# **BIOGRAPHICAL SKETCH**

Provide the following information for the Senior/key personnel and other significant contributors.

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NAME: CHANCE, MARK				
eRA COMMONS USER NAME (agency login): mrch	nance			
POSITION TITLE: Vice Dean for Research				
EDUCATION/TRAINING (Begin with baccalaureate	or other initial pro	ofessional education	, such as nursing,	
include postdoctoral training and residency training if applicable.)				
INSTITUTION AND LOCATION	DEGREE	Completion Date	FIELD OF STUDY	
	(if applicable)	MM/YYYY		
Wesleyan University, Middletown, CT	BA	1980	Biology	
MIT, Boston, MA	OTH	1984	Biochemistry	
University of Pennsylavnia, Philadelphia, PA	PHD	1986	Biophysics	
AT&T Bell Labs, Murray Hill, NJ	Other training	1988	Biophysics	

### A. Personal Statement

Dr. Chance is an internationally renowned scientist in the field of proteomics, systems, and structural biology with over 270 publications. He has a long-standing track record in quantitative mass spectrometry; his laboratory invented mass spectrometry based protein footprinting, a well-known and popular quantitative proteomics technology for examining protein structure. Recently, his work combining proteomics, genomics, and bioinformatics, has provided novel approaches and biomarkers for understanding colon cancer and glioblastoma and identifying key pathways that mediate complications of HIV. He has a long-standing demonstrated experience developing complex, internationally recognized biomedical science projects and Centers, including developing and implementing technologically advanced experimental and computational infrastructure for biomedical research. This includes being PI of a synchrotron biophysics resource center continuously funded by the NIH since 1995 as well as leadership in the Protein Structure Initiative from 1999-2015. In terms of broader experience with developing technologies towards the market in areas of genomics and proteomics, he is the Director of the Translational Technologies & Innovations (TTI) Core and a Co-PI of the Case CTSA grant as well as a Co-PI for the National Center for Accelerating Innovations project funded by the NHLBI.

As Vice Dean for Research, Dr. Chance has been a leader at the institution in developing new training initiatives through the Office of Graduate Education (which reports to him) including multiple initiatives to enhance workforce readiness. To promote CTSC goals, he has established an Office of Translation and Innovation to support faculty connections with industry partners and help faculty build research teams to advance drugs and devices towards the market. He has reorganized the school's core facilities to be more efficient and visible and has championed a core utilization pilot-funding model to encourage core staff and faculty interaction. In this project as Co-PI of the CTSC program and member of the Executive Committee, he will lead the Translational Endeavors component and serve as co-lead of the Translational Workforce Development sub-component. He will also co-lead the Community and Collaboration component. He will devote 20% overall to the project (10% as TE lead, 5% as CC co-lead, and 5% as Co-PI).

- Shi W, Robinson H, Sullivan M, Abel D, Toomey J, Berman LE, Lynch D, Rosenbaum G, Rakowsky G, Rock L, Nolan B, Shea-McCarthy G, Schneider D, Johnson E, Sweet RM, Chance MR. Beamline X29: a novel undulator source for X-ray crystallography. J Synchrotron Radiat. 2006 Sep;13(Pt 5):365-72. PubMed PMID: <u>16924132</u>.
- Takamoto K, Chance MR. Radiolytic protein footprinting with mass spectrometry to probe the structure of macromolecular complexes. Annu Rev Biophys Biomol Struct. 2006;35:251-76. PubMed PMID: <u>16689636</u>.
- 3. Chance MR, Bresnick AR, Burley SK, Jiang JS, Lima CD, Sali A, Almo SC, Bonanno JB, Buglino JA, Boulton S, Chen H, Eswar N, He G, Huang R, Ilyin V, McMahan L, Pieper U, Ray S, Vidal M, Wang LK.

Structural genomics: a pipeline for providing structures for the biologist. Protein Sci. 2002 Apr;11(4):723-38. PubMed PMID: <u>11910018</u>; PubMed Central PMCID: <u>PMC2373525</u>.

 Burley SK, Almo SC, Bonanno JB, Capel M, Chance MR, Gaasterland T, Lin D, Sali A, Studier FW, Swaminathan S. Structural genomics: beyond the human genome project. Nat Genet. 1999 Oct;23(2):151-7. PubMed PMID: <u>10508510</u>.

