

## Documents

- 1) Elshafei, S.O., Mahmoud, N.A., Almofti, Y.A.

**Immunoinformatics, molecular docking and dynamics simulation approaches unveil a peptide vaccine candidate against avian leukosis virus**

(2024) *Scientific Reports*, 14 (1), art. no. 2870, .

- 2) Kashif, M., Waseem, M., Subbarao, N.

**In silico prediction of CD8+ and CD4+ T cell epitopes in Leishmania major proteome: U**

(2024) *Journal of Molecular Graphics and Modelling*, 129, art. no. 108759, .

- 3) Das, N.C., Gorai, S., Gupta, P.S.S., Panda, S.K., Rana, M.K., Mukherjee, S.

**Immune targeting of filarial glutaredoxin through a multi-epitope peptide-based vaccine approach**

(2024) *International Immunopharmacology*, 133, art. no. 112120, .

- 4) Malviya, J., Yadav, S., Rathore, P., Barik, A., Mohapatra, S.S., Sareen, S., Sahoo, B., Singh, S.

**Exploring the Function of Predicted T-Cell Epitopes in Enhancing Influenza Virus Vaccine**

(2024) *Macromolecular Symposia*, 413 (2), art. no. 2300116, .

- 5) Disha, S., Yathisha, U.G., Harshitha, M., Maiti, B.

**In silico evaluation of outer membrane protein S2 as a suitable vaccine candidate against infection of fish**

(2024) *North American Journal of Aquaculture*, 86 (2), pp. 193-201.

- 6) Alsaiani, A.A., Hakami, M.A., Alotaibi, B.S., Alkhalil, S.S., Hazazi, A., Alkhorayef, N., Jalal, K.,

**Rational design of multi-epitope-based vaccine by exploring all dengue virus serotypes: immunoinformatic approach**

(2024) *Immunologic Research*, 72 (2), pp. 242-259.

7) Rezaei, M., Habibi, M., Ehsani, P., Karam, M.R.A., Bouzari, S.

**Design and computational analysis of an effective multi-epitope vaccine candidate used as a build-in adjuvant against urinary tract infections**  
(2024) *BioImpacts*, 14 (1), .

8) Mohapatra, S., Kumar, S., Kumar, S., Singh, A.K., Nayak, B.

**Immunodominant conserved moieties on spike protein of SARS-CoV-2 renders virulent epitope-based peptide vaccines**  
(2023) *VirusDisease*, 34 (4), pp. 456-482.

9) Oladipo, E.K., Ojo, T.O., Olufemi, S.E., Irewolede, B.A., Adediran, D.A., Abiala, A.G., Hezekia Y.G., Ikuomola, M.O., Olayinka, A.T., Akanbi, G.O., Idowu, U.A., Olubodun, O.A., Odunlami, F.O.P., Adegoke, H.M., Folakanmi, E.O., Usman, T.A., Oladokun, E.F., Oluwasanya, G.J., Awot Akintibubo, S.A., Jimah, E.M.

**Proteome based analysis of circulating SARS-CoV-2 variants: approach to a universal**  
(2023) *Genes and Genomics*, 45 (12), pp. 1489-1508.

10) Hiu, J.J., Fung, J.K.Y., Tan, H.S., Yap, M.K.K.

**Unveiling the functional epitopes of cobra venom cytotoxin by immunoinformatics analysis**  
(2023) *Scientific Reports*, 13 (1), art. no. 12271, .

11) Alam, R., Samad, A., Ahammad, F., Nur, S.M., Alsaiani, A.A., Imon, R.R., Talukder, M.E.K., N Mohammad, F., Karpiński, T.M.

**In silico formulation of a next-generation multiepitope vaccine for use as a prophylactic against Congo hemorrhagic fever**  
(2023) *BMC Medicine*, 21 (1), art. no. 36, .

12) Khalaj-Hedayati, A., Moosavi, S., Manta, O., Helal, M.H., Ibrahim, M.M., El-Bahy, Z.M., Supriyati, N.

**Identification and In Silico Characterization of a Conserved Peptide on Influenza Hemagglutinin as a Potential Antigen for Universal Influenza Vaccine Development**  
(2023) *Nanomaterials*, 13 (20), art. no. 2796, .

13) Asoudeh Moghanloo, S., Forouzanfar, M., Jafarinia, M., Fazlollahi, M.R., Kardar, G.A.

**Allergen-specific immunotherapy by recombinant Der P1 allergen-derived peptide-based mouse model**

(2023) *Immunity, Inflammation and Disease*, 11 (6), art. no. e878, .

- 14) Jin, Y., Fayyaz, A., Liaqat, A., Khan, A., Alshammari, A., Wang, Y., Gu, R.-X., Wei, D.-Q.

**Proteomics-based vaccine targets annotation and design of subunit and mRNA-based virus (MPXV) against the recent outbreak**

(2023) *Computers in Biology and Medicine*, 159, art. no. 106893, .

- 15) Santoni, D.

**Peptide Hamming Graphs: A network representation of peptides presented through s potential epitope clusters**

(2023) *Journal of Immunological Methods*, 517, art. no. 113474, .

- 16) Hashimi, T., Joyce, D., Nasir, S.M., Masarudin, M.J., Salleh, A., Othman, S.

