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Ian A Wilson

The Scripps Research Institute, USA

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The major surface antigen, the hemagglutinin (HA) of in uenza virus is the main target of neutralizing antibodies. However, until recently, most antibodies were thought to be strain-speci c and protect only against highly related strains within the same subtype. However, in the past few years, many human antibodies have been isolated that are much broader a neutralize across subtypes and groups of in uenza A and B viruses through binding to functionally conserved sites. We have determined structures of many broadly neutralizing antibodies with HAs and determined that their epitopes map to highly conserved sites on the HA fusion domains (stem) and receptor binding sites (head). e identi cation and characterization of the epitopes and mode of binding of these antibodies have elucidated recognition motifs and conserved sites of vulnerability that provide exciting new opportunities for structure-assisted vaccine design as well as for design of therapeutics that a ord greater protection against in uenza viruses.

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Ian A Wilson has received his BSc in Biochemistry from Edinburgh University, DPhil in Molecular Biophysics from Oxford University and did Postdoctoral research at Harvard University. He has been a Professor at The Scripps Research Institute since 1982 and is Hansen Professor of Structural Biology and Chair of the Department Integrative Structural and Computational Biology. His laboratory focuses on recognition of microbial pathogens by the immune system and structure-based design of vaccines and therapeutics. He is a Fellow of the Royal Society, Fellow of the Royal Society of Edinburgh, Member of the American Academy of Arts and Sciences and has a DSc degree from Oxford University and published over 665 papers.

wilson@scripps.edu

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