

In silico identification of vaccine targets for 2019-nCoV

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Citation Report

#	ARTICLE	IF	CITATIONS
1	An immunoinformatics study on the spike protein of SARS-CoV-2 revealing potential epitopes as vaccine candidates. <i>Heliyon</i> , 2020, 6, e04865.	1.4	8
2	The role of host genetics in the immune response to SARS-CoV-2 and COVID-19 susceptibility and severity. <i>Immunological Reviews</i> , 2020, 296, 205-219.	2.8	175
3	Immunodominant regions prediction of nucleocapsid protein for SARS-CoV-2 early diagnosis: a bioinformatics and immunoinformatics study. <i>Pathogens and Global Health</i> , 2020, 114, 463-470.	1.0	20
4	SARS-CoV-2 Epitopes Are Recognized by a Public and Diverse Repertoire of Human T Cell Receptors. <i>Immunity</i> , 2020, 53, 1245-1257.e5.	6.6	194
5	Epitope-Based Immunoinformatics Approach on Nucleocapsid Protein of Severe Acute Respiratory Syndrome-Coronavirus-2. <i>Molecules</i> , 2020, 25, 5088.	1.7	33
6	Polymorphism and Selection Pressure of SARS-CoV-2 Vaccine and Diagnostic Antigens: Implications for Immune Evasion and Serologic Diagnostic Performance. <i>Pathogens</i> , 2020, 9, 584.	1.2	16
7	Genetic gateways to COVID-19 infection: Implications for risk, severity, and outcomes. <i>FASEB Journal</i> , 2020, 34, 8787-8795.	0.2	111
8	HLA-B*44 and C*01 Prevalence Correlates with Covid19 Spreading across Italy. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5205.	1.8	73
9	Computationally Optimized SARS-CoV-2 MHC Class I and II Vaccine Formulations Predicted to Target Human Haplotype Distributions. <i>Cell Systems</i> , 2020, 11, 131-144.e6.	2.9	50
10	SARS-CoV-2 Vaccine Development: Current Status. <i>Mayo Clinic Proceedings</i> , 2020, 95, 2172-2188.	1.4	96
11	Immunoinformatics-guided design of an epitope-based vaccine against severe acute respiratory syndrome coronavirus 2 spike glycoprotein. <i>Computers in Biology and Medicine</i> , 2020, 124, 103967.	3.9	62
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14	Designing a multi-epitope peptide based vaccine against SARS-CoV-2. <i>Scientific Reports</i> , 2020, 10, 16219.	1.6	87
15	Vaccines for COVID-19: perspectives from nucleic acid vaccines to BCG as delivery vector system. <i>Microbes and Infection</i> , 2020, 22, 515-524.	1.0	23
16	Computationally validated SARS-CoV-2 CTL and HTL Multi-Patch vaccines, designed by reverse epitomics approach, show potential to cover large ethnically distributed human population worldwide. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 2369-2388.	2.0	10
17	Potential CD8+ T Cell Cross-Reactivity Against SARS-CoV-2 Conferred by Other Coronavirus Strains. <i>Frontiers in Immunology</i> , 2020, 11, 579480.	2.2	42
18	Binding affinities of 438 HLA proteins to complete proteomes of seven pandemic viruses and distributions of strongest and weakest HLA peptide binders in populations worldwide. <i>Hla</i> , 2020, 96, 277-298.	0.4	89

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20	Genetics and genomics of SARS-CoV-2: A review of the literature with the special focus on genetic diversity and SARS-CoV-2 genome detection. Genomics, 2021, 113, 1221-1232.	1.3	126
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37	COMPUTER SIMULATION IN THE DEVELOPMENT OF VACCINES AGAINST COVID-19 BASED ON HLA-SYSTEM ANTIGENS. Journal of Clinical Practice, 0, , .	0.2	0

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39	Frequency of HLA alleles among COVID-19 infected patients: Preliminary data from Saudi Arabia. <i>Virology</i> , 2021, 560, 1-7.	1.1	18
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41	Immunoinformatics and molecular modeling approach to design universal multi-epitope vaccine for SARS-CoV-2. <i>Informatics in Medicine Unlocked</i> , 2021, 24, 100578.	1.9	41
42	The SARS-Coronavirus Infection Cycle: A Survey of Viral Membrane Proteins, Their Functional Interactions and Pathogenesis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1308.	1.8	83
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65	T Cell Epitope Discovery in the Context of Distinct and Unique Indigenous HLA Profiles. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	4
66	Reverse vaccinology-based prediction of a multi-epitope SARS-CoV-2 vaccine and its tailoring to new coronavirus variants. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, , 1-22.	2.0	4
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