**Characterisation of the Putative Antigenic Genes of the Outer Membrane Proteins of I Strain PMTB2.1 through in silico Analysis**

(2023) *Pertanika Journal of Tropical Agricultural Science*, 46 (1), pp. 277-313.

- 17) Ismail, M., Bai, B., Guo, J., Bai, Y., Sajid, Z., Muhammad, S.A., Shaikh, R.S.

**Experimental Validation of MHC Class I and II Peptide-Based Potential Vaccine Candid Virus Using Sprague-Dawley Models**

(2023) *Molecules*, 28 (4), art. no. 1687, .

- 18) de Miranda Mariano, I.H., Silva, B.F., da S. Machado, M., Blanco, R.M., Romero, E.C., Andr E.A.L., da Silva, J.B.

**Analysis of LruC lipoprotein and identification of peptides candidates for vaccine dev leptospirosis**

(2023) *PLoS ONE*, 18 (2 February), art. no. e0281344, .

- 19) Ghosh, P., Patra, P., Mondal, N., Chini, D.S., Patra, B.C.

**Multi Epitopic Peptide Based Vaccine Development Targeting Immobilization Antigen A Computational Approach**

(2023) *International Journal of Peptide Research and Therapeutics*, 29 (1), art. no. 11, .

20) Cai, Y., Chen, R., Gao, S., Li, W., Liu, Y., Su, G., Song, M., Jiang, M., Jiang, C., Zhang, X.

**Artificial intelligence applied in neoantigen identification facilitates personalized cancer**  
(2023) *Frontiers in Oncology*, 12, art. no. 1054231, .

21) Bondhopadhyay, B., Hussain, S., Kasherwal, V.

**The differential effect of the immune system in breast cancer**  
(2023) *Exploration of Medicine*, 4 (6), pp. 1094-1108.

22) Sinha, M., Pandit, S., Singh, P., Chauhan, S.S., Parthasarathi, R.

**Visualizing chemical functionality and structural insights into SARS-CoV-2 proteins**  
(2023) *Stem Cells: an Alternative Therapy for COVID-19 and Cytokine Storm*, pp. 257-275.

23) Razali, S.A., Shamsir, M.S., Ishak, N.F., Low, C.-F., Azemin, W.-A.

**Riding the wave of innovation: immunoinformatics in fish disease control**  
(2023) *PeerJ*, 11, art. no. 16419, .

24) Kumari R, S., Sethi, G., Krishna, R.

**Development of multi-epitope based subunit vaccine against Mycobacterium Tuberculosis using**  
**immunoinformatics approach**  
(2023) *Journal of Biomolecular Structure and Dynamics*, .

25) Mukhtar, M., Qadir, M.I.

**QadirVax-19: A multi epitope-based vaccine against COVID-19**  
(2023) *Kuwait Journal of Science*, 50 (1), .

26) Alsaiari, A.A., Hakami, M.A., Alotaibi, B.S., Alkhalil, S.S., Alkhorayef, N., Khan, K., Jalal, K.

**Delineating multi-epitopes vaccine designing from membrane protein CL5 against all**  
**pangenome reverse vaccinology approach**  
(2023) *Journal of Biomolecular Structure and Dynamics*, .

27) Adetunji, C.O., Ogundolie, F.A., Olaniyan, O.T., Olatunde, S.K., Pius, O.O., Kanmodi, K.K., I

**In silico Approaches to Vaccine Design**  
(2023) *Advances in Bioinformatics and Big Data Analytics*, pp. 57-80.

28) Chakraborty, A., Bayry, J., Mukherjee, S.

**Immunoinformatics Approaches in Designing Vaccines Against COVID-19**  
(2023) *Methods in Molecular Biology*, 2673, pp. 431-452.

29) Sarmadi, A., Hassanzadeganroudsari, M., Soltani, M.

**Artificial Intelligence and Machine Learning Applications in Vaccine Development**  
(2023) *Bioinformatics Tools for Pharmaceutical Drug Product Development*, pp. 233-253.

30) Hamed, S.M., Sakr, M.M., El-Housseiny, G.S., Wasfi, R., Aboshanab, K.M.

**State of the art in epitope mapping and opportunities in COVID-19**  
(2023) *Future Science OA*, 9 (1), art. no. 2680160, .

31) Zhang, X., Yuan, H., Mahmmod, Y.S., Yang, Z., Zhao, M., Song, Y., Luo, S., Zhang, X.-X., Yi

**Insight into the current *Toxoplasma gondii* DNA vaccine: a review article**  
(2023) *Expert Review of Vaccines*, 22 (1), pp. 66-89.

32) Ezzemani, W., Windisch, M.P., Altawalah, H., Guessous, F., Saile, R., Benjelloun, S., Kettan

**Design of a multi-epitope Zika virus vaccine candidate—an in-silico study**  
(2023) *Journal of Biomolecular Structure and Dynamics*, 41 (9), pp. 3762-3771.

33) da Silva, M.K., Azevedo, A.A.C., Campos, D.M.D.O., de Souto, J.T., Fulco, U.L., Oliveira, J.I

**Computational vaccinology guided design of multi-epitope subunit vaccine against a Americas**  
(2023) *Journal of Biomolecular Structure and Dynamics*, 41 (8), pp. 3321-3338.

