A signed statement by the applicant that the research work under reference has not been given any award.

The following two research work was not submitted for any award for which the award has been claimed.

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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