### **B.** Positions and Honors

#### **Positions and Employment**

1985 - 1987	Postdoctoral Research Associate, AT&T Bell Laboratories, Institute for Structural and Functional Studies, Murray Hills, NJ	
1988 - 1992	Assistant Professor, Department of Chemistry, Georgetown University, Washington, DC	
1993 - 1998	Associate Professor, Department of Physiology & Biophysics, Albert Einstein College of Medicine, New York, NY	
1995 -	Director, Center for Synchrotron Biosciences, National Synchrotron Light Source , Brookhaven National Labs, Upton, NY	
1998 - 2005	Professor, Departments of Physiology & Biophysics and Biochemistry , Albert Einstein College of Medicine, Bronx, NY	
2005 -	Director, Center for Proteomics and Bioinformatics, Case Western Reserve University, Cleveland, OH	
2005 - 2010	Professor, Department of Physiology & Biophysics, School of Medicine, Case Western Reserve University, Cleveland, OH	
2009 -	Chief Scientific Officer, NeoProteomics, Inc., Cleveland, OH	
2010 -	Professor, Department of Genetics and Genome Sciences, School of Medicine, Case Western Reserve University, Cleveland, OH	
2010 - 2012	Interim Chair, Department of Genetics and Genome Sciences, School of Medicine, Case Western Reserve University, Cleveland, OH	
2010 - 2014	Professor, Department of General Medical Sciences, School of Medicine, Case Western Reserve University, Cleveland, OH	
2011 -	Charles W. and Iona A. Mathias Professor of Cancer Research, School of Medicine, Case Western Reserve University, Cleveland, OH	
2011 -	Vice Dean for Research, School of Medicine, Case Western Reserve University, Cleveland, OH	
2015 -	Professor, Department of Nutrition, School of Medicine, Case Western Reserve University, Cleveland, OH	
Other Experience and Professional Memberships		

- 1995 1998 Member, Scientific Advisory Board, ELETTRA Synchrotron, Trieste, Italy
- 1995 2005 Director, NIH Funded Molecular Biophysics Training Program, Albert Einstein College of Medicine
- 2000 2001 Chair, User Executive Committee, National Synchrotron Light Source, Brookhaven National Laboratory
- 2001 2003 Chair, NIH-NCRR Biomedical Technology Center Directors' Organization
- 2003 2007 Regular Member, NIH Biomedical Research & Training Committee-A
- 2003 2014 Member, Scientific Advisory Committee, Protein Crystallography Research Resource, Brookhaven National Laboratory
- 2007 Member, Biophysics Proposal Review Panel, Advanced Light Source, Lawrence Berkeley National Laboratory
- 2007 2007 Member, NIGMS, Systems Biology P50 Review Panel
- 2007 2009 Member, Experimental Facilities Advisory Committee, National Synchrotron Light Source-II, Brookhaven National Laboratory
- 2009 Member, External Advisory Committee, NIH/NIGMS Mass Spectrometry Resource Washington University, St. Louis

2010 - Editorial Board Member, Molecular and Cellular Proteomics

2013 - 2014 Member, NIGMS, Systems Biology P50 Review Panel

#### <u>Honors</u>

1985	NIH/NHLBI Cardiovascular Fellow, University of Pennsylvania
1990	Upjohn Company Research Award, W.E. Upjohn Institute for Employment Research
1995	Joseph & Anne Wunsch Fellow in Biophysical Engineering, Albert Einstein College of Medicine
1996	Irma T. Hirschl Career Scientist Award, Albert Einstein College of Medicine
2003	Dean's Achievement Award, Albert Einstein College of Medicine
2011	Charles W. and Iona A. Mathias Chair in Cancer Research, Case Western Reserve University School of Medicine
2014	Naomi Kanof Investigator Award Lectureship and Medal for Distinguished Achievement in Clinical Investigation, Society of Investigative Dermatology