34) Parmar, M., Thumar, R., Sheth, J., Patel, D.

**Designing multi-epitope based peptide vaccine targeting spike protein SARS-CoV-2 E using computational approaches**  
(2022) *Structural Chemistry*, 33 (6), pp. 2243-2260.

35)

García-Machorro, J., Ramírez-Salinas, G.L., Martínez-Archundia, M., Correa-Basurto, J.

**The Advantage of Using Immunoinformatic Tools on Vaccine Design and Development fo**  
(2022) *Vaccines*, 10 (11), art. no. 1844, .

36) Shen, C., Zhu, X., Xu, X., Chang, H., Ni, Y., Li, C., He, K., Chen, L., Chen, L., Hou, M., Ji, M

**Identification and Characterization of Antigenic Properties of Schistosoma japonicum Derived Peptides**

(2022) *Pathogens*, 11 (11), art. no. 1238, .

37) Seadawy, M.G., Zekri, A.R.N., Saeed, A.A., San, E.J., Ageez, A.M.

**Candidate Multi-Epitope Vaccine against Corona B.1.617 Lineage: In Silico Approach**

(2022) *Life*, 12 (11), art. no. 1715, .

38) Bi, J., Zheng, Y., Wang, C., Ding, Y.

**An Attention Based Bidirectional LSTM Method to Predict the Binding of TCR and Epi**

(2022) *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 (6), pp. 32

39) Li, R.-H., Yin, G.-R.

**Research advances of multi-epitope vaccine candidates against toxoplasmosis**

(2022) *Chinese Journal of Parasitology and Parasitic Diseases*, 40 (5), pp. 661-667.

40) Hossain, F., Kandalai, S., Zhou, X., Zhang, N., Zheng, Q.

**Chemical and Synthetic Biology Approaches for Cancer Vaccine Development**

(2022) *Molecules*, 27 (20), art. no. 6933, .

41) Dar, H.A., Almajhdi, F.N., Aziz, S., Waheed, Y.

**Immunoinformatics-Aided Analysis of RSV Fusion and Attachment Glycoproteins to I Vaccine**

(2022) *Vaccines*, 10 (9), art. no. 1381, .

42) Pissarra, J., Dorkeld, F., Loire, E., Bonhomme, V., Sereno, D., Lemesre, J.-L., Holzmüller, P.

**SILVI, an open-source pipeline for T-cell epitope selection**

(2022) *PLoS ONE*, 17 (9 September), art. no. e0273494, .

43) Mahapatra, S.R., Dey, J., Jaiswal, A., Roy, R., Misra, N., Suar, M.

**Immunoinformatics-guided designing of epitope-based subunit vaccine from *Pilus* as *Acinetobacter baumannii* bacteria**

(2022) *Journal of Immunological Methods*, 508, art. no. 113325, .

44) Alves, M.L.F., Ferreira, M.R.A., Rodrigues, R.R., Conceição, F.R.

***Clostridium haemolyticum*, a review of beta toxin and insights into the antigen design**

(2022) *Molecular Immunology*, 148, pp. 45-53.

45) Moodley, A., Fatoba, A., Okpeku, M., Emmanuel Chiliza, T., Blessing Cedric Simelane, M., F

**Reverse vaccinology approach to design a multi-epitope vaccine construct based on tuberculosis biomarker PE\_PGRS17**

(2022) *Immunologic Research*, 70 (4), pp. 501-517.

46) Huisman, B.D., Dai, Z., Gifford, D.K., Birnbaum, M.E.

**A high-throughput yeast display approach to profile pathogen proteomes for MHC-II b**

(2022) *eLife*, 11, art. no. e78589, .

47) Shahriari, S., Monajjemi, M., Mollaamin, F.

**DETERMINATION OF PROTEINS SPECIFICATION WITH SARS- COVID-19 BASED LIGA**

(2022) *Journal of the Chilean Chemical Society*, 67 (2), pp. 5468-5476.

48) Almalki, S., Beigh, S., Akhter, N., Alharbi, R.A.

**In silico epitope-based vaccine design against influenza a neuraminidase protein: Co established on B- and T-cell epitope predictions**

(2022) *Saudi Journal of Biological Sciences*, 29 (6), art. no. 103283, .

49) Chakraborty, S., Deb, B., Nath, D., Monoswita, D.

**Identification of promising CD8 and CD4 T cell epitopes for peptide vaccine formulation**

(2022) *Archives of Microbiology*, 204 (5), art. no. 242, .

50) Gao, Z., Chen, L., Song, T., Pan, X., Li, X., Lu, G., Tang, Y., Wu, X., Zhao, B., Zhang, R.

**A candidate multi-epitope vaccine against porcine reproductive and respiratory syndrome virus induces robust humoral and cellular response in mice**  
(2022) *Vaccine*, 40 (16), pp. 2370-2378.

51) Koşaloğlu-Yalçın, Z., Lee, J., Greenbaum, J., Schoenberger, S.P., Miller, A., Kim, Y.J., Sette, J.

**Combined assessment of MHC binding and antigen abundance improves T cell epitope prediction**  
(2022) *iScience*, 25 (2), art. no. 103850, .

