CIRM Scientific and Medical Research Funding Working Group
Biographical information of candidates nominated to serve as Scientific Members of the Working Group

Stephen Friend, MD, PhD
Dr. Friend is the President of Sage Bionetworks. He received his BA in philosophy, his PhD in biochemistry, and his MD from Indiana University. He is an authority in the field of cancer biology and a leader in efforts to make large scale, data-intensive biology broadly accessible to the entire research community.

Dr. Friend has been a senior advisor to the National Cancer Institute (NCI), several biotech companies, a Trustee of the American Association for Cancer Research (AACR), and is an American Association for the Advancement of Science (AAAS) and Ashoka Fellow as well as an editorial board member of *Open Network Biology*. Dr. Friend was previously Senior Vice President and Franchise Head for Oncology Research at Merck & Co., Inc. where he led Merck's Basic Cancer Research efforts.

Prior to joining Merck, Dr. Friend was recruited by Dr. Leland Hartwell to join the Fred Hutchinson Cancer Research Center's Seattle Project, an advanced institute for drug discovery. While there Drs. Friend and Hartwell developed a method for examining large patterns of genes that led them to co-found Rosetta Inpharmatics in 2001. Dr. Friend has also held faculty positions at Harvard Medical School from 1987 to 1995 and at Massachusetts General Hospital from 1990 to 1995.

Christie Gunter, PhD
Dr. Gunter is the HudsonAlpha director of research affairs. She earned her BS degree in both genetics and biochemistry from the University of Georgia in 1992, and a PhD in genetics from Emory University in 1998. Her research was centered on human genetics, and specifically on Fragile X syndrome, the most common inherited form of mental retardation. She then completed postdoctoral work at Case Western Reserve University, examining the mechanism of mammalian X-chromosome inactivation.

Dr. Gunter has also earned publishing experience at several journals, including editorial positions at *Human Molecular Genetics* and *Science*. From 2002-2008, she served as the editor for genetics and genomics manuscripts at the international journal *Nature*, the most highly-cited general science journal in the world. She then started at HudsonAlpha in 2008 and coordinates research activities in genetics and genomics. Her primary job is to create and maintain an academic environment at HudsonAlpha, including a vibrant seminar series and creation of an international conference on immunogenomics. In addition, Dr. Gunter communicates HudsonAlpha's research in a variety of different formats and public venues. She holds adjunct appointments at three universities (University of Pennsylvania, University of Alabama Birmingham, and University of Alabama Huntsville), and currently serves on the Program Committee and as the chair of the Communications Committee for the American Society of Human Genetics.

Leroy Hood, MD, PhD
Dr. Hood is the President and Co-founder of the Institute for Systems Biology (ISB) ISB is a non-profit research organization based in Seattle, Washington that was established as an untraditional institution, where scientific collaboration could take place across disciplines, where biologists and technologists could commingle, and where the future of research and medicine could take foot. ISB pioneered systems biology, which harnesses and integrates the respective insights of biologists, geneticists, computer scientists, chemists, engineers, mathematicians, immunologists and others to answer some of society's most challenging questions related to health and the environment.

Dr. Hood is a pioneer in the systems approach to biology and medicine. He received his MD from the John Hopkins School of Medicine and his PhD in Biochemistry from the California Institute of Technology. His research has focused on the study of molecular immunology, biotechnology and genomics. Dr. Hood's professional career began at Caltech, where he and his colleagues developed the DNA gene sequencer and synthesizer and the protein synthesizer and sequencer––four instruments that paved the way for the successful mapping of the human genome. A pillar in the biotechnology field, Dr. Hood has played a role in founding more than fourteen biotechnology companies, including Amgen, Applied Biosystems, Darwin, The Accelerator and Integrated Diagnostics.

At the ISB, the Hood group is integrating biology, technology and computation to create a predictive, personalized, preventive and participatory approach to medicine. This P4 Medicine will use a systems or holistic approach and new computational and mathematical tools to analyze the enormous amounts of molecular, cellular, phenotypic and medical data that now can be generated for each individual. By viewing medicine as an informational science, P4 medicine will draw on an understanding of the networks underlying health and disease. The goals are to treat and prevent disease by identifying perturbations in biological networks, and countering those perturbations through therapeutic intervention. Furthermore, a systems approach to biology will create knowledge with far-reaching implications for agriculture, energy production, environmental protection, and many other human activities. The Hood group is working on technology-driven projects including identification of disease genes through the complete genome sequencing of families affected by particular diseases; establishing the computational infrastructure needed to analyze the thousands and eventually millions of human genome sequences that will become available over the next ten years; supporting a human proteome project that will parallel the human genome project; and developing clinical assays that use genomic, proteomic and cellular analyses, including the use of induced pluripotent stem (iPS) cells, to explore development and to stratify disease.

