1.

Record Nr.	UNINA9910795975103321
Autore	Li Robert Y.
Titolo	Cardiovascular diseases : from molecular pharmacology to evidence-based therapeutics / / Y. Robert Li
Pubbl/distr/stampa	Hoboken, New Jersey : , : John Wiley & Sons Inc., , 2015 2015
ISBN	1-118-88994-0 1-118-88991-6
Descrizione fisica	1 online resource (504 pages) : illustrations (some color)
Disciplina	616.1/061
Soggetti	Cardiovascular system - Diseases - Chemotherapy Cardiovascular system - Diseases - Diagnosis
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references and index.

2.

Record Nr.	UNINA9910619470903321
Autore	Piorkowska Katarzyna
Titolo	Pig Genomics and Genetics
Pubbl/distr/stampa	MDPI - Multidisciplinary Digital Publishing Institute, 2022
ISBN	3-0365-5357-6
Descrizione fisica	1 online resource (318 p.)
Soggetti	Biology, life sciences Research and information: general Zoology and animal sciences
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Sommario/riassunto	In this Special Issue, we present the state of the art in the field of pig genetics and genomics, including the identification of gene candidates linked to important pig traits and to nutritional modifications, with the aim of collecting the most recent advances. The published manuscripts focused on high-throughput methodologies, such as RNA sequencing, ATAC-seq, MACE-seq, chip-seq, and RRBS, and covered other fields of pig genetics. The pig (Sus scrofa) is the most common large mammal in the world. The Sus genus includes domestic pig and wild boar. Since the draft reference genome sequence of S. scrofa was assembled in 2012, the processes of identification of genes related to important phenotypic traits and of search of genetic markers for pig selection have been significantly refined. In addition, the newest wide-range high-throughput techniques, including microarrays, next-generation sequencing, and the recent PacBio sequencing platform providing ultra-long sequencing reads, allow identifying gene mutations and gene candidates throughout the whole genome, transcriptome, or epigenome and estimating quantitative traits important for breeding as well as the genetic backgrounds of inherited diseases.