52) Anam, K., Endharti, A.T., Poeranto, S., Sujuti, H., Hidayati, D.Y.N., Prawiro, S.R.

**Shigella flexneri vaccine development: Oral administration of peptides derived from toxin subunit activates the intestinal immune response in mice**  
(2022) *Veterinary World*, 15 (2), pp. 281-287.

53) Pirmoradi, S.

**Development of a New Epitope Immunogenic Structure Based on the Coronavirus SARS-CoV-2 Using Immunoinformatics Tools**  
(2022) *Infection, Epidemiology and Microbiology*, 8 (4), pp. 365-378.

54) Waseem, M., Basheer, A., Anwer, F., Shahid, F., Zaheer, T., Ali, A.

**Genomics, metagenomics, and pan-genomics approaches in COVID-19**  
(2022) *Omics Approaches and Technologies in COVID-19*, pp. 23-39.

55) Arya, H., Bhatt, T.K.

**Vaccine regulation and ethics**  
(2022) *System Vaccinology: The History, the Translational Challenges and the Future*, pp. 3-12.

56) Samavia, N., Fahed, P., Yasir, W., Tasneem, A., Syeda, N.

**Prediction of promiscuous epitopes in ORF2 of Hepatitis E virus: an In-Silico approach**  
(2022) *African Health Sciences*, 22 (3), pp. 626-639.

57) Umar, A., Liaquat, S., Fatima, I., Rehman, A., Rasool, D., Alshammari, A., Alharbi, M., Rajok, U.A., Haque, A.



**Vaccinomics to Design a Multiepitope Vaccine against Legionella pneumophila**  
(2022) *BioMed Research International*, 2022, art. no. 4975721, .

58) Arwansyah, A., Arif, A.R., Kade, A., Taiyeb, M., Ramli, I., Santoso, T., Ningsih, P., Natsir, H.,

**Molecular modelling on multiepitope-based vaccine against SARS-CoV-2 using immunodocking, and molecular dynamics simulation**

(2022) *SAR and QSAR in Environmental Research*, 33 (9), pp. 649-675.

59) Yurina, V., Adianingsih, O.R.

**Predicting epitopes for vaccine development using bioinformatics tools**

(2022) *Therapeutic Advances in Vaccines and Immunotherapy*, 10, .

60) Weidenbacher, P.A.-B., Rodriguez-Rivera, F.P., Sanyal, M., Visser, J.A., Do, J., Bertozzi, C.F

**Chemically Modified Bacterial Sacculi as a Vaccine Microparticle Scaffold**

(2022) *ACS Chemical Biology*, .

61) Ali, I., Shoukat, T., Parveen, T., Raza, S., Jamil, F., Kanwal, S., Ibrahim, M., Rasheed, M.A.

**Multi Epitope Based Vaccine Design and Analysis against Mycoplasma bovis Using Ir**

(2022) *Pakistan Veterinary Journal*, 42 (1), pp. 33-40.

62) Michalik, M., Djahanschiri, B., Leo, J.C., Linke, D.

**An Update on “Reverse Vaccinology”: The Pathway from Genomes and Epitope Prediction to Recombinant Vaccines**

(2022) *Methods in Molecular Biology*, 2412, pp. 45-71.

63) Martínez-Archundia, M., Ramírez-Salinas, G.L., García-Machorro, J., Correa-Basurto, J.

**Searching Epitope-Based Vaccines Using Bioinformatics Studies**

(2022) *Methods in Molecular Biology*, 2412, pp. 471-479.

64) Lari, A., Lari, N., Biabangard, A.

**Immunoinformatics Approach to Design a Novel Subunit Vaccine Against Visceral Leishmaniasis**

(2022) *International Journal of Peptide Research and Therapeutics*, 28 (1), art. no. 34, .

65) Sethi, G., Varghese, R.P., Krishna, R.

**Identification and design of a multi-epitope subunit vaccine against the opportunistic epidermidis: An immunoinformatics approach**

(2022) *Journal of Biomolecular Structure and Dynamics*, 40 (24), pp. 13859-13871.

66) Vivekanandam, R., Rajagopalan, K., Jeevanandam, M., Ganesan, H., Jagannathan, V., Selva K., Selvan Christyraj, J.R.S., Mohan, M.

**Designing of cytotoxic T lymphocyte-based multi-epitope vaccine against SARS-CoV: approach**

(2022) *Journal of Biomolecular Structure and Dynamics*, 40 (24), pp. 13711-13726.

67) Sunita, Singh, Y., Beamer, G., Sun, X., Shukla, P.

**Recent developments in systems biology and genetic engineering toward design of v**

(2022) *Critical Reviews in Biotechnology*, 42 (4), pp. 532-547.

68) Mohammadzadeh, R., Soleimanpour, S., Pishdadian, A., Farsiani, H.

**Designing and development of epitope-based vaccines against Helicobacter pylori**

(2022) *Critical Reviews in Microbiology*, 48 (4), pp. 489-512.

69) Prado, L.C.D.S., Giacchetto Felice, A., Rodrigues, T.C.V., Tiwari, S., Andrade, B.S., Kato, R. Barh, D., Azevedo, V.A.D.C., Jaiswal, A.K., Soares, S.D.C.

