eRA COMMONS USER NAME (credential, e.g., agency login): ZINAGOOD

POSITION TITLE: Assistant Professor of Medicine

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

| INSTITUTION AND LOCATION | DEGREE *(if applicable)* | Completion Date MM/YYYY | FIELD OF STUDY |
|---|---|---|---|
| University of British Columbia, Vancouver, BC, Canada | B.S. | 05/2008 | Microbiology & Immunology |
| University of British Columbia, Vancouver, BC, Canada | M.S. | 05/2012 | Microbiology & Immunology |
| Stanford University, Stanford, CA | Ph.D. | 04/2018 | Computational & Systems Immunology |
| Stanford University, Stanford, CA | Postdoc | 01/2023 | Cell Therapy & Systems Immunology |
| Stanford University, Stanford, CA | Instructor | 12/2024 | Cell Therapy & Systems Immunology |

## A. Personal Statement

I am an Assistant Professor at Stanford University's Department of Medicine, with joint appointments in the Division of Immunology and Rheumatology and the Division of Computational Medicine. I also serve as the Director of the Data Hub at the Stanford Center for Cancer Cell Therapy. My masters training in experimental immunology, doctoral training in computational and systems immunology, and postdoctoral work on chimeric antigen receptor (CAR) T cell therapies have uniquely positioned my research program to tackle complex challenges in cancer immunotherapy through innovative computational approaches. My lab develops **advanced algorithms** for high-dimensional single-cell, spatial, and clinical data to identify **mechanisms of therapy resistance** based on **primary patient samples**. We leverage internal and public clinical multi-omic T cell therapy datasets to build **artificial intelligence systems** for enhanced T cell designs with improved predicted clinical outcomes. This approach enables us to test novel T cell design strategies preclinically in models that recapitulate clinical resistance mechanisms and gather sufficient data for clinical translation.

My work has already made significant contributions to the field. As a Parker Scholar and a Ph.D. student with Dr. Garry Nolan and Dr. Sean Bendall, I developed a method for tracking cell proliferative history, which led to the construction of a system to map and steer human T cell differentiation *ex vivo* (*Nat Biotech*, 2019). Further, my computational tool for single-cell developmental classification enabled deconstructing 'broken' B cell development to identify a developmental transition window linked to clinical outcome in acute lymphoblastic leukemia (*Nat Med*, 2018). As a Parker Bridge Fellow, an NIH K99/R00 Fellow, and a postdoctoral fellow with Dr. Crystal Mackall and Dr. Sylvia Plevritis, I developed algorithms to learn actionable insights from multimodal single-cell and spatial data from patients receiving CAR T cell therapies for cancer. With these tools, I identified post-infusion CAR T regulatory cells as a biomarker for resistance to CD19-CAR therapy in large B cell lymphoma (LBCL; *Nat Med*, 2022). Since the launch of my independent lab in January 2025, we performed a lineage tracing study to define ‘therapeutic’ CD19-CAR T cells in LBCL (senior author: *In Preparation*) and applied this workflow to CD22-CAR therapy for LBCL (co-senior author: *Nat Cancer – Under Review*), GD2-CAR therapy for DMG (*In Submission*), and CD5-CAR therapy for T-ALL (*In Preparation*). We have also identified pre-existing mechanisms of CD19-CAR resistance in the LBCL tumor microenvironment (senior author: *Cancer Cell – Under Review*) and built the first two AI models for CAR T cell design (senior author: *ICML, 2025; NeurIPS, 2025*) and broadly applicable biomedical AI models (senior author: *ICML – In Press;* co-senior author: *arXiv, 2026; bioRxiv, 2026*). I look forward to building on these initial successes by developing advanced systems to optimize engineered T cell therapies for clinical efficacy in hematologic cancers and solid tumors.

