

NIH BIOGRAPHICAL SKETCH COMMON FORM

Name: Pearlman, Alexander

Persistent Identifier (PID) of the Senior/Key Person: <https://orcid.org/0000-0002-0465-5886>

Position Title: Consultant

Organization and Location: Self Employed, Boca Raton, Florida, United States

PROFESSIONAL PREPARATION

INSTITUTION AND LOCATION	DEGREE	Start Date	Completion Date	FIELD OF STUDY
New York University, New York, New York, United States	Doctor of Philosophy (PHD)	04/2004	05/2009	Computational Biology
New York University, New York, New York, United States	Master of Science (MS)	01/1998	05/1999	Molecular Biology
New York Institute of Technology, Brookville, New York, United States	Bachelor of Science (BS)	09/1991	05/1996	Biomedical Engineering

Appointments and Positions

2020 - present Consultant, Self Employed, Boca Raton, Florida, United States

2020 - 2023 Chief Scientific Officer, Hursana, LLC, White Plains, New York, United States

2020 - 2022 Consultant, Albert Einstein College of Medicine, Cancer Center, Bronx, New York, United States

2017 - 2020 Associate, Albert Einstein College of Medicine, Cancer Center, Department of Radiology, Bronx, New York, United States

2011 - 2017 Instructor, Albert Einstein College of Medicine, Department of Pathology, Bronx, New York, United States

2002 - 2011 Research Scientist, NYU Langone School of Medicine, New York, New York, United States

1999 - 2002 Research Scientist, The Rockefeller University, New York, New York, United States

Products**Products Closely Related to the Proposed Project**

1. Pearlman A, Upadhyay K, Cole K, Loke J, Sun K, Fineberg S, Freedland SJ, Shao Y, Ostrer H. Robust genomic copy number predictor of pan cancer metastasis. Genes Cancer. 2018 Jan;9(1-2):66-77. PubMed Central PMCID: [PMC5931251](#).
2. Pearlman A, Campbell C, Brooks E, Genshaft A, Shajahan S, Ittman M, Bova GS, Melamed J, Holcomb I, Schneider RJ, Ostrer H. Clustering-Based Method for Developing a Genomic Copy Number Alteration Signature for Predicting the Metastatic Potential of Prostate Cancer. J Probab Stat. 2012;2012(2012):873570. PubMed Central PMCID: [PMC4240515](#).
3. Fofanov VY, Upadhyay K, Pearlman A, Loke J, O V, Shao Y, Freedland S, Ostrer H. Rapid Next-Generation Sequencing Method for Prediction of Prostate Cancer Risks. J Mol Diagn. 2019 Jan;21(1):49-57. PubMed Central PMCID: [PMC6334266](#).
4. Ostrer H, Loke JC, Pearlman A., inventors. Robust genomic predictor of breast and lung cancer metastasis. United States 12,227,809 B2. 2025 February 18.
5. Ostrer H, Pearlman A., inventors. Genomic signatures of metastasis in prostate cancer. United States 10,519,505 B2. 2019 December 31.

Other Significant Products Highlighting Contributions to Science

1. Loke J, Pearlman A, Upadhyay K, Tesfa L, Shao Y, Ostrer H. Functional variant analyses (FVAs) predict pathogenicity in the BRCA1 DNA double-strand break repair pathway. Hum Mol Genet. 2015 Jun 1;24(11):3030-7. PubMed PMID: [25652403](#).
2. Syeda MM, Upadhyay K, Loke J, Pearlman A, Klugman S, Shao Y, Ostrer H. Prediction of breast cancer risk based on flow-variant analysis of circulating peripheral blood B cells. Genet Med. 2017 Sep;19(9):1071-1077. PubMed PMID: [28301456](#).
3. Atzmon G, Hao L, Pe'er I, Velez C, Pearlman A, Palamara PF, Morrow B, Friedman E, Oddoux C, Burns E, Ostrer H. Abraham's children in the genome era: major Jewish diaspora populations comprise distinct genetic clusters with shared Middle Eastern Ancestry. Am J Hum Genet. 2010 Jun 11;86(6):850-9. PubMed Central PMCID: [PMC3032072](#).