**New putative therapeutic targets against Serratia marcescens using reverse vaccinolo**

(2022) *Journal of Biomolecular Structure and Dynamics*, 40 (20), pp. 10106-10121.

70) Rajput, V.S., Sharma, R., Kumari, A., Vyas, N., Prajapati, V., Grover, A.

**Engineering a multi epitope vaccine against SARS-CoV-2 by exploiting its non structu**

(2022) *Journal of Biomolecular Structure and Dynamics*, 40 (19), pp. 9096-9113.

71) Ayyagari, V.S., Venkateswarulu, T.C., Abraham Peele, K., Srirama, K.

**Design of a multi-epitope-based vaccine targeting M-protein of SARS-CoV2: an immu**

(2022) *Journal of Biomolecular Structure and Dynamics*, 40 (7), pp. 2963-2977.

72)

Bell, D.R., Domeniconi, G., Yang, C.-C., Zhou, R., Zhang, L., Cong, G.

**Dynamics-Based Peptide-MHC Binding Optimization by a Convolutional Variational Auto Model for CASTELO**

(2021) *Journal of Chemical Theory and Computation*, 17 (12), pp. 7962-7971.

73) Fotakis, G., Trajanoski, Z., Rieder, D.

**Computational cancer neoantigen prediction: current status and recent advances**

(2021) *Immuno-Oncology and Technology*, 12, art. no. 100052, .

74) Naz, S., Ahmad, S., Abbasi, S.W., Ismail, S., Waseem, S., Tahir ul Qamar, M., Almatroudi, A

**Identification of immunodominant epitopes in allelic variants VK210 and VK247 of *Plasmodium circumsporozoite* immunogen**

(2021) *Infection, Genetics and Evolution*, 96, art. no. 105120, .

75) Madlala, T., Adeleke, V.T., Fatoba, A.J., Okpeku, M., Adeniyi, A.A., Adeleke, M.A.

**Designing multiepitope-based vaccine against *Eimeria* from immune mapped protein immunoinformatic approach**

(2021) *Scientific Reports*, 11 (1), art. no. 18295, .

76) Yousafi, Q., Amin, H., Bibi, S., Rafi, R., Khan, M.S., Ali, H., Masroor, A.

**Subtractive Proteomics and Immuno-informatics Approaches for Multi-peptide Vaccine against *Klebsiella oxytoca* and Validation Through In Silico Expression**

(2021) *International Journal of Peptide Research and Therapeutics*, 27 (4), pp. 2685-2701.

77) Yang, Z., Bogdan, P., Nazarian, S.

**An in silico deep learning approach to multi-epitope vaccine design: a SARS-CoV-2 case study**

(2021) *Scientific Reports*, 11 (1), art. no. 3238, .

78) Rezaei, S., Sefidbakht, Y., Uskoković, V.

**Tracking the pipeline: immunoinformatics and the COVID-19 vaccine design**

(2021) *Briefings in Bioinformatics*, 22 (6), art. no. bbab241, .

79) Jabarzadeh, S., Samiminemati, A., Zeinoddini, M.

**In Silico Design of a New Multi-Epitope Peptide-Based Vaccine Candidate Against Q Fever**  
(2021) *Molecular Biology*, 55 (6), pp. 950-960.

80) De Mesa Herrera, L.R., Bisa, E.P.

**In silico analysis of highly conserved cytotoxic T-cell epitopes in the structural proteins of Q fever**  
(2021) *Veterinary World*, 14 (10), pp. 2625-2633.

81) Ramchandani, R., Hossenbaccus, L., Ellis, A.K.

**Immunoregulatory T cell epitope peptides for the treatment of allergic disease**  
(2021) *Immunotherapy*, 13 (15), pp. 1283-1291.

82) Cai, X., Li, J.J., Liu, T., Brian, O., Li, J.

**Infectious disease mRNA vaccines and a review on epitope prediction for vaccine design**  
(2021) *Briefings in Functional Genomics*, 20 (5), pp. 289-303.

83) Sharma, A., Pal, S., Panwar, A., Kumar, S., Kumar, A.

**In-silico immunoinformatic analysis of SARS-CoV-2 virus for the development of putative epitopes**  
(2021) *Immunobiology*, 226 (5), art. no. 152134, .

84) Saba, A.A., Adiba, M., Saha, P., Hosen, M.I., Chakraborty, S., Nabi, A.H.M.N.

**An in-depth in silico and immunoinformatics approach for designing a potential multi-epitope vaccine to combat against SARS-CoV-2 encompassing various epitopes**  
(2021) *Computers in Biology and Medicine*, 136, art. no. 104703, .

85) Alves, M.L.F., Ferreira, M.R.A., Donassolo, R.A., Rodrigues, R.R., Conceição, F.R.

**Clostridium septicum: A review in the light of alpha-toxin and development of vaccine**  
(2021) *Vaccine*, 39 (35), pp. 4949-4956.

86) Caoili, S.E.C.

**Beyond B-cell epitopes: Curating positive data on antipeptide paratope binding to support vaccine design**  
(2021) *Protein and Peptide Letters*, 28 (8), pp. 953-962.

87) Sarma, V.R., Olotu, F.A., Soliman, M.E.S.