Ongoing and recently completed projects that I would like to highlight include:

**2P01CA049605** Negrin, Miklos (MPI) 09/01/2024 – 06/30/2030
NIH/NCI
*Bone Marrow Grafting and Cellular Therapy for Leukemia and Lymphoma*
Role: Project 2 Co-Lead; Core C Co-I; transition to Project 2 Lead planned in Year 1; wrote Project 2 proposal

**1OT2OD038101** Mackall, Gevaert, Good (MPI) 01/23/2025 – 01/22/2027
NIH Office of the Director
*Multimodal AI Modeling of T Cell therapies to Predict Patient Response & Nominate Cell Design Strategies*
Role: Co-PI & Project Manager; wrote proposal & serving as a project lead

**1K99CA293149, 4R00CA293149** Good (PI) 07/01/2024 – 12/31/2027
NIH/NCI
*Learning Features of Optimal CAR T Cells for LBCL from Patient Data*
Role: PI

**Parker Bridge Fellow** Good (PI) 02/01/2023 – 01/31/2026
Parker Institute for Cancer Immunotherapy
*Defining a Therapeutic CAR T Cell in Patients with Cancer*
Role: PI

Citations:

a. Tsui KY*, Rodrigues KB*, Zhan X*, Chen Y, Mo KC, Mackall CL, Miklos DB, Gevaert O[§], **Good Z**[§]. (2025). Patient-level prediction from single-cell data using attention-based multiple instance learning with regulatory priors. ***Proceedings to the 39th Conference on Neural Information Processing Systems,*** AI4DS: 16. PDF: https://openreview.net/attachment?id=Y3Dqqv1RYQ&name=pdf.
b. **Good Z***, Spiegel JY*, Sahaf B, Malipatlolla MB, Ehlinger ZJ, Kurra S, Desai MH, Reynolds WD, Wong Lin A, Vandris P, Wu F, Prabhu S, Hamilton MP, Tamaresis JS, Hanson PJ, Patel S, Feldman SA, Frank MJ, Baird JH, Muffly L, Claire GK, Craig J, Kong KA, Wagh D, Coller J, Bendall SC, Tibshirani RJ, Plevritis SK, Miklos DB[§], Mackall CL[§]. (2022). Post-infusion CAR $T_{reg}$ cells identify patients resistant to CD19-CAR therapy. ***Nature Medicine***, 28(9): 1860-1871. PMID: 36097223.
c. **Good Z**, Borges L, Vivanco Gonzalez N, Sahaf B, Samusik N, Tibshirani R, Nolan GP[§], Bendall SC[§]. (2019). Proliferative tracing with single-cell mass cytometry optimizes generation of stem cell memory-like T cells. ***Nature Biotechnology***, 37(3): 259-66. PMID: 30742126.
d. **Good Z***, Sarno J*, Jager A, Samusik N, Aghaeepour N, Simonds EF, While L, Lacayo NJ, Fantl WJ, Fazio G, Gaipa G, Biondi A, Tibshirani R, Bendall SC, Nolan GP[§], Davis KL[§]. (2018). Single-cell developmental classification of B cell precursor acute lymphoblastic leukemia at diagnosis reveals predictors of relapse. ***Nature Medicine***, 24(4): 474-83. PMID: 29505032.

*Co-first author; [§]co-senior author. I have previously used another name: Zinaida Tebaykina.

**B. Positions, Scientific Appointments, and Honors**

**Positions and Scientific Appointments**

| | |
|---|---|
| 2025 – Present | Investigator, Weill Cancer Hub West |
| 2025 – Present | Assistant Professor, Division of Immunology & Rheumatology and Division of Computational Medicine, Department of Medicine, Stanford University, Stanford, CA |
| 2024 – Present | Director, Cancer Cell Therapy Data Hub, Center for Cancer Cell Therapy, Stanford Cancer Institute (SCI), Stanford University |
| 2017 – Present | Investigator, Parker Institute for Cancer Immunotherapy |
| 2023 – 2024 | Instructor, SCI and Department of Biomedical Data Science (DBDS), Stanford University |
| 2018 – 2023 | Postdoctoral Fellow, SCI and DBDS, Stanford University |
| 2013 – 2018 | Ph.D. Student, Microbiology & Immunology (M&I) and Pathology, Stanford University |
| 2012 – 2013 | Research Associate, Discovery Oncology, Genentech, Inc., South San Francisco, CA |
| 2011 | Intern, Discovery Oncology, Genentech, Inc. |
| 2008 – 2012 | M.S. Student, M&I, University of British Columbia, Vancouver, BC, Canada |
| 2007 | Intern, Process Virology, Genentech, Inc. |
| 2006 | Intern, Medical Biophysics, BC Cancer Research Center, Vancouver, BC, Canada |
| 2005 | Laboratory Assistant, M&I, University of British Columbia |