Dr. Hood is a member of the National Academy of Sciences, the National Academy of Engineering, and the Institute of Medicine. Of the 6,000+ scientists world-wide who

belong to one or more of these academies, Dr. Hood is one of only fifteen people accepted to all three. He is also a member of the American Philosophical Society and a Fellow of the American Academy of Arts and Sciences. His work has been widely published, and he has coauthored numerous textbooks in biochemistry, immunology, molecular biology and genetics, as well as a popular book on the human genome project, The Code of Codes. He is the recipient of numerous awards, including the Lasker Award for Studies of Immune Diversity, the Kyoto Prize in advanced technology, the Heinz Award for pioneering work in Systems Biology, and most recently, the coveted NAE 2011 Fritz J. and Delores H. Russ Prize for automating DNA sequencing that revolutionized biomedicine and forensic science. In addition to having received 17 honorary degrees from prestigious universities in the US and abroad, Dr. Hood has published more than 700 peer reviewed articles and currently holds 36 patents.

John Mattick, PhD

Dr. Mattick is the Executive Director of the Garvan Institute of Medical Research in Sydney. He received his BSc (with First Class Honours) from the University of Sydney, followed by his PhD from Monash University in Melbourne, on the topic of mitochondrial DNA replication and mutation. He undertook postdoctoral work on the molecular biology of the fatty acid synthase complex at Baylor College of Medicine in House Texas. He then returned to Australia where he worked at the CSIRO Division of Molecular Biology in Sydney from 1982-1988 and, subsequently, at the University of Queensland in Brisbane from 1988-2012, where he was Professor of Molecular Biology and NHMRC Australia Fellow at the Institute for Molecular Bioscience. He has also spent sabbatical periods at the University of Cambridge, the University of Oxford, and the University of Cologne.

Dr. Mattick has made seminal contributions to molecular biology. He was responsible for the development of one of the first recombinant DNA-based vaccines in the world (against ovine footrot), which was recently credited with eradicating footrot from Nepal. In recognition of this work he was awarded the 1989 Pharmacia---LKB Biotechnology Medal by the Australian Biochemical Society. As the Foundation Professor of Molecular Biology and Foundation Director of the Centre for Molecular Biology and Biotechnology (CMBBT) at the University of Queensland, Dr. Mattick devoted considerable energy to the establishment of this Centre and its maturation into one of the largest research institutes in Australia. The CMCB amalgamated with the Centre for Drug Design and Development to form the Institute for Molecular Bioscience (IMB), a systems biology institute whose research activities span the spectrum from genomics and computational biology, genetics and developmental biology, molecular cell biology, structural biology and biological chemistry. Professor Mattick served as both Co-Director and Director of the IMB. Professor Mattick was also the founder and Foundation Director (1996 - 2002) of the Australian Genome Research Facility (AGRF), a designated major national research facility that provides large-scale DNA sequencing, genotyping and related services to the Australian research community. He was also the Foundation Director of the ARC Special Research Centre for Functional and Applied Genomics.

Dr. Mattick's research interests are now focused on the role of regulatory RNAs in the evolution and development of complex organisms. He is pursuing the thesis that the majority of the genome of humans and other complex organisms, previously considered to be "junk", is devoted to a vastly expanded regulatory architecture, which is mainly transacted via digital RNA signals and which contain the endogenous program that directs the trajectories of differentiation and development, via RNA – DNA, RNA – RNA, and RNA – protein interactions that control epigenetic modification, transcription, alternative splicing, etc.

Dr. Mattick has published over 250 research articles and his work has received coverage in *Nature*, *Science*, *Scientific American*, *New Scientist*, and *The New York Times*, among others. He is frequently invited to international meetings to speak on the subject. Dr. Mattick was appointed as an Officer in the Order of Australia (AO) for his services to molecular biology and genomics in Australia. In 2002, he was elected as an Honorary Fellow of the Royal College of Pathologists of Australasia (FRCPA), and in 2003, he was awarded the Centenary Medal by the Australian Government for services to biotechnology. In 2006, he was awarded the CSIRO Eureka Prize for Leadership in Science. In 2007, he was awarded the inaugural Gutenberg Chair at the Université Louis Pasteur De Strasbourg and elected as an Associate (Foreign) Member of the European Molecular Biology Organisation. In 2008, he was elected a Fellow of the Austrlian Academy of Science. He was awarded the 2011 International Union of Biochemistry and Moelcular Biology (IUBMB) Medal and the 2012 Human Genome Organisation Chen Medalfor Distinguished Academic Achievement in Human Genetics and Genomic Research.

Alexander Meissner, PhD

Dr. Meissner is Associate Professor of Stem Cell and Regenerative Biology at Harvard University, Principal Faculty at the Harvard Stem Cell Institute, and Senior Associate Member at the Broad Institute, which is a collaborative, multidisciplinary initiative of Harvard University and the Massachusetts Institute of Technology (MIT), and a Robertson Investigator at the New York Stem Cell Foundation. He received his degree in medical biotechnology at the Technological University of Berlin, and his PhD at MIT's Whitehead Institute, where he also completed a postdoctoral fellowship.

