**Supplementary Table 1:** Highlights of the number of retrieved VP2 protein sequences across the continents.

|  |  |
| --- | --- |
| **Continents** | **Number of sequences retrieved** |
| Africa | 1030 |
| Asia | 1824 |
| Europe | 603 |
| North America | 537 |
| South America  | 472 |
| Australia/Oceania | 43 |
| **Total** | **4509** |

**Supplementary Table 2:** Highlights of the number of retrieved VP3 protein sequences across the continents.

|  |  |
| --- | --- |
| **Continents** | **Number of sequences retrieved** |
| Africa | 7 |
| Asia | 35 |
| Europe | - |
| North America | - |
| South America  | 1 |
| Australia/Oceania | - |
| **Total** | **43** |

**Supplementary Table 3:** Accession list of the retrieved protein sequences

|  |  |  |
| --- | --- | --- |
| **S/N** | **Protein** | **Accession numbers** |
| 1 | VP3 | DQ912981.1, MT951626.1, MN563601.1, MN539755.1, MN539754.1, MN539753.1, MN539752.1, MN539751.1, MN539750.1, ON567385.1, JQ315182.1, JQ315181.1, JQ315180.1, JQ315179.1, JQ315178.1, JQ315177.1, JQ315176.1, JQ315175.1, JQ315174.1, JQ315173.1, JQ315172.1, JQ315171.1, JQ315170.1, JQ315169.1, JQ315168.1, JQ315167.1, JQ315166.1, JQ315165.1, JQ315164.1, JQ315163.1, JF965440.1, EF080961.1, EF080957.1, EF080955.1, EF080963.1, EF080962.1, EF080956.1, OP831905.1, OP831904.1, OP831903.1, OP831902.1, OP831901.1, OP831900.1  |
| 2 | VP3 | KC986368.1, KC986367.1, KC986366.1, KC986365.1, JX096987.1, JX096986.1, JX096982.1, JX096981.1, JX096980.1, JX096979.1, JX096978.1, JX096977.1, JX096976.1, JX096975.1, JX096974.1, JX096973.1, JX096972.1, JX096971.1, JX096970.1, JX096969.1, JX096968.1, JX096967.1, JX096966.1, JX096965.1, JX096964.1, JX096963.1, JX096962.1, JX096961.1, JX096960.1, JX096959.1, KC352669.1, KC352668.1, KC352667.1, KC352666.1, KC352665.1, KC352664.1, KC352663.1, KC352662.1, KC352661.1, KC352660.1, KC352659.1, JQ398618.1, JQ398617.1, JQ277695.1, JQ239172.1, EF544179.1, EF544178.1, EF544177.1, EF544176.1, EF544175.1, EF544174.1, EF544173.1, EF544172.1, EF544171.1, EF544170.1, AY628218.1, AY628217.1, AY628216.1, AY628215.1, AY628214.1, AB306716.1, AB306715.1, AB306714.1, AB200987.2, AB201125.1, AB201124.1, AB200988.1, AB200986.1, AB200985.1, AB200984.1, AB200983.1, AB200982.1, AB200981.1, AB200980.1, AB200979.1, AB200978.1, AB200977.1, AB200976.1, AB200975.1, LN849070.1, LN849069.1, AJ586969.1, 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**Supplementary Table 4:** Summary of the tools, functions, parameters, and thresholds used in the study.