**Honors**

| | |
|---|---|
| 2026 | Laude Institute MOONSHOT // ONE Honorable Mention |
| 2026 | Stanford Center for Digital Health 2026 pilot project award |
| 2025 – 2030 | NIH Program Project Grant Project 2 Co-Lead and Core C Investigator (P01) |
| 2025 – 2029 | Investigator and Project 3 Lead, Team PROMISE, Weill Cancer Hub West |
| 2025 – 2027 | NIH Office of the Director Multimodal AI Initiative Award (OT2) |
| 2024 – 2027 | NIH Pathway to Independence Award (K99/R00) |
| 2024 – 2025 | Kona Innovation Challenge Award, Parker Institute for Cancer Immunotherapy |
| 2024 – 2025 | Institutional Research Grant Pilot Project Award, SCI and American Cancer Society |
| 2024 | Woman in Cancer Research Scholar, American Association for Cancer Research |
| 2024 | NIH Research Accelerator Program (ReCAP) Scholar |
| 2023 – 2026 | Parker Bridge Fellow, Parker Institute for Cancer Immunotherapy |
| 2022 – 2024 | Pilot Project Award, 10x Genomics and Parker Institute for Cancer Immunotherapy |
| 2022 | Fellow, Arthur and Sandra Irving Cancer Immunology Symposium |
| 2022 | NK and Irene Cheung Family Scholar, Keystone Symposia |
| 2020 – 2021 | Stanford Cancer Institute Fellowship, Stanford University |
| 2020 – 2021 | Pilot Project Grant, NIH-U54 Center for Cancer Systems Biology, Stanford University |
| 2019 | Abstract Achievement Award, American Society of Hematology |
| 2019 | Best Q1 2019 Paper, Parker Institute for Cancer Immunotherapy |
| 2019 | Scholarship, Keystone Symposia |
| 2018 – 2020 | Parker Scholar, Parker Institute for Cancer Immunotherapy |
| 2017 | CYTO Image Analysis Challenge Finalist, Int. Society for Advancement of Cytometry |
| 2016 | CYTO Exceptional Student Award Finalist, Int. Society for Advancement of Cytometry |
| 2012 – 2013 | Featured Wikipedia Editor, Wikimedia Foundation (2 times) |
| 2011 | 1st place: DARPA Shredder Challenge, Defense Advanced Research Projects Agency |
| 2009 | 2nd place: Junior Poster Competition, Life Sciences Institute, Vancouver, BC, Canada |
| 2008 | Graduate Entrance Scholarship, University of British Columbia, Vancouver, BC, Canada |

**C. Contribution to Science**

***1. Artificial intelligence systems for T cell therapy design.*** Given the limitations of preclinical assays and animal models, the field of T cell therapies does not yet have an effective method for identifying therapeutic candidates that are optimized for performance in patients. Artificial intelligence (AI) approaches offer an exciting opportunity to tackle this problem by learning unified representations directly from single-cell, spatial, and other primary patient data modalities to uncover patterns imperceptible to human intuition or common statistical approaches. My lab leverages innovation in machine learning and clinical multi-omic T cell therapy datasets to build AI systems that nominate T cell engineering strategies to enhance predicted patient outcomes, which we then validate in preclinical models that mimic clinical mechanisms of resistance. We posit that T cell designs that both perform well in preclinical models and predicted to improve patient outcomes are poised for success during clinical translation compared to designs based on preclinical data alone. My lab has built the first two AI models, *tcellMIL* (*NeurIPS, 2025*) and *tcellNF* (*ICML, 2025*) for single-cell sequencing CAR T data, developed a CAR T Raman method (*bioRxiv, 2026*), and created *SAGE-FM* (*arXiv, 2026*) and *SpatialWhisperer* (*ICML – In Revision*) biomedical AI models. I also contributed to *CellFuse* (*Cancer Research – In Press*), and *MONTAGE* (*Cell – In Revision*) tools for multimodal data and *CELESTA* for spatial proteomics data (*Nat Methods, 2022*).

