1.	Record Nr.	UNISA996393783803316
	Autore	Playford Henry <b. 1657.>
	Titolo	The Banquet of musick, or, A Collection of the newest and best songs sung at court and at publick theatres . The fourth book [[electronic resource]] : with a thorow-bass for the theorbo-lute, bass-viol, harpsichord, or organ / / composed by several of the best masters ; the words by the ingenious wits of this age
	Pubbl/distr/stampa	In the Savoy [London], : Printed by E. Jones, for Henry Playford ..., 1690
	Descrizione fisica	[4] p., 44 p. of music
	Soggetti	Songs (High voice)
	Lingua di pubblicazione	Inglese
	Formato	Musica a stampa
	Livello bibliografico	Monografia
	Note generali	Attributed to Henry Playford by Wing and NUC pre-1956 imprints. Reproduction of original in the Harvard University Library.
	Sommario/riassunto	eebo-0167

2.

Record Nr.	UNINA9910707762203321
Autore	Fike Richard E.
Titolo	The pony express stations of Utah in historical perspective / / Richard E. Fike, John W. Headley
Pubbl/distr/stampa	[Salt Lake City] : , : Bureau of Land Management, Utah, , 1979
Descrizione fisica	1 online resource : illustrations, maps
Collana	Cultural resources series ; ; monograph 2
Soggetti	Pony express - History Historic buildings - Utah Historic buildings Pony express History Utah History Utah
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references.

3. Record Nr.	UNINA9910373913403321
Titolo	The Grape Genome / / edited by Dario Cantu, M. Andrew Walker
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2019
ISBN	3-030-18601-6
Edizione	[1st ed. 2019.]
Descrizione fisica	1 online resource (XXVII, 367 p. 52 illus., 40 illus. in color.)
Collana	Compendium of Plant Genomes, , 2199-4781
Disciplina	581.35
Soggetti	Plant genetics Plant breeding Agriculture Genètica vegetal Plant Genetics and Genomics Plant Breeding/Biotechnology Llibres electrònics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references.
Nota di contenuto	Economic/Academic importance -- Grape taxonomy and germplasm -- Grape domestication -- Ancient DNA sequencing and grape archeology -- Strategies & tools for sequencing -- Gene annotation -- Database -- Molecular mapping of genes & QTLs -- Grape systems biology -- Grape epigenetics -- The genome of the grapevine holobiont -- Genes and water relations in the grapevine -- Genomics of berry ripening -- Grape transcriptomics and viticulture -- Wild grapes and rootstock breeding -- Breeding genetic resistance to biotic diseases -- Grape biotechnology, past present future (genome editing…) -- Future prospects. .
Sommario/riassunto	This book describes the current state of international grape genomics, with a focus on the latest findings, tools and strategies employed in genome sequencing and analysis, and genetic mapping of important agronomic traits. It also discusses how these are having a direct impact on outcomes for grape breeders and the international grape research community. While V. vinifera is a model species, it is not always appreciated that its cultivation usually requires the use of other Vitis

species as rootstocks. The book discusses genetic diversity within the Vitis genus, the available genetic resources for breeding, and the available genomic resources for other Vitis species. Grapes (Vitis vinifera spp. vinifera) have been a source of food and wine since their domestication from their wild progenitor (Vitis vinifera ssp. sylvestris) around 8,000 years ago, and they are now the world’s most valuable horticultural crop. In addition to being economically important, V. vinifera is also a model organism for the study of perennial fruit crops for two reasons: Firstly, its ability to be transformed and micropropagated via somatic embryogenesis, and secondly its relatively small genome size of 500 Mb. The economic importance of grapes made V. vinifera an obvious early candidate for genomic sequencing, and accordingly, two draft genomes were reported in 2007. Remarkably, these were the first genomes of any fruiting crop to be sequenced and only the fourth for flowering plants. Although riddled with gaps and potentially omitting large regions of repetitive sequences, the two genomes have provided valuable insights into grape genomes. Cited in over 2,000 articles, the genome has served as a reference in more than 3,000 genome-wide transcriptional analyses. Further, recent advances in DNA sequencing and bioinformatics are enabling the assembly of reference-grade genome references for more grape genotypes revealing the exceptional extent of structural variation in the species.