

Citation on the Research Work of the Applicant duly signed by the Nominator

Professor Chiranjib Chakraborty is the nominee for the award in the category of Medical Sciences-Basic Research from Sun Pharma Science Foundation.

I found he is one of the best candidates for the award.

Using Immunoinformatics, Professor Chiranjib Chakraborty has created a new line of vaccine development. His vaccine contract using AI, He has developed a dozen immunoinformatics-based next-generation vaccine constructs for various infectious diseases to cancer.

Among his dozen vaccine constructs, the following five works are significant results of his research.

(1) Professor Chakraborty and his co-workers have developed the world's first mutiepitopic next-generation immunoinformatics-based vaccine construct against SARS-CoV-2, published in the Journal of Medical Virology(92(6):618-631.doi: 10.1002/jmv.25736). It's impact factor is 12.7, and the work has been cited 377 times. The technology was granted a South Korean patent (Patent no 10-2425 492; Application Date: 27. 04. 2020. Grant Date: 21.07. 2022).

(ii) Professor Chakraborty and his co-workers have developed the world's first mutiepitopic next-generation immunoinformatics-based vaccine construct against monkeypox. It was developed through the screening of whole genome-encoded proteins of the mpox virus. The work has been published in Travel Medicine and Infectious Disease, (2022, 50:102481.doi: 10.1016/j.tmaid.2022.102481. with a 12.0 impact factor), and A patent was applied for the technology.

(iii) Recently, they have developed an artificial intelligence (AI)-based, mutation-proof, next-generation vaccine construct against SARS-CoV-2. It was the first AI-based vaccine construct. It was published in the International Journal of Biological Macromolecules (2023, 242(Pt 2):124893.doi: 10.1016/j.ijbiomac.2023.124893.) having a impact factor of 8.2.

(iv) *Helicobacter pylori* (*H. pylori*) creates patients' ulcers. They have developed next-generation vaccine construct against *H. pylori* using significant antigens. The work has been published in International Journal of Peptide Research and Therapeutics (IF=2.5), This has been applied for patent and has been cited 37 times.

I feel that The following two are the best:

1. Vaccine Construct Development whole genome encoded proteins: A novel multi-epitopic peptide-based potential vaccine candidate against monkeypox virus through screening its whole genome encoded proteins

The research demonstrates the development of a novel multi-epitopic peptide-based potential vaccine candidate using an immunoinformatics approach against the monkeypox virus. A whole-genome- screening was performed of 176 encoded proteins of MPXV, and the highest antigenic epitopes were used to design the vaccine candidate. Finally, the vaccine was characterized through bioinformatics to understand the physicochemical properties, non-allergenicity, antigenicity, and binding affinity to immune receptors (TLR4/MD2-complex). The designed vaccine has shown the required effectiveness against MPXV without side effects.

Publication: Bhattacharya M, Chatterjee C, Nag S, Dhama K, **Chakraborty C*** (2022) Designing, characterization, and immune stimulation of a novel multi-epitopic peptide-based potential vaccine candidate against monkeypox virus through screening its whole genome encoded proteins: An immunoinformatics approach. **Travel Medicine and Infectious Disease** 50:102481 doi: 10.1016/j.tmaid.2022.102481 **IF: 12.0** (*Corresponding Author)
[<https://pubmed.ncbi.nlm.nih.gov/36265732/>]
(More than 13 citations)

2. AI-enabled mutation-proof, next-generation vaccine development: A novel mutation-proof, next-generation vaccine to fight against upcoming SARS-CoV-2 variants and subvariants, designed through AI-enabled approaches

It was the first AI-based vaccine construct. The study selects nine mutations from 835 RBD mutations AI-enabled, the top-ranked antigenic selection approaches. We selected twelve common antigenic B and T cell epitopes (CTL and HTL) containing the nine RBD mutations and joined them with the adjuvants, PADRE sequence, and suitable linkers. The constructs' binding affinity was confirmed through docking with TLR4/MD2 complex and showed significant binding free energy (-96.67 kcal mol⁻¹) with positive binding affinity. Similarly, the calculated eigenvalue (2.428517e-05) from the NMA of the complex reveals proper molecular motion and superior residues' flexibility. Immune simulation shows that the candidate can induce a robust immune response.

Publication: Bhattacharya M, Alshammari A, Alharbi M, Dhama K, Lee SS, **Chakraborty C.** (2023) A novel mutation-proof, next-generation vaccine to fight against upcoming SARS-CoV-2 variants and subvariants, designed through AI enabled approaches and tools, along with the machine learning based immune simulation: A vaccine breakthrough. **International Journal of Biological** 242(Pt 2):124893.
[<https://pubmed.ncbi.nlm.nih.gov/35952818/>]**IF: 8.2 (More than 1 citations)**

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