Andrej Sali received his BSc degree in chemistry from the University of Ljubljana, Slovenia, in 1987; and his PhD from Birkbeck College, University of London, UK, in 1991, under the supervision of Professor Tom L. Blundell, where he developed the MODELLER program for comparative modeling of protein structures. He was then a postdoc with Professor Martin Karplus at Harvard University as a Jane Coffin Childs Memorial Fund fellow, studying lattice Monte Carlo models of protein folding. From 1995 to 2002, he was first an Assistant Professor and then an Associate Professor at The Rockefeller University. In 2003, he moved to University of California, San Francisco, as a Professor of Computational Biology in the Department of Bioengineering and Therapeutic Sciences, Department of Pharmaceutical Chemistry, and California Institute for Quantitative Biosciences (QB3). He was a Sinsheimer Scholar (1996), an Alfred P. Sloan Research Fellow (1998), an Irma T. Hirschl Trust Career Scientist (2000), the recipient of the Zois Award of Science Ambassador of Republic of Slovenia (2007), and elected a Fellow of International Society for Computational Biology (2014). He has been an Editor of Structure since 2002. He is also a Founder of Prospect Genomix that merged with Structural Genomix (2001); and of Global Blood Therapeutics (2012). Dr. Sali develops and applies computational methods for determining and modulating structures and functions of proteins and their assemblies.