**Integrative immunoinformatics paradigm for predicting potential B-cell and T-cell epitope subunit vaccine design against COVID-19 virulence**

(2021) *Biomedical Journal*, 44 (4), pp. 447-460.

88) Pyasi, S., Sharma, V., Dipti, K., Jonniya, N.A., Nayak, D.

**Immunoinformatics approach to design multi-epitope-subunit vaccine against bovine**

(2021) *Vaccines*, 9 (8), art. no. 925, .

89) Jafari, E., Mahmoodi, S.

**Design, expression, and purification of a multi-epitope vaccine against Helicobacter F adjuvant**

(2021) *Microbial Pathogenesis*, 157, art. no. 104970, .

90) Silva, M.K., Gomes, H.S.S., Silva, O.L.T., Campanelli, S.E., Campos, D.M.O., Araújo, J.M.G Oliveira, J.I.N.

**Identification of promiscuous T cell epitopes on Mayaro virus structural proteins using molecular modeling, and QM:MM approaches**

(2021) *Infection, Genetics and Evolution*, 91, art. no. 104826, .

91) Fadilah, F., Erlina, L., Paramita, R.I., Istiadi, K.A.

**Immunoinformatics Studies and Design of Breast Cancer Multiepitope Peptide Vaccine Approach**

(2021) *Journal of Applied Pharmaceutical Science*, 11 (6), pp. 035-045.

92) Olotu, F.A., Soliman, M.E.S.

**Immunoinformatics prediction of potential B-cell and T-cell epitopes as effective vaccine immunogenic responses against Epstein–Barr virus**

(2021) *Biomedical Journal*, 44 (3), pp. 317-337.

93) da Costa, A.S., Fernandes, T.V.A., Bello, M.L., de Souza, T.L.F.

**Evaluation of potential MHC-I allele-specific epitopes in Zika virus proteins and the effect of MHC-I interaction studied using in silico approaches**

(2021) *Computational Biology and Chemistry*, 92, art. no. 107459, .

94) Chakraborty, C., Sharma, A.R., Bhattacharya, M., Sharma, G., Lee, S.-S.

**Immunoinformatics Approach for the Identification and Characterization of T Cell and Peptide-Based Vaccine against SARS-CoV-2**

(2021) *Archives of Medical Research*, 52 (4), pp. 362-370.

95) Hu, Y., Li, X., Cheng, J., Ma, X., Meng, X., Chen, H., Wu, Y.

**Advances in Food Allergen Epitope Localization Technologies [食物致敏原表位定位技术]**

(2021) *Shipin Kexue/Food Science*, 42 (7), pp. 292-300.

96) Borojeni, G.N., Abasabadi, F., Abiri, R., Alvandi, A., Salari, F.

**Designing B and T Cell Multi-Epitope Vaccine for Cross Protection Against Haemophilus influenzae Type B (Hib) Using Immunoinformatics Approach**

(2021) *Journal of Veterinary Research*, 76 (1), pp. 133-145.

97) Solanki, V., Tiwari, M., Tiwari, V.

**Immunoinformatic approach to design a multiepitope vaccine targeting non-mutational structural and non-structural proteins of the SARS CoV2**

(2021) *PeerJ*, 9, art. no. e11126, .

98) Chukwudozie, O.S., Gray, C.M., Fagbayi, T.A., Chukwuanukwu, R.C., Oyeboji, V.O., Bankole, E.M.

**Immuno-informatics design of a multimeric epitope peptide based vaccine targeting S glycoprotein**

(2021) *PLoS ONE*, 16 (3 March), art. no. e0248061, .

99) Culma, M.F.

**Strongyloides stercoralis proteome: A reverse approach to the identification of potential vaccine targets**

(2021) *Microbial Pathogenesis*, 152, art. no. 104545, .

100) Oyarzun, P., Kashyap, M., Fica, V., Salas-Burgos, A., Gonzalez-Galarza, F.F., McCabe, A., B.

**A Proteome-Wide Immunoinformatics Tool to Accelerate T-Cell Epitope Discovery in the Context of Emerging Infectious Diseases: An Ethnicity-Oriented Approach**

(2021) *Frontiers in Immunology*, 12, art. no. 598778, .

101) Ghosh, N., Sharma, N., Saha, I., Saha, S.

**Genome-wide analysis of Indian SARS-CoV-2 genomes to identify T-cell and B-cell e regions based on immunogenicity and antigenicity**

(2021) *International Immunopharmacology*, 91, art. no. 107276, .

102) Arya, H., Bhatt, T.K.

**Role of Bioinformatics in Subunit Vaccine Design**

(2021) *Molecular Docking for Computer-Aided Drug Design: Fundamentals, Techniques, R Applications*, pp. 425-439.

103) Arya, H.

**Epitope prediction and selection of linkers and adjuvant**

(2021) *The Design and Development of Novel Drugs and Vaccines: Principles and Protoc*

104) Arya, H., Bhatta, T.K.

