1.

Record Nr.	UNINA9910452022803321
Titolo	Alliances for obesity prevention [[electronic resource]] : finding common ground : workshop summary / / Lynn Parker ... [et al.], rapporteurs ; Standing Committee on Childhood Obesity Prevention, Food and Nutrition Board, Institute of Medicine of the National Academies
Pubbl/distr/stampa	Washington, D.C., : National Academies Press, 2012
ISBN	1-280-67629-9 9786613653222 0-309-22473-X
Descrizione fisica	1 online resource (74 p.)
Altri autori (Persone)	ParkerLynn
Disciplina	614.59398
Soggetti	Obesity - Prevention Electronic books.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references.
Nota di contenuto	""Front Matter""; ""Reviewers""; ""Contents""; ""1 Background and Rationale""; ""2 Mission: Readiness""; ""3 Food and Agriculture""; ""4 Physical Activity and the Built Environment""; ""5 Forming Successful Alliances""; ""6 Building Alliances""; ""7 Final Observations""; ""References""; ""Appendix A: Workshop Agenda""; ""Appendix B: Speaker Biographical Sketches""; ""Appendix C: Statement of Task""; ""Appendix D: Acronyms""

2.

Record Nr.	UNINA9910253930203321
Autore	DeKosky Brandon
Titolo	Decoding the Antibody Repertoire : High Throughput Sequencing of Multiple Transcripts from Single B Cells / / by Brandon DeKosky
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2017
ISBN	3-319-58518-5
Edizione	[1st ed. 2017.]
Descrizione fisica	1 online resource (XXVIII, 87 p. 34 illus.)
Collana	Springer Theses, Recognizing Outstanding Ph.D. Research, , 2190-5053
Disciplina	616.0798
Soggetti	Immunoglobulins Genetic engineering Human genetics Cytology Biochemistry Antibodies Genetic Engineering Human Genetics Cell Biology Biochemistry, general
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
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.