BIOGRAPHICAL SKETCH

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NAME: Good, Zinaida

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

POSITION TITLE: Postdoctoral Fellow

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	Postdoctoral	Present	Systems Biology & Immunology

A. Personal Statement

I am a cross-trained scientist with expertise in systems biology, immunology, and oncology. My postdoctoral training with Profs. Crystal Mackall and Sylvia Plevritis at Stanford University is focused on investigating how engineered cellular immunotherapies succeed or fail in patients. Leveraging multimodal single-cell data analysis, tumor microenvironment imaging, and data integration, I aim to identify features of an 'optimal engineered T cell' from patient data. I earned a Ph.D. in Computational and Systems Immunology from Stanford University in 2018, where I trained with Profs. Garry Nolan and Sean Bendall. My background is in immunology (B.S. and M.S. from the University of British Columbia in Vancouver, Canada) and oncology (I worked in Discovery Oncology at Genentech and at the British Columbia Cancer Research Center for a combined 3 years). As a result of my academic training and work experiences, I became an inventor on 2 patent applications, co-authored 12 papers, and published 4 first-author manuscripts. My work and academic potential have been recognized by postdoctoral fellowships from the Parker Institute for Cancer Immunotherapy and the Stanford Cancer Institute, and I have been named an Arthur and Sandra Irving Cancer Immunology Fellow in 2022. My *short-term goal* is to launch an independent academic career spanning the systems biology and cancer immunotherapy fields. My *long-term goal* is to better understand and enhance engineered cellular immunotherapies for patients with cancer.

Citations:

a. **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.

b. **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.

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

2021 – Present	Member, Society for Immunotherapy of Cancer
2019 – Present	Member, American Society of Hematology
2018 – Present	Postdoctoral Fellow, Stanford Cancer Institute / DBDS, Stanford University, Stanford, CA
2017 – Present	Member, Parker Institute for Cancer Immunotherapy
2016 – Present	Member, American Association for Cancer Research
2013 – 2018	Ph.D. Student, M&I / Pathology, Stanford University, Stanford, CA
2012 – 2013	Research Associate, Discovery Oncology, Genentech, Inc., South San Francisco, CA
2011	Intern, Discovery Oncology, Genentech, Inc., South San Francisco, CA
2008 – 2012	M.S. Student, M&I, University of British Columbia, Vancouver, BC, Canada
2007	Intern, Process Virology, Genentech, Inc., South San Francisco, CA
2006	Intern, Medical Biophysics, BC Cancer Research Center, Vancouver, BC, Canada
2005	Laboratory Assistant, M&I, University of British Columbia, Vancouver, BC, Canada

Honors

2022 – 2023	Pilot Project Support, 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, Stanford, CA
2020 – 2021	Pilot Project Grant, NIH-U54 Stanford Center for Cancer Systems Biology, Stanford, CA
2019	Abstract Achievement Award, American Society of Hematology
2019	Best Q1 2019 Paper, Parker Institute for Cancer Immunotherapy, San Francisco, CA
2019	Scholarship, Keystone Symposia
2018 – 2020	Parker Scholar, Parker Institute for Cancer Immunotherapy, San Francisco, CA
2017	CYTO Image Analysis Challenge Finalist, Int. Society for Advancement of Cytometry
2016 – 2018	Stanford Biosciences Travel Grant (3 times), Stanford University, Stanford, CA
2016 – 2017	CYTO Student Travel Award (2 times), 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, San Francisco, CA (2 times)
2011	1st place: DARPA Shredder Challenge, Defense Advanced Research Projects Agency
2011	4th place: Speed Poster Competition, ImmunoVancouver, Vancouver, BC, Canada
2009	2nd place: Junior Poster Competition, Life Sciences Institute, Vancouver, BC, Canada
2008	Graduate Entrance Scholarship, University of British Columbia, Vancouver, BC, Canada
2007	WithinSight National Leadership Conference Delegate, University of British Columbia Vancouver, BC, Canada; Queen's University, Kingston, ON, Canada
2004 – 2008	Dean's Honor List (8 times), University of British Columbia, Vancouver, BC, Canada