# **C.** Contribution to Science

- 1. At Albert Einstein College of Medicine, in collaboration with Michael Brenowitz, Dr. Chance developed a synchrotron-based radiolysis and "footprinting" approach to define the folding mechanism of the Tetrahymena ribozyme on millisecond timescales, revealing fundamental principles of RNA packing. The major findings were published in J. Mol. Bio. and Science (1997 and 1998), these papers have been cited over 500 times. Subsequently, Dr. Chance and Brenowitz defined the equilibrium thermodynamics of the folding in two papers in Nat. Structural Biology in 2000 and 2002. These studies resulted in significant NIH funding for Dr. Chance's laboratory and set the standard for high resolution structural kinetics evaluation of macromolecules.
  - a. Sclavi B, Woodson S, Sullivan M, Chance MR, Brenowitz M. Time-resolved synchrotron X-ray "footprinting", a new approach to the study of nucleic acid structure and function: application to protein-DNA interactions and RNA folding. J Mol Biol. 1997 Feb 14;266(1):144-59. PubMed PMID: <u>9054977</u>.
  - Sclavi B, Sullivan M, Chance MR, Brenowitz M, Woodson SA. RNA folding at millisecond intervals by synchrotron hydroxyl radical footprinting. Science. 1998 Mar 20;279(5358):1940-3. PubMed PMID: <u>9506944</u>.
  - Ralston CY, He Q, Brenowitz M, Chance MR. Stability and cooperativity of individual tertiary contacts in RNA revealed through chemical denaturation. Nat Struct Biol. 2000 May;7(5):371-4. PubMed PMID: <u>10802732</u>.
  - d. Takamoto K, He Q, Morris S, Chance MR, Brenowitz M. Monovalent cations mediate formation of native tertiary structure of the Tetrahymena thermophila ribozyme. Nat Struct Biol. 2002 Dec;9(12):928-33. PubMed PMID: <u>12434149</u>.
- 2. As Dr. Chance developed the nucleic acids footprinting technology, he began to envision an approach to develop protein structure assessment using OH-radical footprinting. With the demonstration of mass spectrometry (MS) detection of OH-radical modifications in peptides in a landmark paper in Analytical Chem. (1999) a new field of protein footprinting was born. The chemistry and MS methods for detecting oxidized residues was established in a series of papers culminating in a major article in Chem. Rev. (2007). These technologies have been uniquely valuable in probing the structure and dynamics of membrane proteins, as seen in many publications (e.g. PNAS 2009 and Nature 2014).
  - Maleknia SD, Brenowitz M, Chance MR. Millisecond radiolytic modification of peptides by synchrotron X-rays identified by mass spectrometry. Anal Chem. 1999 Sep 15;71(18):3965-73. PubMed PMID: <u>10500483</u>.
  - b. Xu G, Chance MR. Hydroxyl radical-mediated modification of proteins as probes for structural proteomics. Chem Rev. 2007 Aug;107(8):3514-43. PubMed PMID: <u>17683160</u>.
  - c. Angel TE, Gupta S, Jastrzebska B, Palczewski K, Chance MR. Structural waters define a functional channel mediating activation of the GPCR, rhodopsin. Proc Natl Acad Sci U S A. 2009 Aug 25;106(34):14367-72. PubMed PMID: <u>19706523</u>; PubMed Central PMCID: <u>PMC2732891</u>.

