

## **MATTHEW REES**

NIH-Cambridge Scholar 2008

Degrees: University of Oxford, M.A., Biochemistry, 2007

Research Interests: Genetics, metabolic disease



Matthew Rees graduated from the University of Oxford, earning a Master's Degree in Molecular and Cellular Biochemistry in four years. Matthew was the recipient of a Departmental Prize for his performance in first-year exams and was a Corpus Christi Scholar from 2004-2007. In addition, Matthew was awarded the 2007 Gibbs Prize as the top student in his class. Matthew was introduced to research as a summer student at Cornell University in 2002, where he studied the effects of knocking out the serine hydroxymethyltransferase gene on folate metabolism in mice. At Oxford, Matthew developed a keen interest in human metabolism and physiology. For his dissertation research, Matthew worked in the lab of Professor Frances Ashcroft, functionally characterizing a novel mutation in the regulatory subunit of the pancreatic ATP-sensitive potassium channel that causes neonatal diabetes. A potential causative modification in protein function was discovered, and this led to the work being published in the Proceedings of the National Academy of Sciences, U.S.A. Since his graduation, Matthew has been working in the laboratory of Dr. Francis Collins at the National Institutes of Health on genetic risk factors for common diseases such as type 2 diabetes and related quantitative traits. This research has included broader-scale high-throughput genotyping, as well as functional studies of a diabetes-predisposing variant in the pancreatic zinc transporter SLC30A8. Outside of the lab, Matthew was a member and officer of numerous clubs and societies at Oxford, participating in a diverse set of activities including rowing, darts, and the Christian Union. He is an avid reader and writer with a particular interest in history and also enjoys nothing more than cooking a rewarding dinner after a long day in lab. Matthew is driven by knowledge gained from new experiences and new ideas and hopes to help in bridging the gap between identified genetic factors of common disease and the influence these factors may have on treatment in the innovative field of personalized medicine.