a. Tsui KY*, Rodrigues KB*, Zhan X*, Chen Y, Mo KC, Mackall CL, Miklos DB, Gevaert O§, **Good Z§**. (2025). Patient-level prediction from single-cell data using attention-based multiple instance learning with regulatory priors. ***Proceedings to the 39th Conference on Neural Information Processing Systems,*** AI4DS: 16. PDF: https://openreview.net/attachment?id=Y3Dqqv1RYQ&name=pdf.
b. Stiber A, Quach B, Ogunlade B, Georgiadis A, Chang K, Li Y, Quinn P, Wang H, Ang C, Sotillo E, Mackall CL§, **Good Z§**, Dionne JA§. Dynamic, single-cell monitoring of CAR T cell identity and activation with Raman spectroscopy. *Nature – In Revision. bioRxiv* (2026). DOI: 10.64898/2026.02.22.707331.
c. Zhan X*, Xu JW*, Zheng Y, **Good Z§**, Gevaert O§. SAGE-FM: A lightweight and interpretable spatial transcriptomics foundation model. *Nature Machine Intelligence – Submitted*. *arXiv* (2026). DOI: 10.48550/arXiv.2601.15504.
d. Kadaba SE*, Eapen AK*, Tsui KY, Pang K, Roth TL§, **Good Z§**. (2025). Conditional normalizing flows for the design of T cell therapies. ***Proceedings of the 42nd International Conference on Machine Learning***, FM4LS: 43. PDF: https://openreview.net/pdf?id=uuQjL4L0J9.

***2. Lineage tracing to define a 'therapeutic' CAR T cell in patients with cancer.*** Only a small fraction of 'therapeutically relevant' CAR T cells persist following infusion. Accordingly, during my postdoctoral work with Dr. Crystal Mackall and Dr. Sylvia Plevritis at Stanford University, I developed a platform for fate mapping studies based on endogenous TCR sequence as a 'barcode' and applied it to CD19-CAR and CD19/CD22-CAR (NCT03233854) T cell therapies for large B cell lymphoma (LBCL) (*AACR, 2024; In Preparation*). This platform is now broadly used, and I mentored two postdoctoral fellows on analyses of CD22-CAR T cell therapy for LBCL (NCT04088890; *Nature Cancer – Under Review*) and GD2-CAR T cell therapy for diffuse midline glioma (NCT04196413; *Nature, 2022*; *In Preparation*). I also contributed to deep profiling of T cell lymphoma after CAR T cell therapy (*NEJM, 2024*) and to advancing single-cell sequencing technologies (*Nat Med, 2022*).

a. Kramer AM, Murty T, Chen Y, Hamilton MP, Desai MH, Kuo A, Ehlinger ZJ, Reynolds WD, Srinagesh HK, Tsui KY, Rietberg S, Mo KC, Baird JH, Su YJ, Agarwal N, Sotillo E, Prabhu S, Sahaf B, Ramakrishna S, Muffly LS, Mackall CL, Miklos DB, **Good Z**[§], Frank MJ[§]. CD22-CAR T cell multiomic features linked to patient outcomes in CD19-CAR resistant large B cell lymphoma. ***Nature Cancer – Under Review.***
b. **Good Z***, Hamilton MP*, Spiegel JY, Kurra S, Desai MH, Prabhu S, Chiou SH, Yeh CY, Chen Y, Yang E, Ozawa MG, Wu F, Frank MJ, Muffly L, Claire GK, Craig J, Iglesias MI, Bharadwaj S, Kong KA, Wagh D, Coller J, Davis MM, Plevritis SK, Sahaf B, Miklos DB[§], and Mackall CL[§]. Lineage tracing of CAR T cells in patients with B cell malignancies. ***American Association for Cancer Research Annual Meeting*** (2024); San Diego, CA.
c. Hamilton MP*, Sugio T*, Noordenbos T*, Shi S, Bulterys PL, Long Liu C, Olsen MN, **Good Z**, Dahiya S, Frank MJ, Sahaf B, Mackall CL, Gratzinger D, Diehn M, Alizadeh AA[§], Miklos DB[§]. (2024). Risk of second malignancies & T-cell lymphoma after chimeric antigen receptor T-cell therapy. ***New England Journal of Medicine***, 390(22): 2047-2060. PMID: 38865660.
d. Majzner RG*, Ramakrishna S*, Yeom KW, Patel S, Chinnasamy H, Schultz LM, Richards RM, Barsan V, Mancusi R, Geraghty AC, **Good Z**, Mochizuki A, Gillespie SM, Martin A, Toland S, Mahdi J, Reschke A, Chau I, Nie E, Chau AJ, Rotiroti MC, Mount CW, Baggott C, Mavroukakis S, Egeler E, Moon J, Erickson C, Green S, Kunicki M, Fujimoto M, Ehlinger Z, Reynolds W, Kurra S, Warren KE, Prabhu S, Vogel H, Rasmussen L, Cornell TT, Partap S, Fisher PG, Campen CJ, Filbin M, Grant G, Sahaf B, Davis KL, Feldman SA, Mackall CL[§], Monje M[§]. (2022). GD2-CAR T cell therapy for H3K27M-mutated diffuse midline gliomas. ***Nature***, 603(7903): 934–941. PMID: 35130560.

