1.	Record Nr.	UNINA9910437617803321
	Autore	Morgan Kevin
	Titolo	Genetic variants in Alzheimer's disease / / Kevin Morgan
	Pubbl/distr/stampa	New York, : Springer, c2013
	ISBN	1-4614-7309-8
	Edizione	[1st ed. 2013.]
	Descrizione fisica	1 online resource (256 p.)
	Disciplina	616.831042
	Soggetti	Alzheimer's disease - Genetic aspects Neurogenetics
	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 and indexes.
	Nota di contenuto	The Genetics of Alzheimer's disease: Introduction and Perspective for the Future -- Apolipoprotein E -- Clusterin -- PICALM -- Complement Component (3b/4b) Receptor 1(CR1) -- Bridging Integrator 1 (BIN1) -- ATP-binding cassette, sub-family A (ABC1), member 7 (ABCA7) -- Membrane-spanning 4-domains subfamily A, MS4A cluster -- Sialic acid binding immunoglobulin-like lectin-3 (CD33) -- Erythropoietin-producing human hepatocellular carcinoma (EphA1) -- CD2-associated protein (CD2AP) -- Other Genes Implicated in Alzheimer's Disease -- The Future Role of Biomarkers in Alzheimer's Disease Diagnostics -- Index.
	Sommario/riassunto	Since 2009, a revolution has been witnessed in Alzheimer's Disease genetics. New genetic links are being discovered at an unprecedented pace and our understanding of the molecular mechanisms of neurodegeneration have taken a quantum leap forward. This book provides a thorough description of the genes that have been implicated in the aetiology of late-onset Alzheimer's disease (LOAD) based on evidence of genetic association. These "AD susceptibility genes" are described both in their genomic and cellular context, as well as with respect to their known or suspected molecular functions. Although these genes are not sufficient to explain all of the genetic contributions to LOAD, they represent the best replicated set of genes to date. Undoubtedly the list will grow as more advanced genomic approaches towards the identification of novel LOAD genes progresses.