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| 1. Record Nr.           | UNISALENT0991000961909707536  |
| Autore                  | Burdea, Grigore   |
| Titolo                  | Force and touch feedback for Virtual Reality / Grigore C. Burdea  |
| Pubbl/distr/stampa      | New York : Wiley, c1996   |
| ISBN                    | 0471021415  |
| Descrizione fisica      | xiv, 339 p., [8] p. of plates : ill. 24 cm  |
| Disciplina              | 006   |
| Soggetti                | Human-computer interaction<br>Virtual reality   |
| Lingua di pubblicazione | Inglese   |
| Formato                 | Materiale a stampa  |
| Livello bibliografico   | Monografia  |
| Nota di bibliografia    | Includes bibliographical references and index   |
| 2. Record Nr.           | UNINA9910298441903321   |
| Titolo                  | Advances in the Understanding of Biological Sciences Using Next Generation Sequencing (NGS) Approaches / / edited by Gaurav Sablok, Sunil Kumar, Saneyoshi Ueno, Jimmy Kuo, Claudio Varotto |
| Pubbl/distr/stampa      | Cham : , : Springer International Publishing : , : Imprint : Springer, , 2015   |
| ISBN                    | 3-319-17157-7   |
| Edizione                | [1st ed. 2015.]   |
| Descrizione fisica      | 1 online resource (248 p.)  |
| Disciplina              | 570   |
| Soggetti                | Plant breeding<br>Plant genetics<br>Plant physiology<br>Plant Breeding/Biotechnology<br>Plant Genetics and Genomics<br>Plant Physiology   |
| Lingua di pubblicazione | Inglese   |
| Formato                 | Materiale a stampa  |

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| Livello bibliografico | Monografia   |
| Note generali         | Description based upon print version of record.  |
| Nota di bibliografia  | Includes bibliographical references at the end of each chapters and index.   |
| Nota di contenuto     | Expression analysis and genome annotations with RNA sequencing -- The application of Next Generation Sequencing techniques to Plant Epigenomics -- Whole genome sequencing to identify genes and QTL in rice -- Variant calling using NGS data in European aspen ( <i>Populus tremula</i> ) -- Leafy Spurge Genomics: A Model Perennial Weed To Investigate Development, Stress Responses, And Invasiveness -- Utilization of NGS and proteomic-based approaches to gain insights on cellular responses to singlet oxygen and improve energy yields for bacterial stress adaptation -- Experimental evolution and next generation sequencing illuminate the evolutionary trajectories of microbes -- Plant carbohydrate active enzyme (CAZyme) repertoires: a comparative Study -- Metagenomics of Plant- Microbe Interactions -- Genes and trans-factors underlying embryogenic transition in plant soma-cells -- Bioinformatics tools to analyze the proteome and genome data -- High through-put transcriptome analysis of plant stress responses -- CNV and structural variation in plants: prospects of NGS Approaches. |
| Sommario/riassunto    | This work is a compiled catalogue of such findings, where several NGS technologies ranging from the genomics, transcriptomics, metagenomics, single cell genomics, QTL, patho-genomics and patho-transcriptomics have been applied to delineate the mystery of the associated mutations, biological pathway transitions, transcriptional fluxes and patterns of host associated or adaptations to certain climatic conditions. The aims and scope of this book focuses more on the biological underpinning to initiate the cross-talks across the traits acquired or lost during the course of evolution. The structured framework of the present volume provides the applicative point of view of the NGS technologies and demonstrates the conceptual way of linking the experimentation to the NGS technologies, to aid in researchers to place their biological hypothesis in a larger context.  |