C. Contribution to Science

1. Identification of strategies to prevent relapse in colorectal and breast cancer. Tumor re-initiating cells (TRICs) are malignant cells that survive chemotherapy regimens and initiate cancer relapse. Working with Dr. Kevin G. Leong within Discovery Oncology at Genentech, I co-developed an orthotopic xenograft mouse model of colorectal cancer (*Enquist IB, Good Z, et al. 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 (*Franci C, …, Good Z, et al. 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 the oncology research during my two eight-month internships. In the laboratory of Dr. Aly Karsan at the British Columbia Cancer Research Center, I refined a TLR signaling pathway in endothelial cells that drives tumor angiogenesis (*Dauphinee SM, …, Tebaykina Z, et al. Am J Physiol Heart Circ Physiol, 2011*). Working with Dr. Bin Yang in Process Virology at Genentech, I defined distinct mechanisms of enveloped and

non-enveloped viral clearance during biotherapeutic antibody manufacturing (*Strauss DM, …, Tebaykina Z, et al. Biotechnol Bioeng, 2009*).

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. Dauphinee SM, Voelcker V, **Tebaykina Z**, Wong F, Karsan A. (2011). Heterotrimeric Gi/Go proteins modulate endothelial TLR signaling independent of the MyD88-dependent pathway. ***American Journal of Physiology – Heart and Circulatory Physiology***, 301(6): H2246-53. PMID: 21949112.

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.

2. Characterization of processing bodies in T and B lymphocytes. Translational control is an active area of research within immunology. In my M.S. work with Prof. Michael R. Gold at the University of British Columbia, I was fortunate to pursue my own idea about a novel mechanism of immune memory, with a long-term goal of a better immune control. Utilizing the protocol that I developed for dual analysis of proteins and mRNA transcripts in lymphocytes by flow cytometry and confocal microscopy, I characterized three types of mRNA processing bodies (P-bodies) in primary T and B lymphocytes. Using the OT-I model of immune memory, I found that non-degrading P-bodies in memory $CD8^+$ T cells co-localize with interferon-γ mRNA, indicating that P-bodies may store pre-synthesized effector mRNAs, and this concept merits further exploration.

a. **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.

b. **Tebaykina Z**, Choi K, Osborne LC, Abraham N, Gold MR. The role of mRNA processing bodies in memory $CD8^+$ T cells. ***Oral Presentation, 24th Canadian Society for Immunology Meeting*** (2011); Lake Louise, AB, Canada.

3. Algorithms to construct and control lymphocyte differentiation trajectories in human 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, such as mass cytometry and single-cell RNA-sequencing (scRNA-seq), 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 Profs. Garry P. Nolan and Sean C. Bendall at Stanford University, I developed an assay to trace cell proliferative history by mass cytometry 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 (*Good Z, et al. 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 (*Good Z, et al. Nat Med, 2018*). These studies resulted in two patent applications 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* (*Samusik N, Good Z, et al. Nat Methods, 2016*). This software is now 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.

4. Identification of CAR T_{Reg} cells as limiting CAR T cell expansion, efficacy, and toxicity. Engineered CAR T cell therapies have demonstrated extraordinary response rates in hematologic malignancies and hold promise for other types of cancer. However, limited CAR T cell expansion, persistence, and hostile tumor microenvironment restrict efficacy of CAR T cell therapies, especially in solid tumors. In my postdoctoral work with Profs. Crystal L. Mackall and Sylvia K. Plevritis at Stanford University, I identified a subset of CAR^+ T_{Reg} cells associated with reduced CAR T cell expansion, efficacy, and toxicity in patients with large B cell lymphoma (LBCL) receiving axi-cel, an FDA-approved CD19-targeted CAR T cell therapy (*Good Z, et al. Invited Talk at the 2021 Annual Meeting of the Society for Immunotherapy of Cancer;* Good Z, *et al. Nat Med, 2022*). In my proposed work, I will be addressing outstanding questions related to the CAR T_{Reg} cell origins and modulating this subset to achieve better efficacy while managing toxicity. Early in my postdoctoral training, I completed the analysis of two large single-cell datasets on the mechanisms of CAR T cell exhaustion (*Lynn RC, …, Good Z, et al. Nature, 2019; Weber EW, …, Good Z, et al. Science, 2021*) and contributed to a study that demonstrated reversal of human immune aging (*Fahy GM, …, Good Z, et al. Aging Cell, 2019*).

