

List of 10 best papers

1. Bhattacharya M, Sharma AR, Patra P, Ghosh G, Sharma G, Patra BC, Lee SS*, **Chakraborty C*** (2020) Development of epitope-based peptide vaccine against novel Coronavirus 2019 (SARS-CoV-2): Immunoinformatics approach. **Journal of Medical Virology** 92(6):618-631.doi:10.1002/jmv.25736 (*Corresponding Author) **IF: 12.7** (More than 301 citations) [<https://pubmed.ncbi.nlm.nih.gov/32108359/>](**More than 377 citations**)
2. Bhattacharya M, Sharma AR, Ghosh P, Lee SS*, **Chakraborty C***(2021) A next-generation vaccine candidate using alternative epitopes to protect against Wuhan and all significant mutant variants of SARS-CoV-2: an Immunoinformatics approach. **Aging and Disease** doi: 10.14336/AD.2021.0518 (*Corresponding Author) **IF: 7.4** [<http://www.aginganddisease.org/EN/10.14336/AD.2021.0518>] (**More than 19 citations**)
3. 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**)
- 4.. Bhattacharya M, Alshammari A, Alharbi M, Dhama K, Lee SS, **Chakraborty C*** (2022) 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. *Int J Biol Macromol.* 2023 Jul 1;242(Pt 2):124893. doi: 10.1016/j.ijbiomac.2023.124893. **IF: 8.2** (*Corresponding Author) (**More than 1 citations**)
5. Ghosh P, Bhakta S, Bhattacharya M, SharmaAR,, Sharma G, Lee SS, **Chakraborty C***(2021) A novel multi-epitopic peptide vaccine candidate against *Helicobacter pylori*: In-silico identification, design, cloning and validation through molecular dynamics. **International Journal of Peptide Research and Therapeutics** : 27(2):1149-1166. doi: 10.1007/s10989-020-10157-w.(*Corresponding Author)**IF: 2.5** [<https://pubmed.ncbi.nlm.nih.gov/33495694/>](**More than 37 citations**)
6. Doss. CGP, **Chakraborty C**, Syed Haneef SA, NagaSundaram N, Chen L, Zhu H (2014) Evolution- and structure-based computational strategy reveals the impact of deleterious missense mutations on MODY 2 (maturity-onset diabetes of the young, type 2). **Theranostics** 4(4):366-385. **IF: 12.4** [<https://pubmed.ncbi.nlm.nih.gov/24578721/>] (**More than 56 citations**)
7. Doss CGP, Rajith B, **Chakraborty C**, Naga Sundaram N, Shabana Kouser Ali, Zhu H (2014) Structural signature of the G719S-T790M double mutation in the EGFR kinase domain and its response to inhibitors. **Scientific Reports** 4: 5868 | DOI: 10.1038/srep05868 **IF: 4.6** [<https://pubmed.ncbi.nlm.nih.gov/25091415/>] (**More than 46 citations**)
8. Nagasundaram N, George Priya Doss C, **Chakraborty C**, Karthick V, Thirumal Kumar D, Balaji V, Siva R, Lu A, Zhang G, Zhu H. (2016) Mechanism of artemisinin resistance for malaria PfATP6 L263 mutations and discovering potential antimalarials: An integrated computational approach. **Scientific Reports** 6:30106. **IF: 4.6** [<https://pubmed.ncbi.nlm.nih.gov/27471101/>] (**More than 38 citations**)

9. Chakraborty C*, Sharma AR, Bhattacharya M, Agoramoorthy G and Lee SS* (2021) Newly emerging SARS-CoV-2 variants, evolution, their mode of transmission and mutational landscape. **mBio** 12(4):e0114021. doi: 10.1128/mBio.01140-21 (*Corresponding Author) **IF: 6.4** [<https://pubmed.ncbi.nlm.nih.gov/34465019/>] (**More than 55 citations**)

10. Bhattacharya M#, Sharma AR, Dhama K, Agoramoorthy G, **Chakraborty C*#** (2022) Omicron variant (B.1.1.529) of SARS-CoV-2: Understanding mutations in the genome, S-glycoprotein, and antibody binding regions. **GeroScience** doi: 10.1007/s11357-022-00532-4 (*Corresponding Author) **IF: 5.6** (# equally contributed) [<https://pubmed.ncbi.nlm.nih.gov/35258772/>] (**More than 41 citations**)

Overview of research contribution in light of the above ten research articles

The nominee (Professor Chiranjib Chakraborty) has performed translational research significantly, and his area is primarily confined to three directions. (i) Mutation in diseases development, drug resistance, and the creation of virus variants (ii) The role of ncRNA (non-coding RNA), especially miRNA, in various diseases such as diabetes, cancer, rheumatoid arthritis, etc. (iii) Immunoinformatics based vaccine construct development

- **Immunoinformatics based vaccine construct development**

He has developed a dozen of immunoinformatics-based next-generation vaccine constructs for various infectious diseases to cancer.

(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.

- **Mutation in diseases development, drug resistance, and the creation of virus variants**

(v) They have worked on mutation in disease creation and illustrated the structural role of glucokinase (gck) mutation in MODY 2. They have Evolution- and structure-based computational models explaining deleterious missense mutations' impact on MODY 2. The work was published in *Theranostics* (4(4):366-385) (IF=12.4 which was cited more than 56 times).

(vi) His research contributed to Mutation in Drug Resistance. PfATP6, a SERCA-type Ca²⁺-ATPase enzyme, is observed in the malaria parasite. It is a significant protein target for artemisinin. The study analyzed the binding affinity and efficacy between PfATP6 and artemisinin. The study demonstrates the role of mutations in PfATP6 (especially L263K and L263E). It showed that the binding affinity was affected due to the mutation/mutations. The study also found novel compounds that offered a good result for the critical relationship with the mutant protein. It was cited more than 46 times

(vii) His research tried to unfold the mutations that created the viral variants. His research describes the Evolution of emerging variants of SARS-CoV-2, their mutational landscape, and their transmission approach. The VOCs (B.1.617.2, B.1.1.7, B.1.351, and P.1) and the significant VOIs were illustrated in that direction along with their mutations. We also critically evaluated the significant mutations in VOCs and VOIs. The structural landscape of important spike protein mutations (E484K, K417T/N, N501Y, and D614G) has been discussed, impacting public health. The work was published in *mBio* (12(4):e0114021. doi: 10.1128/mBio.01140-21) (IF: 6.4) The work has been cited more than 55 times.

He has significantly contributed to medical bioinformatics, immunoinformatics, mutation, and infectious disease. Not only he is engaged in knowledge creation, but he is also involved in disseminating knowledge nationally and internationally. Professor Chakraborty is also a visiting Professor at Hallym University, College of Medicine, South Korea, and Visiting Research Professor at the Department of Marine Biotechnology and Resources, National Sun Yat-sen University, Taiwan. (2006-2007) (QS World University Ranking 428 in the year 2023).

For his translational research, he was selected for India's highly prestigious "**Tata Innovation Fellowship**" for 2022-2023 from the Department of Biotechnology, Ministry of Science and Technology, Govt. of India. He was listed top 2% of Scientists in the World by Stanford University, USA/Elsevier BV for three consecutive years (2020, 2021, and 2022).