## BIOGRAPHICAL SKETCH

Provide the following information for the key personnel and other significant contributors in the order listed on Form Page 2.
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| NAME | POSITION TITLE |
|---|---|
| Garry P. Nolan, Ph.D. | Rachford and Carlota A. Harris Professor |
| eRA COMMONS USER NAME<br>nolan.garry | |

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

| INSTITUTION AND LOCATION | DEGREE *(if applicable)* | YEAR(mm/yy) | FIELD OF STUDY |
|---|---|---|---|
| Cornell University, Ithaca, NY | B.S. | 05/83 | Biology/Genetics |
| Stanford University, Stanford, CA | Ph.D. | 06/89 | Genetics |
| Stanford University, Stanford, CA | Postdoc | 06/90 | Genetics |
| MIT, Cambridge / Rockefeller University, NY | Postdoc | 06/93 | Biochemistry |

### A. Personal Statement

I am a Professor in Microbiology and Immunology. My areas of expertise include signaling biology, immunology, cancer biology, retroviral design, bioinformatics, and genetics. My laboratory's recent interests include studying signaling alterations at the single cell level in leukemia and lymphomas, cancer stem cells, and determining which of these signaling attributes correlate with patient outcome, drug reactivity, and mechanism of disease progressions. Similarly, we work on global representations of signaling attributes and capabilities in the immune system in autoimmune diseases such as systemic lupus erythematosus and rheumatoid arthritis. We develop and apply advanced tools in informatics, such as machine learning, as implemented specifically for single cell analysis and use of perturbation analysis. In addition, we have an extensive program in the development of hardware algorithm implementations (using both field programmable gate arrays as well as graphical processing units) for highly parallelized machine learning of network structures.

### B. Positions and Honors.

**Professional Experience:**

1979-1983 Cornell University. B.S., Biology, specialization in Genetics
Research: Rhizobium/Legume microbial genetics. Advisor: **Dr. Aladar Szalay**

1983-1989 Ph.D. student, Department of Genetics, Stanford University
Research: Immunogenetics, individual cell gene expression. Advisor: **Dr. Leonard Herzenberg**

1989-1990 Postdoctoral Fellow, Department of Genetics, Stanford University
Research: Epigenetics of mammalian gene expression; Whole animal cell sorting.
Advisor: **Dr. Leonard Herzenberg**

1990-1993 NIH Fellow; Leukemia Society Special Fellow, Laboratory of **Prof. David Baltimore**
Whitehead Institute for Biomedical Research (1990-June 1991)
The Rockefeller University (June 1991-1993). Advisor: **Dr. David Baltimore**

1993-1999 Assistant Professor, Department of Molecular Pharmacology and Department of Microbiology & Immunology (Joint Appointment) Stanford University School of Medicine

1999-2001 Associate Professor, Department of Molecular Pharmacology and Department of Microbiology & Immunology (Joint Appointment) Stanford University School of Medicine

2002-2009 Associate Professor, Baxter Laboratory in Genetic Pharmacology, Department of Microbiology & Immunology, Stanford University School of Medicine

2009-2011 Professor, Baxter Laboratory for Stem Cell Biology, Department of Microbiology & Immunology, Stanford University School of Medicine

2011-present Rachford and Carlota A. Harris Professor, Baxter Laboratory for Stem Cell Biology, Department of Microbiology & Immunology, Stanford University School of Medicine

**Honors and Fellowships:**

National Institutes of Health Fellowship: June 1990-June 1992
Leukemia Society Special Fellow: July 1992 -June 1995
Board of Trustees, Leukemia Society of America, Northern California Chapter: 1995-1998
Burroughs Wellcome Fund New Investigator Award in Pharmacology: July 1996 - June 2000

Leukemia and Lymphoma Society: Stohlman Scholar. January 2000 – December 2000
Nature "Outstanding Research Achievement for 2011"
Department of Defense "Teal Innovator Award" for work on Ovarian Single Cell. 2012-2017.