4. Campbell CL, Palamara PF, Dubrovsky M, Botigué LR, Fellous M, Atzmon G, Oddoux C, Pearlman A, Hao L, Henn BM, Burns E, Bustamante CD, Comas D, Friedman E, Pe'er I, Ostrer H. North African Jewish and non-Jewish populations form distinctive, orthogonal clusters. Proc Natl Acad Sci U S A. 2012 Aug 21;109(34):13865-70. PubMed Central PMCID: [PMC3427049](#).
5. Pearlman A, Rahman MT, Upadhyay K, Loke J, Ostrer H. Ectopic Otoconin 90 expression in triple negative breast cancer cell lines is associated with metastasis functions. PLoS One. 2019;14(2):e0211737. PubMed Central PMCID: [PMC6375562](#).

Certification:

I certify that the information provided is current, accurate, and complete. This includes, but is not limited to, information related to current, pending, and other support (both foreign and domestic) as defined in 42 U.S.C. § 6605.

In accordance with Section 10632 of the CHIPS and Science Act of 2022 (42 U.S.C. § 19232), each individual identified as a senior/key person must certify that they are not a party to a malign foreign talent recruitment program.

Research Security Training Requirement for Federal Award Personnel: In accordance with Section 10634 of the CHIPS and Science Act of 2022 (42 U.S.C. § 19234), each individual identified as a senior/key person must certify that they have completed the requisite research security training that meets the requirements specified in Item 2 of Important Notice No. 149 within 12 months prior to proposal submission.

Misrepresentations and/or omissions may be subject to prosecution and liability pursuant to, but not limited to, 18 U.S.C. §§287, 1001, 1031 and 31 U.S.C. §§3729-3733 and 3802.

Certified by Pearlman, Alexander in SciENcv on 2026-10-09 10:53:26

NIH BIOGRAPHICAL SKETCH SUPPLEMENT

Name: Pearlman, Alexander

Persistent Identifier (PID) of the Senior/Key Person: <https://orcid.org/0000-0002-0465-5886>

Position Title: Consultant

Organization and Location: Self Employed, Boca Raton, Florida, United States

Personal Statement

For more than 15 years I have developed clinical-grade genomic diagnostic algorithms end to end — design, analytical validation, and regulatory readiness in oncology. My work centers on the question at the heart of this project: whether tumor genomic copy-number alteration (CNA) patterns can predict metastatic potential across cancers.

At NYU Langone and then at Albert Einstein College of Medicine I developed a copy-number signature of metastatic potential in prostate cancer (Pearlman et al., 2012), extended it into a pan-cancer predictor of metastasis (Pearlman et al., 2018) and co-developed a next-generation sequencing assay for clinical specimens (Fofanov et al., 2019). This body of work is patented and published.

My validation philosophy is conservative: performance standards set against real-world outcomes rather than optimistic benchmarks, mandatory replication in independent cohorts, and a clear separation between what a test measures and what it has earned the right to claim. More recently, as an independent consultant, I have re-engineered the signature platform for the multimodal-data era, harmonizing genomic copy number alterations across whole-exome and whole-genome sequencing platforms. In preliminary, unpublished analyses of public data sets I have also harmonized copy number with RNA-seq gene expression from the same tumors and begun examining copy-number signal in ctDNA/cfDNA. The cross-platform work directly supports the pipeline-integration and reproducibility work of Aim 1; the cfDNA work is an early step toward the MRD-timing analysis of Aim 3.3.

In this project I will serve as consultant and senior computational biologist. I will lock the panMPS pipeline and its copy-number cutoffs before any validation data are scored, score the partner and academic cohorts in Aims 1 and 2, and hand the scores and analysis code to Dr. Xue for the statistical analyses.

