

1. Record Nr.	UNINA9910350351803321
Titolo	Single Molecule and Single Cell Sequencing [[electronic resource] /] / edited by Yutaka Suzuki
Pubbl/distr/stampa	Singapore : , : Springer Singapore : , : Imprint : Springer, , 2019
ISBN	981-13-6037-5
Edizione	[1st ed. 2019.]
Descrizione fisica	1 online resource (VI, 150 p. 56 illus., 51 illus. in color.)
Collana	Advances in Experimental Medicine and Biology, , 0065-2598 ; ; 1129
Disciplina	611.01816 599.935
Soggetti	Human genetics Bioinformatics Human Genetics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Chapter1. Strategies for converting RNA to amplifiable cDNA for single-cell RNA sequencing methods -- Chapter2. Integrated Fluidic Circuits for single cell omics and multi-omics applications -- Chapter3. Single-cell DNA-Seq and RNA-Seq in cancer using the C1 system -- Chapter4. Nx1-Seq (Well based Single-Cell Analysis System) -- Chapter5. Quantitation of mRNA transcripts and proteins using the BD Rhapsody™ Single-Cell Analysis System -- Chapter6. An Informative Approach to Single-Cell Sequencing Analysis -- Chapter7. Bionano Genome Mapping: High-Throughput, Ultra-Long Molecule Genome Analysis System for Precision Genome Assembly and Haploid-Resolved Structural Variation Discovery -- Chapter8. Informatics for PacBio long reads -- Chapter10. On-site MinION sequencing.
Sommario/riassunto	This book presents an overview of the recent technologies in single molecule and single cell sequencing. These sequencing technologies are revolutionizing the way of the genomic studies and the understanding of complex biological systems. The PacBio sequencer has enabled extremely long-read sequencing and the MinION sequencer has made the sequencing possible in developing countries. New developments and technologies are constantly emerging, which will further expand sequencing applications. In parallel, single cell

sequencing technologies are rapidly becoming a popular platform. This volume presents not only an updated overview of these technologies, but also of the related developments in bioinformatics. Without powerful bioinformatics software, where rapid progress is taking place, these new technologies will not realize their full potential. All the contributors to this volume have been involved in the development of these technologies and software and have also made significant progress on their applications. This book is intended to be of interest to a wide audience ranging from genome researchers to basic molecular biologists and clinicians. .