**An overview of vaccine design**

(2021) *The Design and Development of Novel Drugs and Vaccines: Principles and Protoc*

105) Elhassan, R.M., Alsony, N.M., Othman, K.M., Izz-Aldin, D.T., Alhaj, T.A., Ali, A.A., Abashir, I

**Epitope-Based Immunoinformatic Approach on Heat Shock 70 kDa Protein Complex var. grubii**

(2021) *Journal of Immunology Research*, 2021, art. no. 9921620, .

106) Mustafa, M.I., Shantier, S.W., Abdelmageed, M.I., Makhawi, A.M.

**Epitope-based peptide vaccine against Bombali Ebolavirus viral protein 40: An immi molecular docking studies**

(2021) *Informatics in Medicine Unlocked*, 25, art. no. 100694, .

107) Alom, M.W., Shehab, M.N., Sujon, K.M., Akter, F.

**Exploring E, NS3, and NS5 proteins to design a novel multi-epitope vaccine candida in-silico approach**

(2021) *Informatics in Medicine Unlocked*, 25, art. no. 100644, .

- 108) Naqvi, S.T.Q., Yasmeen, M., Ismail, M., Muhammad, S.A., Nawazish-I-Husain, S., Ali, A., M  
**Designing of Potential Polyvalent Vaccine Model for Respiratory Syncytial Virus by 5 Immunoinformatics Approaches**  
(2021) *BioMed Research International*, 2021, art. no. 9940010, .
- 109) Bappy, S.S., Sultana, S., Adhikari, J., Mahmud, S., Khan, M.A., Kibria, K.M.K., Rahman, M  
**Extensive immunoinformatics study for the prediction of novel peptide-based epitop confirmation against envelope protein of Chikungunya virus: a computational biolog**  
(2021) *Journal of Biomolecular Structure and Dynamics*, 39 (4), pp. 1139-1154.
- 110) Ismail, M., Sajid, Z., Ali, A., Wu, X., Muhammad, S.A., Shaikh, R.S.  
**Prediction of prophylactic peptide vaccine candidates for human papillo-mavirus (H<sub>1</sub> reverse vaccinology approaches**  
(2021) *Current Proteomics*, 18 (2), pp. 178-192.
- 111) Rashidian, E., Forouharmehr, A., Nazifi, N., Jaydari, A., Shams, N.  
**Computer-aided design of a novel poly-epitope protein in fusion with an adjuvant as leptospirosis**  
(2021) *Current Proteomics*, 18 (2), pp. 105-115.
- 112) Krishnan G, S., Joshi, A., Akhtar, N., Kaushik, V.  
**Immunoinformatics designed T cell multi epitope dengue peptide vaccine derived fr**  
(2021) *Microbial Pathogenesis*, 150, art. no. 104728, .
- 113) Hossain, M.S., Hossan, M.I., Mizan, S., Moin, A.T., Yasmin, F., Akash, A.-S., Powshi, S.N.,  
**Immunoinformatics approach to designing a multi-epitope vaccine against Saint Lou**  
(2021) *Informatics in Medicine Unlocked*, 22, art. no. 100500, .
- 114) Ahmadi, K., Hasaniazad, M., Kalani, M., Faezi, S., Ahmadi, N., Enayatkhani, M., Mahdavi,  
**Comparative study of the immune responses to the HMS-based fusion protein and c molecules as vaccine candidates in a mouse model of Staphylococcus aureus syste**  
(2021) *Microbial Pathogenesis*, 150, art. no. 104656, .



- 115) Bharadwaj, K.K., Srivastava, A., Panda, M.K., Singh, Y.D., Maharana, R., Mandal, K., Mani M., Murmu, D., Kabi, S.K.

**Computational Intelligence in Vaccine Design Against COVID-19**

(2021) *Studies in Computational Intelligence*, 923, pp. 311-329.

- 116) Enayatkhani, M., Hasaniazad, M., Faezi, S., Gouklani, H., Davoodian, P., Ahmadi, N., Eina Ahmadi, K.

**Reverse vaccinology approach to design a novel multi-epitope vaccine candidate against COVID-19: an in silico study**

(2021) *Journal of Biomolecular Structure and Dynamics*, 39 (8), pp. 2857-2872.

- 117) Monajjemi, M., Esmkhani, R., Mollaamin, F., Shahriari, S.

**Prediction of proteins associated with covid-19 based ligand designing and molecular docking**

(2020) *CMES - Computer Modeling in Engineering and Sciences*, 125 (3), pp. 907-926.

- 118) Tahir ul Qamar, M., Rehman, A., Tusleem, K., Ashfaq, U.A., Qasim, M., Zhu, X., Fatima, I.,

**Designing of a next generation multiepitope based vaccine (MEV) against SARS-CoV-2 using in silico approaches**

(2020) *PLoS ONE*, 15 (12 December 2020), art. no. e0244176, .

- 119) Vergni, D., Gaudio, R., Santoni, D.

**The farther the better: Investigating how distance from human self affects the proper presentation of peptides on cell surface by MHC class I molecules, the case of *Trypanosoma cruzi***

(2020) *PLoS ONE*, 15 (12 December), art. no. e0243285, .

- 120) Singh, N., Rai, S.N., Singh, V., Singh, M.P.

**Molecular characterization, pathogen-host interaction pathway and in silico approach for COVID-19**

(2020) *Journal of Chemical Neuroanatomy*, 110, art. no. 101874, .

