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Nota di bibliografia	Includes bibliographical references at the end of each chapters and index.
Nota di contenuto	Background -- High-throughput Sequencing of the Paired Human Immunoglobulin Heavy and Light Chain Repertoire -- In-Depth Determination and Analysis of the Human Paired Heavy and Light Chain Antibody Repertoire -- Paired VH:VL Analysis of Naïve B Cell Repertoires and Comparison to Antigen-Experienced B Cell Repertoires in Healthy Human Donors -- Conclusions and Future Perspectives -- Appendices.
Sommario/riassunto	This thesis outlines the development of the very first technology for high-throughput analysis of paired heavy and light-chain antibody sequences, opening the door for the discovery of new antibodies and the investigation of adaptive immune responses to vaccines and diseases. By designing two new technologies for sequencing multiple

mRNA transcripts from up to 10 million isolated, single cells, the author directly addresses the limitations to provide information on the identity of immune receptor pairs encoded by individual B or T lymphocytes. Previous methods for high-throughput immune repertoire sequencing have been unable to provide such information. The techniques developed in this thesis have enabled comprehensive investigation of human B-cell repertoires and have been applied for the rapid discovery of new human antibodies, to gain new insights into the development of human antibody repertoires, and for analysis of human immune responses to vaccination and disease.