- d. Gupta S, Chai J, Cheng J, D'Mello R, Chance MR, Fu D. Visualizing the kinetic power stroke that drives proton-coupled zinc(II) transport. Nature. 2014 Aug 7;512(7512):101-4. PubMed PMID: <u>25043033</u>; PubMed Central PMCID: <u>PMC4144069</u>.
- 3. Over his entire career, Dr. Chance has made major contributions to the field of metalloprotein spectroscopy As a Post-Doctoral scholar in the lab of Dr. Joel Friedman he participated in confirming the precise structure-function relationships of protein conformational substates in optical studies of hemeproteins published in Science in 1987. In the early 1990s, with Dr. Michael Summers, he tackled the issue of metal binding by the nucleocapsid (NC) protein in retroviruses related to HIV, and Dr. Chance utilized his expertise in x-ray spectroscopy to confirm that the Zn-ion was a core element of the NC structure, Dr. Chance and Dr. Summers published these results in Protein Science and PNAS in 1992. More recently, he has established high throughput methods for x-ray spectroscopy published in Genome Research (2004 and 2011) and elsewhere.
  - Campbell BF, Chance MR, Friedman JM. Linkage of functional and structural heterogeneity in proteins: dynamic hole burning in carboxymyoglobin. Science. 1987 Oct 16;238(4825):373-6. PubMed PMID: <u>3659921</u>.
  - b. Summers MF, Henderson LE, Chance MR, Bess JW Jr, South TL, Blake PR, Sagi I, Perez-Alvarado G, Sowder RC 3rd, Hare DR. Nucleocapsid zinc fingers detected in retroviruses: EXAFS studies of intact viruses and the solution-state structure of the nucleocapsid protein from HIV-1. Protein Sci. 1992 May;1(5):563-74. PubMed PMID: <u>1304355</u>; PubMed Central PMCID: <u>PMC2142235</u>.
  - c. Chance MR, Sagi I, Wirt MD, Frisbie SM, Scheuring E, Chen E, Bess JW Jr, Henderson LE, Arthur LO, South TL. Extended x-ray absorption fine structure studies of a retrovirus: equine infectious anemia virus cysteine arrays are coordinated to zinc. Proc Natl Acad Sci U S A. 1992 Nov 1;89(21):10041-5. PubMed PMID: <u>1332027</u>; PubMed Central PMCID: <u>PMC50273</u>.
  - d. Chance MR, Fiser A, Sali A, Pieper U, Eswar N, Xu G, Fajardo JE, Radhakannan T, Marinkovic N. High-throughput computational and experimental techniques in structural genomics. Genome Res. 2004 Oct;14(10B):2145-54. PubMed PMID: <u>15489337</u>; PubMed Central PMCID: <u>PMC528931</u>.
- 4. Since coming to Cleveland to establish the Center for Proteomics and Bioinformatics, Dr. Chance has developed core resource and technologies to provide advanced systems biology assessment of disease, resulting in novel biomarkers and disease classifiers.
  - Nibbe RK, Markowitz S, Myeroff L, Ewing R, Chance MR. Discovery and scoring of protein interaction subnetworks discriminative of late stage human colon cancer. Mol Cell Proteomics. 2009 Apr;8(4):827-45. PubMed PMID: <u>19098285</u>; PubMed Central PMCID: <u>PMC2667362</u>.
  - Nibbe RK, Koyutürk M, Chance MR. An integrative -omics approach to identify functional sub-networks in human colorectal cancer. PLoS Comput Biol. 2010 Jan 15;6(1):e1000639. PubMed PMID: <u>20090827</u>; PubMed Central PMCID: <u>PMC2797084</u>.
  - c. Schlatzer DM, Sugalski J, Dazard JE, Chance MR, Anthony DD. A quantitative proteomic approach for detecting protein profiles of activated human myeloid dendritic cells. J Immunol Methods. 2012 Jan 31;375(1-2):39-45. PubMed PMID: <u>21945394</u>; PubMed Central PMCID: <u>PMC3253886</u>.
  - d. Patel VN, Gokulrangan G, Chowdhury SA, Chen Y, Sloan AE, Koyutürk M, Barnholtz-Sloan J, Chance MR. Network signatures of survival in glioblastoma multiforme. PLoS Comput Biol. 2013;9(9):e1003237. PubMed PMID: <u>24068912</u>; PubMed Central PMCID: <u>PMC3777929</u>.

# **D. Research Support**

#### Selected Ongoing and Prior Research Support

P30-EB-009998 , NIH CHANCE, MARK (PI) 09/01/09-08/01/19 Case Center for Synchrotron Biosciences This center assists NIH funded users in accessing structural biology beamlines for their research in crystallography, nucleic acid and protein footprinting, and x-ray spectroscopy. Role: PI

P30-CA-043703, NIH GERSON, STANFORD (PI) 07/01/07-06/01/18 Case Comprehensive Cancer Center Proteomics Core To provide proteomics and bioinformatics services to cancer center investigators. Role: PI Ohio Pre-Maturity Consortium, MARCH OF DIMES MUGLIA, LOU (PI) 07/01/13-06/01/18 Systems Biology of Progesterone Signaling To use systems biology and bioinformatics approaches to explore pre-mature birth mechanisms Role: Co-Investigator UL1-TR-000439, NIH Konstan, Mike (PI) 09/01/07-08/01/17 CTSA The goal of this grant is to accelerate translational research in Cleveland Role: CPI DBI-1228549, NSF CHANCE, MARK (PI) 08/01/12-07/01/17 MRI Consortium: Development of a Damping Wiggler Beamline for X-Ray Footprinting at NSLS II Role: PI R01-LM-11247, NIH KOYUTURK, MEHMET (PI) 08/01/12-07/01/16 Enhancing Genome Wide Association Studies with Integrative Network Analysis Role: CPI P30-AI-036219, NIH KARN, JONATHAN (PI) 05/01/15-04/01/20 Case Center for AIDS Research-Proteomics and Systems Biology Core Role: PI U54HL119810, NIH CHANCE, MARK (PI) 08/01/13-07/30/18 The Cleveland Clinic Innovation Accelerator-CWRU Site The goal of this project is to accelerate the advancement of NHLBI-related research discoveries and innovations into improvements in human health and educating researchers to be full parameters in this translation process Role: PI