I maintain an active collaboration with the Department of Pathology at Albert Einstein College of Medicine, where I was an Instructor from 2011 to 2017; I was then an Associate in the Cancer Center and Department of Radiology (2017–2020) and a Consultant to the Cancer Center (2020–2022). I currently mentor bioinformatics students from Brown University and CUNY. From 2020 to 2023 I was Chief Scientific Officer of Hursana, LLC, where I led real-world-data programs, including a pharmacoepidemiology study of cannabis use and opioid prescribing in New York primary-care practices; Hursana holds no rights to the panMPS signature or assay. I bring the technical depth, validation discipline, and collaborative track record needed to carry out the proposed work.

Honors

2013 Genome Technology · Seventh Annual: “Tomorrow's PIs”, GenomeWeb

Contributions to Science

1. Genomic copy-number signatures of metastatic potential, built for clinical specimens. I invented a clustering-based method for constructing genomic copy-number alteration (CNA) signatures and used it to build a prognostic signature that predicts the metastatic potential of prostate cancer from clinical specimens, including needle biopsies (Pearlman et al., 2012). I subsequently led the extension of this approach into a robust pan-cancer copy-number predictor of metastasis, replicated in independent retrospective cohorts across multiple epithelial cancers (Pearlman et al., 2018), with mechanistic follow-up identifying ectopic Otoconin 90 expression associated with metastasis functions in triple-negative breast cancer (Pearlman et al., 2019). To make the signature work on the small, imperfect samples real patients provide, I co-developed a rapid next-generation sequencing method for prediction of prostate cancer risks designed for clinical workflows (Fofanov et al., 2019). The signature and assay are patented (US 10,519,505; US 12,227,809). As an independent consultant I continue to develop this platform for the multimodal-data era.
2. Functional assays for inherited cancer risk. With colleagues at Albert Einstein College of Medicine, I contributed to the

development of functional variant analyses (FVAs) - flow-cytometric functional readouts of DNA-repair pathway variants - demonstrating that they predict pathogenicity in the BRCA1 DNA double-strand-break repair pathway (Loke et al., 2015) and that flow-variant analysis of circulating peripheral-blood B cells predicts breast cancer risk (Syeda et al., 2017). This work underlies a patented functional assay for assessing germline cancer risk from DNA-repair variants (US 12,253,524), on which I am a co-inventor.

3. Population genetics and genetic ancestry. Earlier in my career I contributed to foundational studies of Jewish population structure, including the demonstration that major Jewish diaspora populations comprise distinct genetic clusters with shared Middle Eastern ancestry (Atzmon et al., 2010) and that North African Jewish and non-Jewish populations form distinctive, orthogonal clusters (Campbell et al., 2012). This work informs ancestry-aware genomic analysis - an important consideration for building cancer predictors that generalize across populations.
4. Metabolic interventions in cancer. As Co-Principal Investigator of a translational presurgical ketogenic-diet breast-cancer study at Albert Einstein College of Medicine, I coordinated clinical, pathology, and tumor-omics data across the study's human and mouse arms, serving as the cross-functional bridge among scientific, clinical, and analytical groups. The mouse-arm work demonstrated the effect of a ketogenic diet and its synergy with rapamycin in a model of breast cancer (Zou et al., 2020).

Certification:

I certify that the information provided is current, accurate, and complete. This includes, but is not limited to, information related to current, pending, and other support (both foreign and domestic) as defined in 42 U.S.C. § 6605.

In accordance with Section 10632 of the CHIPS and Science Act of 2022 (42 U.S.C. § 19232), each individual identified as a senior/key person must certify that they are not a party to a malign foreign talent recruitment program.

Research Security Training Requirement for Federal Award Personnel: In accordance with Section 10634 of the CHIPS and Science Act of 2022 (42 U.S.C. § 19234), each individual identified as a senior/key person must certify that they have completed the requisite research security training that meets the requirements specified in Item 2 of Important Notice No. 149 within 12 months prior to proposal submission.

Misrepresentations and/or omissions may be subject to prosecution and liability pursuant to, but not limited to, 18 U.S.C. §§287, 1001, 1031 and 31 U.S.C. §§3729-3733 and 3802.

Certified by Pearlman, Alexander in SciENcv on 2026-10-0910:53:26