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| --- | --- | --- | --- | --- | --- |
| **S/N** | **Tools** | **Function**  | **Link** | **Parameters for Threshold**  | **Threshold** |
| 1 | National Centre for Biotechnology Information (NCBI)  | To retrieve protein sequences  | https://www.ncbi.nlm.nih.gov/protein | - | - |
| 2 | Vaxijen v2.0 Server  | To determine the antigenicity of the referenced sequence  | http://www.ddg-pharmfac.net/VaxiJen/VaxiJen/VaxiJen.html | - | 0.52 |
| 3 | NetMHCpan-4.1 server  | To predict Cytotoxic T-cell Lymphocyte (CTL) epitopes | https://services.healthtech.dtu.dk/service.php?NetMHCpan-4.1 | Threshold for strong binder (% Rank):1Threshold for weak binder (% Rank): 5 | IC50 |
| 4 | MixMHC2 pred server | To select the highest quality MHC class I CLA alleles  | http://ec2-18-188-210-66.us-east-2.compute.amazonaws.com:4000/# | - | - |
| 5 | AllerTop v2.0  | To assess the allergenicity of the epitopes | https://www.ddg-pharmfac.net/AllerTOP/ | - | Defaul-t  |
| 6 | ToxinPred 2 server | To predict the toxicity of the epitopes  | https://webs.iiitd.edu.in/raghava/toxinpred2/ | Hybrid (RF+BLAST+MERCI) | Default (0.6) |
| 7 | NetMHCIIPan-4.0 | To predict Helper T- cell Lymphocytes (HTL) epitopes that can bind to MHC class II HLA alleles | https://services.healthtech.dtu.dk/services/NetMHCIIpan-4.0/1-Submission.php | - | 0.40 |
| 8 | IFN-γ epitope tool | To predict the ability of the epitopes to induce interferon gamma (IFN-γ) cytokine  | http://crdd.osdd.net/raghava/ifnepitope/ | Motif and SVM hybrid IFN-gamma versus Non IFN-gamma | Default  |
| 9 | IL4pred | To predict the ability of the epitopes to induce interleukin 4 (IL-4)  | http://crdd.osdd.net/raghava/il4pred/predict.php | - | - |
| 10 | IL10 pred | To predict the ability of the epitopes to induce interleukin 10 (IL-10)  | http://crdd.osdd.net/raghava/il10pred/predict.php | - | - |
| 11 | ABCpred | To analyze the antigenic consensus sequences so as to find antigens that can stimulate the B-cell immune response | <http://crdd.osdd.net/raghava/abcpred/> | Threshold [ 0.1 to 1 ]Window length to use for prediction: 16  | 0.70 |
| 12 | BEPIpred | To analyze the antigenic consensus sequences in order to find antigens that can stimulate the B-cell immune response | <http://tools.iedb.org/bcell/> |  -  | 0.50 |
| 13 | ElliPro server | To observe the solvent exposure and flexibilities, as well as the linear and structural forms of the epitopes | http://tools.iedb.org/ellipro/ | - | - |
| 14 | IEDB population coverage tool  | To estimate the population size that is immune responsive to the constructed vaccine | http://tools.iedb.org/population/ | - | - |
| 15 | Expasy Protparam server | To determine the physicochemical properties of the construct | https://web.expasy.org/protparam/ | - |  |
| 16 | ProteinSol server | To determine the solubility of the construct. | https://protein-sol.manchester.ac.uk/ | - | - |
| 17 | SOPMA | To significantly improve the secondary structure prediction of the mRNA vaccine | <https://npsa-prabi.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_sopma.html> | Number of conformational states: 4(Helix, Sheet, TurnSimilarity threshold :8Window width: 17 | Default  |
| 18 | AlphaFold2 | For the prediction of the tertiary structure of the vaccine construct | [https://colab.research.google.com/github/sokrypton/ColabFold/blob/main/AlphaFold2.ipynb#scrollTo=G4yBrceuFbf3](https://colab.research.google.com/github/sokrypton/ColabFold/blob/main/AlphaFold2.ipynb) | - | - |
| 19 | GalaxyRefne server  | To enhance the quality of the structure, the prediction of tertiary structure of the designed protein vaccine | <https://galaxy.seoklab.org/cgi-bin/submit.cgi?type=REFINE> | - | - |
| 20 | SAVES 2.0 server  | To validate the model vaccine  | <https://saves.mbi.ucla.edu/> | - | - |
| 21 | ProSA-web server  | To analyze the stereochemical properties of the model vaccine  | <https://prosa.services.came.sbg.ac.at/prosa.php> | - | - |
| 22 | HDock server | To study the interactions between the refined model of the tertiary construct with toll-like receptors (TLRs)  | http://hdock.phys.hust.edu.cn/ | - | - |
| 23 | UniprotKB server  | To retrieve the three-dimensional structures of the selected toll-like receptors (TLRs)  | https://www.uniprot.org/ | - | - |
| 24 | Water simulation tool | To study the physical basis of the structure and function of the complex | https://simlab.uams.edu/index.php | - | - |
| 25 | C-ImmSimm server | To ascertain the interaction between the vaccine construct and the host immune system | https://kraken.iac.rm.cnr.it/C-IMMSIM/ | - | - |