**Invited Speaker (Selected List):**

2006 Keynote Speaker, Sydney Royal Society of Pathology.
2006 Opening Speaker, International Society of Analytic Cytometry, ISAC, Quebec
2007 Memorial Sloan Kettering, New York, NY
2008 Eastern Cooperative Oncology Group, Ft. Lauderdale, FL
2009 "Omics Meets Cell Biology" Keystone Symposia Plenary Speaker
2009 ETH Zurich, Biosystems Science and Engineering, Basel, Switzerland
2010 14th International Congress of Immunology, Kobe, Japan
2011 St. Jude Children's Research Hospital, Memphis, TN
2012 CYTO 2012, Leipzig, Germany
2012 Trinity College, Oxford, England

**Selected peer-reviewed publications. (Publications selected from 172 peer-reviewed publications)**

1. Perez OD and GP Nolan. (2002). Simultaneous measurement of multiple kinase activation states by polychromatic flow cytometry. Nat Biotechnol. Vol 20 155-162. PMID: 11821861
2. Krutzik PO and Nolan GP. (2003). Intracellular phospho-protein staining techniques for flow cytometry: Monitoring single cell signaling events. Cytometry. Oct;55A(2):61-70. PMID: 14505311
3. Perez OD, Krutzik PO, and Nolan GP. (2004). Flow Cytometric Analysis of Kinase Signaling Cascades. Methods in Molecular Biology: Flow Cytometry Protocols, 2nd ed. Humana Press. PMID: 14976361
4. Krutzik PO, Irish JM, Nolan GP and Perez OD. (2004). Analysis of protein phosphorylation and cellular signaling events by flow cytometry: techniques and clinical applications. Clin Immunol. Mar;110(3):206-21 PMID: 15047199
5. Irish JM, Hovland R, Krutzik PO, Perez OD, Bruserud O, Gjertsen BT, Nolan GP. (2004) Single Cell Profiling of Potentiated Phospho-Protein Networks in Cancer Cells. Cell. Jul 23;118(2):217-228. PMID: 15260991
6. Sachs K, Perez O, Pe'er D, Lauffenburger DA, Nolan GP. (2005) Causal protein-signaling networks derived from multiparameter single-cell data. Science. Apr 22;308(5721):523-9. PMID: 15845847
7. Irish J.M., Kotecha N. and Nolan G.P. (2006), Mapping normal and cancer cell signalling networks: towards single-cell proteomics. Nature Reviews Cancer 6, 146-155. PMID: 16491074
8. Krutzik P.O. and Nolan G.P. (2006) Fluorescent cell barcoding in flow cytometry allows high-throughput drug screening and signaling profiling. Nature Methods 3, 361-368. PMID: 16628206
9. Nolan G.P. (2006). Deeper insights into hematological oncology disorders via single-cell phospho-signaling analysis. Hematology Am Soc Hematol Educ Program. 123-7, 509. PMID: 17124050
10. Nolan GP. (2007). What's wrong with drug screening today. Nat Chem Biol. Apr;3(4):187-91. PMID: 17372598
11. Krutzik PO, Crane JM, Clutter MR, Nolan GP. (2008) High-content single-cell drug screening with phosphospecific flow cytometry. Nat Chem Biol. Feb;4(2):132-42. PMID: 18157122
12. Kotecha, N., Flores, NJ., Irish, JM., Simonds, S., Sakaguchi, D., Archambeault, S., Diaz-Flores, E., Coram, M., Shannon, K. Nolan, GP.*, and Loh, ML. (2008) Single Cell Profiling Identifies Aberrant STAT5 Activation in Myeloid Malignancies with Specific Clinical and Biologic Correlates. Cancer Cell. Oct 7;14(4):335-43. (cover article)., *co-last author. PMID: 18835035 PMCID: PMC2647559
13. Bendall SC, Simonds EF, Qiu P, Amir el-AD, Krutzik PO, Finck R, Bruggner RV, Melamed R, Trejo A, Ornatsky OI, Balderas RS, Plevritis SK, Sachs K, Pe'er D, Tanner SD, Nolan GP. (2011) Single-cell mass cytometry of differential immune and drug responses across a human hematopoietic continuum. Science. May 6;332(6030):687-96. PMID: 21551058. NIHMS304953
14. Qiu P, Simonds EF, Bendall SC, Gibbs KD, Bruggner RV, Linderman MD, Sachs K, Nolan GP, Plevritis SK. (2011) Extracting a cellular hierarchy from high-dimensional cytometry data with SPADE. Nat Biotechnol. 2011;29(10) - PubMed PMID: 21964415 CID: PMC3196363
15. K.D.. Gibbs, Jr., A. Jager, O. Crespo, Y. Goltsev, A. Trejo, C. E. Richard, and Garry P. Nolan (2012) Decoupling of Tumor-Initiating Activity from Stable Immunophenotype In HoxA9-Meis1 Driven AML. Cell Stem Cell (In Press)