a. **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.

b. Lynn RC, Weber EW, Sotillo E, Gennert D, Xu P, **Good Z**, Anbunathan H, Lattin J, Jones R, Tieu V, Granja J, DeBourcy C, Xu P, Majzner R, Satpathy AT, Quake SR, Chang H, Mackall CL. (2019). c-Jun overexpression in CAR T cells induces exhaustion resistance. ***Nature***, 576(7786): 293-300. PMID: 31802004.

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. Fahy GM, Brooke RT, Watson JP, **Good Z**, Vasanawala SS, Maecker H, Leipold M, Lin DTS, Kobor MS, Horvath S. (2019). Reversal of epigenetic aging and immunosenescent trends in humans. ***Aging Cell***, 18(6): e13028. PMID: 31496122.

5. Lineage tracing to define a 'therapeutic' CAR T cell in patients with cancer. Despite diverse *in vitro* assays and mouse models, the field of engineered cell therapies does not yet have an effective method for identifying therapeutic candidates that perform best in patients and has not yet defined the best 'therapeutic' CAR T cell (Bucktrout SL, …, Good Z, *et al. Nat Med,* 2022). Accordingly, this proposal includes fate mapping studies in patients treated with axi-cel or bispecific CD19/CD22-targeted CAR T cells for LBCL (NCT03233854) (Aim 1), with initial results from the axi-cel cohort recently presented (*Good Z, et al. Oral Presentation at the 2022 Annual Meeting of the American Association for Cancer Research*). In preliminary work towards Aim 2, I defined scRNA-seq correlates of response in GD2-targeted CAR T cells from our first four pediatric patients with diffuse midline glioma (DMG), a universally lethal cancer of the central nervous system (NCT04196413; *Majzner RG, …, Good Z, et al. Nature, 2022)*. To set the stage for Aim 3, I developed an integrative analysis pipeline for single-cell sequencing and CODEX high-dimensional imaging data. I successfully used this pipeline to build a single-cell atlas of head and neck squamous cell carcinoma (HNSCC), an example of a solid tumor and the next frontier for CAR T cell therapies (*Zhang W, …, Good Z, et al. Nat Methods, 2022; Good Z, et al. Oral Presentation at the 7th Annual Stanford Center for Cancer Systems Biology Symposium, 2021; Zhang W and Good Z, et al. In Preparation*). I also contributed to the development of a PET probe for tracking CAR T cells *in vivo* (*Simonetta F, …, Good Z, et al. Clin Cancer Res, 2020)*. As one of the inaugural graduates from Stanford's new Computational and Systems Immunology (CSI) Ph.D. track, I contributed to Stanford's CSI training program enhancement and described key aspects of implementing a similar program at another institution (*Good Z, et al. Trends Immunol, 2019*).

a. Bucktrout SL, Banovich NE, Butterfield LH, Cimen-Bozkus C, Giles JR, **Good Z**, Goodman D, Jonsson V, Laraeu C, Marson A, Maurer DM, Munson PV, Stubbington M, Taylor S, and Cutchin A. Advancing T cell-based cancer therapy with single cell technologies. (2022). ***Nature Medicine***, 28(9): 1761-1764. PMID: 36127419.

b. 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.

c. Zhang W, Li I, Reticker-Flynn NE, **Good Z**, Chang S, Samusik N, Saumyaa S, Li Y, Zhou X, Liang R, Kong CS, Le QT, Gentles AJ, Sunwoo JB, Nolan GP, Engleman EG, Plevritis SK. (2022). Identification of cell types in multiplexed in situ images by combining protein expression and spatial location using CELESTA reveals spatial biology. ***Nature Methods***, 19(6): 759-769. PMID: 35654951.

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.

Complete List of Published Work in MyBibliography:

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