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Titolo	Novel Coronavirus 2019 : in-silico vaccine design and drug discovery // Amit Kumar [and four others]
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Descrizione fisica	1 online resource (IX, 78 p. 83 illus., 51 illus. in color.)
Collana	SpringerBriefs in applied sciences and technology. Forensic and medical bioinformatics
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Soggetti	COVID-19 (Disease)
Lingua di pubblicazione	Inglese
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Livello bibliografico	Monografia
Nota di contenuto	1. COVID19 and The Novel Corona Virus 2019 -- 2. The Genomic and Evolutionary Studies of Novel Corona Virus 2019 -- 3. Comparative proteomic analysis of NCoV and MERS Corona Virus -- 4. Physiochemical Characterization and Domain annotation of ORF1ab polyprotein of Novel Corona Virus 19 -- 5. Docking studies of the RNA dependent RNA polymerase domain of ORF1AB protein with the selected ligands of Novel Coronavirus 19 -- 6. Noted Herbs in the Treatment of COVID19 and Improving Human Immunity -- 7. Architecture of COVID-19 and SARS CoV-spike structural and functional aspects with ACE2 receptor: In-Silico analysis -- 8. Plasma Therapy towards COVID treatment -- 9. Identification and analysis of Possible Vaccine Candidates for COVID19 -- 10. Development of KITS for Rapid Diagnosis of COVID19.
Sommario/riassunto	This book highlights the genomic findings, observations, and analysis of DNA/RNA sequences and protein structure of the dreadful virus of this decade- COVID-19. The Corona group of viruses though known species, the strain that caused the Pandemic of 2019 is a completely new strain, belonging to the same corona family with a novel genetic make-up. This makes it a new pathogen which is causing the current outbreak leaving the global scientific community clueless of any therapeutic breakthrough. NCOV enjoys life threatening pathogenicity with mysterious genetic annotations. This book details and offers

insights into its viral genetic arrangement, Virulence factors, probable mutations leading to the evolution of this new strain and more. It contains chapters on Virus evolutionary status and Genetic makeup leading to its pathogenicity which can be a new insight in understanding the nature of this clever microorganism and can pave way to the development of new drugs and Vaccines or a novel diagnostic approach for the early prognosis of the disease. A dedicated chapter on annotation of NCOV-19 virulence genes, translation of the genes to protein product, annotation of the antigenic sites on these proteins is also included. In all, this brief is a complete genomic annotation insight of NCOV-19 using AI, Data analytics and Bioinformatics analysis. In the current situation, this book is an extensive preliminary resource for Medical practitioners, Researchers, Academicians, Scientists, Biochemists, Bioinformaticians and other professionals interested in understanding the genetics of Novel Coronavirus 19, the best possible drug targets, ideal vaccine candidates and novel prognostic and diagnostic biomarkers.