**C. Research Support.**

**Ongoing**

U19 AI057229 (Davis, M.) 04/01/09-03/31/14
NIH
Program title: "Protective Mechanisms Against Pandemic Respiratory Virus"

Project D PI: Nolan, G.P. (Arvin, A. co-investigator)
Project D title: “Activation States of Immune Cells”
The major goal of the Program is to use vaccine-induced and naturally acquired influenza immunity as a model for comprehensive, integrated analyses of adaptive and innate immune mechanisms that protect the respiratory tract. The specific aims of project D are to develop multiparameter flow cytometry assays to detect activated T, B, and NK cells and to adapt these assays for phenotypic and functional analysis of peripheral blood APCs.

1R01CA130826 (Nolan, G.P.) 09/26/08-07/31/13
NCI
"Software & Hardware Inference Engines for Automated Determination of Primary Cells"
The major goal of this project is to create a Bioengineering Research Partnership (BRP) between four research labs to combine their expertise in cancer signaling, systems biology, modeling, algorithm and hardware, to fully develop this approach for the study of signaling networks within cancer and the infiltrating and global immune response.

DR1-01477 (Slamon, D.J.) 09/01/10-04/30/14
CIRM
"Therapeutic Opportunities to Target Tumor Initiating Cells in Solid Tumors"
The major goal of this subproject is to identify therapeutic targets to tumor initiating cells in solid tumors.

U54CA149145 (Plevritis, S.) 05/01/10-02/28/15
NCI
“Modeling the Role of Differentiation in Cancer Progression”
The Stanford Center for Systems Biology of Cancer (CCSB) aims to discover molecular mechanisms underlying cancer progression by studying cancer as a complex biological system that is driven, in part, by impaired differentiation.

5U54CA143907 (Gambhir, S.S.) 09/28/09-07/31/14
NCI
“Multi-scale Complex Systems Transdisciplinary Analysis of Response to Therapy”
The objectives of this subaward are to discover, quantitatively describe and create a platform for the predictive analysis of two fundamental cancer states: acute myelogenous leukemia (AML) and non-Hodgkin lymphoma (NHL).

RB2-01592 (Nolan, G.P.) 08/01/10-07/31/13
CIRM Basic Biology II Award
"Kinase signaling analysis of iPS cell reprogramming and differentiation"
The goal is to elucidate the signaling networks underlying pluripotency and cell fate transitions. By identifying the regulatory events required for both reprogramming and differentiation of iPS cells, we aim to create improved methods for regenerative therapy.

N01-HV-00242 (Nolan, G.P.) 08/15/10-08/14/15
NHLBI, NIH
“Proteomics of Inflammation, Immunity, and Pulmonary Arterial Hypertension”
The objectives are to promote the further development of novel proteomic technologies in the context of relevant clinical settings, understand new biological principles related to the interaction(s) of PAH and immunity, and progress (and co-develop) therapeutics and diagnostics for the amelioration of PAH and related disease syndromes.