Dr. Meissner's laboratory uses genomic tools to study stem cell biology with a particular focus on epigenetic reprogramming. The term epigenetic refers to stable modifications of the chromatin and DNA that do not alter the primary nucleotide sequence. The global epigenetic makeup of a cell is a powerful indicator of its developmental state and potential. His laboratory applies next generation sequencing technologies to study the epigenome in early development, stem cells and cancer. He is developing and applying high-throughput bisulfite sequencing (HTBS) technologies for genome-wide (nucleotide resolution) DNA methylation analysis. To gain insights into the interaction and regulation of epigenetic modifications (histone modifications and DNA methylation), Dr. Meissner's

laboratory uses loss of function and gain of function systems. Pluripotent stem cells have enormous potential for regenerative medicine, and provide a powerful tool for studies in developmental biology and pharmacology. Recent advances in transforming somatic cells directly into pluripotent (iPS) cells provide an attractive avenue for generating patient-specific stem cells. Dr. Meissner is identifying the epigenetic changes and components involved in reprogramming and maintaining cellular states.

Dr. Meissner has published in many peer-reviewed journals including *Nature*, *Nature Genetics, Nature Biotechnology*, *Nature Methods*, *Cell*, and *Trends in Molecular Medicine*. He has received several awards, and has been nominated for Technology Review's "Top Innovators Under 35" award. Support for his research includes funding from the National Institutes of Health's Roadmap Epigenomics initiative, the NIGMS and the NYSCF.

Maynard Olson, PhD
Dr. Olson is Professor Emeritus of Medicine and Genome Sciences at the University of Washington. His undergraduate education was at the California Institute of Technology, and he received his PhD in chemistry from Stanford University in 1970. After earlier faculty appointments at Dartmouth College and Washington University, he came to the University of Washington in 1992.

During his research career, Olson developed a number of experimental and computational methods, such as high-resolution, clone-based physical mapping, sequence-tagged-site-content mapping, and yeast-artificial-chromosome cloning that have been widely used in genome analysis. He also carried out numerous studies of natural genetic variation in the human and bacterial genomes. Dr. Olson participated extensively in the formulation of policy for the Human Genome Project, serving on the original National Research Council Committee on Mapping and Sequencing of the Human Genome, the National Advisory Council of the National Human Genome Research Institute, and numerous other advisory groups, as well as testifying several times about the Human Genome Project in front of Congressional Committees. Last year, Olson served on a National Research Council Committee that issued the report "Toward Precision Medicine," and he currently serves of the Board of Scientific Advisors of Illumina, Inc.

Dr. Olson has received several awards for his contributions to genome research, including the Genetics Society of America Medal in 1992, the City of Medicine Award in 2000, the Gairdner International Award in 2002, and the Gruber Genetics Prize in 2007; he was elected to the National Academy of Sciences in 1994.

Jared Roach, M.D., Ph.D.
Dr. Roach is Senior Research Scientist at the Institute for Systems Biology. He received his B.S. from Cornell University and his M.D. and his Ph.D. in Immunology under the mentorship of Dr. Leroy Hood from the University of Washington. He

studied Internal Medicine at the University of Utah. His areas of expertise include Computational Biology, Genetics, Genomics, and Immunology.

Dr. Roach is interested in basic and translational analyses and applications of high-throughput systems-biology data. He is currently focusing on understanding the genetics of complex neurodegenerative diseases, including Huntington's disease. Dr. Roach is pioneering approaches for the analysis of whole genome sequencing data in the context of family pedigrees. His past studies have included (1) the systems biology of the macrophage, particularly in its role as an information processing device, at the levels of cell surface receptors, signal transduction, and nuclear regulation, (2) the molecular phylogenetics of vertebrate gene families, particularly those genes relevant to macrophage information processing, and (3) analysis and interpretation of transcript enumeration data, including RNAseq and microarray transcriptomics.

Dr. Roach was a co-developer of the pairwise end-sequencing technique. The translational impact of Dr. Roach's research contributes to clinical areas including neurodegeneration, autoimmunity, rare genetic diseases, diabetes, inflammation, and vaccine development.

Azim Surani, PhD, FMedSCi, FRS

Dr. Surani, who was born in Kenya, is the Marshall-Walton Professor, Head of Wellcome Laboratories and Principal Investigator at the Wellcome Trust Cancer Research UK Gurdon Institute, and a Professorial Fellow at King's College Cambridge. He obtained his PhD in Mammalian Development in 1975 at Cambridge University under Professor Sir Robert Edwards FRS, a Nobel Prize winner in Physiology or Medicine in 2010. Dr. Surani established his first research group at the Babraham Institute in 1979, where he discovered the phenomenon of Genomic Imprinting in 1984. He and his colleagues went onto identify several novel imprinted genes and their functions, and contributed to the mechanism of imprinting involving the establishment and erasure of DNA methylation. He returned to the University of Cambridge in his current capacity in 1992.

Dr. Surani's work over the past twelve years has revealed for the first time the genetic basis for mammalian germ cell specification, and its intimate link with the initiation of the unique and extensive epigenetic reprogramming in early germ cells. He has received several awards, including election as a Fellow of the Royal Society in 1990 and a Royal Medal in 2010 for his contributions to advances in epigenetic mechanisms and pivotal contributions to early mammalian development.