***2. Identification of CAR $T_{reg}$ cells as limiting CAR T cell expansion, efficacy, and toxicity.*** CAR T cell therapies have demonstrated remarkable response rates in hematologic malignancies and hold promise for other types of cancer, autoimmune diseases, and transplantation. However, limited CAR T cell expansion and persistence, as well as hostile tumor microenvironment (TME), restrict efficacy of CAR T cell therapies. In postdoctoral training, I found that $CAR^+$ $T_{reg}$ cells are associated with reduced CD19-CAR T cell expansion, efficacy, and toxicity in patients with LBCL (*Nat Med, 2022*), and this discovery was independently validated by Marcela Maus' group (*Nat Med, 2022*). I had the opportunity to mentor a postbaccalaureate trainee on the TME analysis, and we found that $CCL8^+CCL13^+$ tumor-associated macrophages drive early resistance to CAR T cell therapy for LBCL (*Cancer Cell – Under Review*). I also contributed to studies on the mechanisms of CAR T cell exhaustion (*Nature, 2024; Nature, 2019; Science, 2021*), CD22-CAR (*Cancer Discovery, 2025*), CAR TME (*Cancer Cell – In Press*) and the first reversal of human immune aging (*Aging Cell, 2019*). Finally, I contributed to Stanford's Computational and Systems Immunology Ph.D. training program improvement and described key aspects of implementing a similar program at another institution (*Trends Immunol, 2019*).

a. Mo KC*, Kramer AM*, Yeh CY, Hamilton MP, Spiegel JY, Desai MH, Ehlinger ZJ, Reynolds WD, Yang E, Ozawa MG, Chen Y, Rietberg S, Prabhu S, Lee C, Frank MJ, Muffly L, Claire GK, Bharadwaj S, Dahiya S, Kong KA, Sotillo E, Sahaf B, Plevritis SK, Miklos DB[§], Mackall CL[§], **Good Z**[§]. $CCL8^+CCL13^+$ tumor-associated macrophages drive early resistance to CAR T cell therapy in large B cell lymphoma. ***Cancer Cell – Under Review.***
b. **Good Z***, Spiegel JY*, Sahaf B, Malipatlolla MB, Ehlinger ZJ, Kurra S, Desai MH, Reynolds WD, Wong Lin A, Vandris P, Wu F, Prabhu S, Hamilton MP, Tamaresis JS, Hanson PJ, Patel S, Feldman SA, Frank MJ, Baird JH, Muffly L, Claire GK, Craig J, Kong KA, Wagh D, Coller J, Bendall SC, Tibshirani RJ, Plevritis SK, Miklos DB[§], Mackall CL[§]. (2022). Post-infusion CAR $T_{reg}$ cells identify patients resistant to CD19-CAR therapy. ***Nature Medicine***, 28(9): 1860-1871. PMID: 36097223.
c. Weber EW, Lynn RC, Parker KR, Lattin J, Anbunathan H, Sotillo E, **Good Z**, Malipatlolla M, Xu P, Vandris P, Majzner RG, Chen L-C, Wandless TJ, Chang HY, Satpathy AT, Mackall CL. (2021). Transient rest

restores functionality in exhausted CAR-T cells through epigenetic remodeling. ***Science***, 2;372(6537): eaba1786. PMID: 33795428.

d. **Good Z**, Glanville G, Gee MH, Davis MM, Khatri P. (2019). Computational and systems immunology: a students' perspective. ***Trends in Immunology***, 40(8): 665-8. PMID: 31288986.