HEALTH.2010.1.2-1: (Landegren, Ulf.) 11/01/10-10/31/14
European Commission
“DiaTools - Tools for minimally invasive diagnostics”
Stanford will serve as a flow cytometry "core" for sample handling by CyTOF, data repository and analysis center for high dimensional flow cytometry at the single cell level.

Merck (Nolan, G.P.) 12/02/11-12/01/13
Merck, Sharp, and Dohme Research Labs
Stanford - Merck CyTOF collaboration agreement
Using a primary sample set taken from patients with rheumatoid arthritis to determine 1) whether ex-vivo stimulation-CyTOF-based measurements correlate with clinical-, laboratory-, and imaging-based assessments of disease activity; 2) whether ex-vivo stimulation-CyTOF-based measurements at baseline can predict

response to anti-TNF therapy; and 3) whether ex-vivo stimulation-CyTOF can be incorporated into Phase I Clinical Trial study sites.

Novo Nordisk Biotech, Inc. (Nolan, G.P.) 03/15/12-03/14/14
Novo Nordisk Biotech, Inc.
Mechanistic study of Novo Nordisk targets in rheumatoid arthritis, using single cell network profiling and mass cytometry

41000411217 (Maecker, H.T.) 05/01/2012-04/30/2013
Prime Sponsor: National Institutes of Health
Baylor Research Institute
Immune MonitoringTechnologies Hands-On Course

Gilead Sciences, Inc. (Nolan, G.P.) 03/22/12-03/21/14
Gilead Sciences, Inc.
Signaling Networks and Functional Responses in Immune Cell Subsets and Their Relation to Host Control of HIV Infection

Celgene (Nolan, G.P.) 08/27/12-08/26/13
Celgene Corporation
Mass Spectrometry Analysis of Erythropoiesis

Alliance for Lupus Research (Utz, P.J.) 02/01/12 - 01/31/15
SLE Target Identification Using CyTOF and
Multiplexed Assays
To identify which autoantibodies are most active in which patients using CyTOF to analyze patient blood cells to study their defects and responses to potential therapies such as rituximab (Rituxan) and belimumab (Benlysta). To explore whether defects in the way these proteins communicate and interact with each other could also be useful biomarkers and/or novel targets for drugs.

5-24927 (Ulevich, R.) 09/01/2012-08/31/2017
Prime Sponsor: National Institutes of Health
The Scripps Research Institute
Systems Approach to Immunity and Inflammation Core E - CyTOF Flow Cytometry
Major Goals: Create and standardize Ab and single cell expression of mRNA panels to cover all major surface markers and intracellular signaling in immune subsets relevant for the biology being interrogated in Projects 1-3 towards the creation of an “immune system reference map” with associated correlative immune maps.

Department of Defense (Nolan, G.P.) 09/30/12-09/29/17
(CDMRP) Ovarian Cancer Teal Innovator Award
“Organizing the Cellular and Molecular Heterogeneity in High-Grade Serous Ovarian Cancer by Mass Cytometry”
Major Goals: to identify markers that delineate tumor cell sub-sets, determine the functional significance of these subsets for tumor initiation and maintenance, define key signaling pathways within these subsets, and assess their response to current agents as well as agents in therapeutic development.

Food And Drug Administration (Nolan, G.P.) 10/01/12 - 09/30/14
FDA BAA-12-00118
“Cross-Species Immune System Reference”
Major Goals: 1. To understand the degree to which people of different ages, genders and ethnicities will respond differently to biological countermeasures that modulate cellular signaling. 2. To understand how accurately animal models reflect the signaling events observed in humans. 3. To that end, we propose to compare the signaling events that occur in different humans, rhesus macaques, cynomolgus macaques and mice upon treatment with prominent biological stimuli and biothreat agents. The resulting data will be placed in an open-access resource.

**Completed**

N01-HV-28183 (Nolan, G.P.) 09/30/02-09/29/09
NIH, NHLBI
“Proteomic Analysis of Blood Components in Autoimmune Disease”
The major goal of this project is to develop proteomic approaches to studying autoimmune disease.