

1.	Record Nr.	UNIBAS000033499
	Autore	Baader, Franz : von
	Titolo	Filosofia erotica / Franz von Baader ; introduzione, traduzione e note di Lidia Procesi Xella
	Pubbl/distr/stampa	Milano : Rusconi, 1982
	Descrizione fisica	682 p. ; 22 cm
	Collana	I classici del pensiero . Sez. 3 , Filosofia moderna
	Disciplina	193
	Soggetti	Erotismo - Filosofia
	Lingua di pubblicazione	Italiano
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
2.	Record Nr.	UNINA9910482286403321
	Autore	Anon
	Titolo	Het avijs, der ijnquizicie van Spaengien bewijsinghe dat in alle de Nederlanden geen papist oft catholijcke personen en sijn na het geluyt der selver ijnquisicie van Spaengien [[electronic resource]]
	Pubbl/distr/stampa	Leuven, : [s.n.], 1571
	Descrizione fisica	Online resource (8°)
	Lingua di pubblicazione	Olandese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Note generali	Reproduction of original in Koninklijke Bibliotheek, Nationale bibliotheek van Nederland.

3. Record Nr.	UNINA9910144561303321
Titolo	The handbook of plant genome mapping [[electronic resource]] : genetic and physical mapping / / edited by Khalid Meksem and Gunter Kahl
Pubbl/distr/stampa	Weinheim, : Wiley-VCH, c2005
ISBN	1-280-51974-6 9786610519743 3-527-60351-4 3-527-60443-X
Descrizione fisica	1 online resource (404 p.)
Altri autori (Persone)	MeksemKhalid KahlGunter
Disciplina	572.862 581.35015118
Soggetti	Plant genome mapping Botany
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 index.
Nota di contenuto	The Handbook of Plant Genome Mapping; Preface; Contents; List of Contributors; Part I Genetic Mapping; 1 Mapping Populations and Principles of Genetic Mapping; Overview; Abstract; 1.1 Introduction; 1.2 Mapping Populations; 1.2.1 Mapping Populations Suitable for Self-fertilizing Plants; 1.2.1.1 F(2) Populations; 1.2.1.2 Recombinant Inbred Lines; 1.2.1.3 Backcross Populations; 1.2.1.4 Introgression Lines: Exotic Libraries; 1.2.1.5 Doubled Haploid Lines; 1.2.2 Mapping Populations for Cross-pollinating Species; 1.2.3 Two-step Strategies for Mapping Mutants and DNA Fragments 1.2.4 Chromosome-specific Tools for Mapping1.2.5 Mapping in Natural Populations/Breeding Pools; 1.2.6 Mapping Genes and Mutants to Physically Aligned DNA; 1.2.7 Specific Mapping Problems; 1.3 Discussion; Acknowledgments; References; 2 Molecular Marker Systems for Genetic Mapping; Abstract; 2.1 Introduction; 2.2 DNA-based Markers Popularly Used in Genetic Mapping; 2.2.1 RFLP; 2.2.1.1 Conventional RFLP Analysis; 2.2.1.2 PCR-RFLP; 2.2.1.3 Mismatch PCR-

RFLP; 2.2.2 RAPD; 2.2.3 SSR Markers; 2.2.3.1 Conventional SSR Analysis; 2.2.3.2 ISSR; 2.2.3.3 STMP; 2.2.4 AFLP; 2.2.4.1 Conventional AFLP Analysis; 2.2.4.2 f-AFLP; 2.2.4.3 cDNA-AFLP and HiCEP; 2.2.4.4 TE-AFLP; 2.2.4.5 MEGA-AFLP; 2.2.4.6 MITE-AFLPs; 2.2.4.7 AFLP Conversion; 2.2.5 REMAP and IRAP; 2.2.5.1 IRAP; 2.2.5.2 REMAP; 2.2.6 SRAP; 2.3 Discussion; References; 3 Methods and Software for Genetic Mapping; Overview; Abstract; 3.1 Introduction; 3.1.1 Methods and Tools for Genetic Linkage Mapping in Plants; 3.1.1.1 Statement of the Problem; 3.1.2 Locus Grouping; 3.1.3 Locus Ordering; 3.1.4 Multilocus Distance Estimation; 3.1.5 Using Variant and Mixed Cross Designs; 3.1.5.1 Outbreeding Species; 3.1.5.2 Autopolyploid Species; 3.1.5.3 Combining Datasets; 3.1.6 Linkage-mapping Software Availability, Interfaces, and Features; 3.2 Methods and Tools for QTL Mapping in Plants; 3.2.1 Statement of the Problem; 3.2.2 Single-marker Association; 3.2.2.1 Metric Traits; 3.2.2.2 Categorical Traits; 3.2.3 Interval Mapping: Simple (SIM); 3.2.3.1 ML Methods; 3.2.3.2 Least-squares (Regression) and Nonparametric Methods; 3.2.4 Interval Mapping: Composite (CIM); 3.2.5 Significance Testing; 3.2.6 Interval Mapping: Multiple-QTL Model Building; 3.2.6.1 Stepwise and Exhaustive-search Methods for Building Multiple-QTL Models; 3.2.6.2 Markov Chain Monte Carlo (MCMC) Methods; 3.2.6.3 Genetic Algorithms; 3.2.7 Multiple-trait (MT) QTL Mapping; 3.2.8 Multiple-cross (MC) QTL Mapping; 3.2.9 Computational Optimization Methods; 3.3 Future Directions in Mapping Methods and Tools; 3.3.1 Future of Linkage and QTL Mapping; 3.3.2 Adequacy of Software Tools for Plant Mapping; 3.3.2.1 Software Merit Criteria; 3.3.2.2 Analytical Scope; 3.3.2.3 Ease of Learning and Use; 3.3.2.4 Accessibility and Extensibility; 3.3.3 A Development Model for Public Genetic Mapping Software; References

4 Single nucleotide Polymorphisms: Detection Techniques and Their Potential for Genotyping and Genome Mapping

Sommario/riassunto

While the complete sequencing of the genomes of model organisms such as a multitude of bacteria and archaea, the yeast *Saccharomyces cerevisiae*, the worm *Caenorhabditis elegans*, the fly *Drosophila melanogaster*, and the mouse and human genomes have received much public attention, the deciphering of plant genomes was greatly lagging behind. Up to now, only two plant genomes, one of the model plant *Arabidopsis thaliana* and one of the crop species rice (*Oryza sativa*) have been sequenced, though a series of other crop genome sequencing projects are underway. Notwithstanding this public bias towards