***4. Algorithms to construct and control lymphocyte differentiation trajectories in health and cancer***. Cellular differentiation is a coordinated process that integrates complex signaling networks to make decisions about cell identity, proliferation, and death. Emerging technologies for deep single-cell phenotyping enabled viewing differentiation as a continuous process, where individual cells are aligned onto a trajectory based on their phenotypes. In my Ph.D. work with Dr. Garry Nolan and Dr. Sean Bendall at Stanford University, I developed an assay to trace cell proliferative history and built a single-cell map of human T cell differentiation in the context of expansion for immunotherapy. Regulatory signaling on this map informed a strategy to steer differentiation towards a clinically desirable T stem cell memory subset (*Nat Biotechnol, 2019*). I further demonstrated clinical utility of a known cell differentiation trajectory. By aligning single B-lineage leukemia cells onto a scaffold of normal human B cell development, I identified a signaling state at a developmental transition from late pro-B to early pre-B cells that predicted relapse based on a diagnostic bone marrow biopsy (*Nat Med, 2018*). This work resulted in a PICI multinational patent and led to several ongoing projects at Stanford and beyond. I also co-developed a novel software for single-cell data embedding, clustering, and visualization called *VorteX* (*Nat Methods, 2016*), which became widely used for single-cell data analysis.

a. **Good Z**, Borges L, Vivanco Gonzalez N, Sahaf B, Samusik N, Tibshirani R, Nolan GP[§], Bendall SC[§]. (2019). Proliferative tracing with single-cell mass cytometry optimizes generation of stem cell memory-like T cells. ***Nature Biotechnology***, 37(3): 259-66. PMID: 30742126.

b. **Good Z***, Sarno J*, Jager A, Samusik N, Aghaeepour N, Simonds EF, While L, Lacayo NJ, Fantl WJ, Fazio G, Gaipa G, Biondi A, Tibshirani R, Bendall SC, Nolan GP[§], Davis KL[§]. (2018). Single-cell developmental classification of B cell precursor acute lymphoblastic leukemia at diagnosis reveals predictors of relapse. ***Nature Medicine***, 24(4): 474-83. PMID: 29505032.

c. **Good Z**. (2018). Lymphocyte differentiation trajectories in human health and cancer. ***Stanford University Libraries Digital Repository***, winter 2018 collection: Ph.D. thesis in Immunology.

d. Samusik N, **Good Z**, Spitzer MH, Davis KL, Nolan GP. (2016). Automated mapping of phenotype space with single-cell data. ***Nature Methods***, 13(6): 493-6. PMID: 27183440.

***5. Identification of strategies to prevent therapy resistance in solid tumors.*** Tumor re-initiating cells (TRICs) are malignant cells that survive chemotherapy and initiate cancer relapse. Working with Dr. Kevin Leong within Discovery Oncology at Genentech, I co-developed an orthotopic xenograft mouse model of colorectal cancer (*Nat Commun, 2014*), which we utilized to characterize and target TRICs. Using a genetically engineered mouse model of breast cancer, I further identified drug targets of TRICs in breast cancer (*PLoS One, 2013*). Based on these targets, we developed several potential therapeutic leads for the Genentech preclinical drug development pipeline. Prior to this work, I contributed to cancer research during two eight-month internships in the laboratories of Dr. Aly Karsan at the British Columbia Cancer Research Center (*Am J Physiol Heart Circ Physiol, 2011*) and Dr. Bin Yang at Genentech (*Biotechnol Bioeng, 2009*). Finally, I contributed to understanding the mechanisms of immune memory during my M.S. studies with Dr. Michael Gold at the University of British Columbia.

a. Enquist IB, **Good Z**, Jubb AD, Fuh G, Wang X, Junttila MR, Jackson EL, Leong KG. (2014). Lymph node-independent liver metastasis in a model of metastatic colorectal cancer. ***Nature Communications***, 26(5): 3530. PMID: 24667486.

b. Franci C, Zhou J, Jiang Z, Modrasan Z, **Good Z**, Jackson EL, Kouros-Mehr H. (2013). Biomarkers of residual disease, disseminated tumor cells, and metastases in the MMTV-PyMT breast cancer model. ***PLoS One***, 8(3): e58183. PMID: 23520493.

c. **Tebaykina Z**. (2012). Characterization of processing bodies in T and B lymphocytes. ***clRcle Library at the University of British Columbia***, spring 2012 collection: M.S. thesis in Microbiology and Immunology.

d. Strauss DM, Lute S, **Tebaykina Z**, Frey DD, Ho C, Blank GS, Brorson K, Chen Q, Yang B. (2009). Understanding the mechanism of virus removal by Q sepharose fast flow chromatography during the purification of CHO-cell derived biotherapeutics. ***Biotechnology & Bioengineering***, 104(2): 371-80. PMID: 19575414.

Complete List of Published Work in MyBibliography:

https://www.ncbi.nlm.nih.gov/myncbi/zinaida.good.1/bibliography/public/