- 121) Rappazzo, C.G., Huisman, B.D., Birnbaum, M.E.

**Repertoire-scale determination of class II MHC peptide binding via yeast display imp**

(2020) *Nature Communications*, 11 (1), art. no. 4414, .

122) Ahmadi, F., Dorosti, H., Ghasemi, Y., Nezafat, N.

**In Silico Design of Epitope-Based Allergy Vaccine Against *Bellatella germanica* Cockroach**  
(2020) *International Journal of Peptide Research and Therapeutics*, 26 (4), pp. 1739-1749.

123) Kadam, A., Sasidharan, S., Saudagar, P.

**Computational design of a potential multi-epitope subunit vaccine using immunoinformatics**  
(2020) *Infection, Genetics and Evolution*, 85, art. no. 104464, .

124) Meng, Q., Wu, Y., Sui, X., Meng, J., Wang, T., Lin, Y., Wang, Z., Zhou, X., Qi, Y., Du, J., Gao, Y.

**POTN: A Human Leukocyte Antigen-A2 Immunogenic Peptides Screening Model and Antigen Prediction**  
(2020) *Frontiers in Immunology*, 11, art. no. 02193, .

125) Aranha, M.P., Jewel, Y.S.M., Beckman, R.A., Weiner, L.M., Mitchell, J.C., Parks, J.M., Smit, A.M.

**Combining three-dimensional modeling with artificial intelligence to increase specific MHC binding predictions**  
(2020) *Journal of Immunology*, 205 (7), pp. 1962-1977.

126) Zawawi, A., Else, K.J.

**Soil-Transmitted Helminth Vaccines: Are We Getting Closer?**  
(2020) *Frontiers in Immunology*, 11, art. no. 576748, .

127) Anand, R., Biswal, S., Bhatt, R., Tiwary, B.N.

**Computational perspectives revealed prospective vaccine candidates from five structural models of SARS-CoV-2**  
(2020) *PeerJ*, 8, art. no. e9855, .

128) Ortega-Tirado, D., Arvizu-Flores, A.A., Velazquez, C., Garibay-Escobar, A.

**The role of immunoinformatics in the development of T-cell peptide-based vaccines against tuberculosis**  
(2020) *Expert Review of Vaccines*, 19 (9), pp. 831-841.

129)

Kim, S.H., Ryu, Y.C., Wang, H.-M.D., Hwang, B.H.

**Optimally Fabricated Chitosan Particles Containing Ovalbumin Induced Cellular and Humoral Immunity in Mice**

(2020) *Biotechnology and Bioprocess Engineering*, 25 (5), pp. 681-689.

- 130) Ortega-Tirado, D., Niño-Padilla, E.I., Arvizu-Flores, A.A., Velazquez, C., Espitia, C., Serran Sumoza-Toledo, A., Garibay-Escobar, A.

**Identification of immunogenic T-cell peptides of Mycobacterium tuberculosis PE\_PGRS**

(2020) *Molecular Immunology*, 125, pp. 123-130.

- 131) Cruz-Rosas, H.I., Riquelme, F., Ramírez-Padrón, A., Buhse, T., Cocho, G., Miramontes, P.

**Molecular shape as a key source of prebiotic information**

(2020) *Journal of Theoretical Biology*, 499, art. no. 110316, .

- 132) Bhattacharya, M., Sharma, A.R., Sharma, G., Patra, P., Mondal, N., Patra, B.C., Lee, S.-S.

**Computer aided novel antigenic epitopes selection from the outer membrane protein of Escherichia coli and its analyses**

(2020) *Infection, Genetics and Evolution*, 82, art. no. 104320, .

- 133) Estrada, E.

**COVID-19 and SARS-CoV-2. Modeling the present, looking at the future**

(2020) *Physics Reports*, 869, pp. 1-51.

- 134) Naz, A., Shahid, F., Butt, T.T., Awan, F.M., Ali, A., Malik, A.

**Designing Multi-Epitope Vaccines to Combat Emerging Coronavirus Disease 2019 (COVID-19): An Immuno-Informatics Approach**

(2020) *Frontiers in Immunology*, 11, art. no. 1663, .

- 135) Panda, P.K., Arul, M.N., Patel, P., Verma, S.K., Luo, W., Rubahn, H.-G., Mishra, Y.K., Suar

**Structure-based drug designing and immunoinformatics approach for SARS-CoV-2**

(2020) *Science Advances*, 6 (28), art. no. eabb8097, .

- 136) Choga, W.T., Anderson, M., Zumbika, E., Phinius, B.B., Mbangiwa, T., Bhebhe, L.N., Barut Musonda, R.M., Bell, T.G., Moyo, S., Blackard, J.T., Gaseitsiwe, S.

**In Silico Prediction of Human Leukocytes Antigen (HLA) Class II Binding Hepatitis B Virus in Botswana**

(2020) *Viruses*, 12 (7), art. no. 731, .

- 137) Muhammad, S.A., Zafar, S., Rizvi, S.Z., Imran, I., Munir, F., Jamshed, M.B., Ali, A., Wu, X., Q.

**Experimental analysis of T cell epitopes for designing liver cancer vaccine predicted by immunoinformatics approach**

(2020) *American Journal of Physiology - Gastrointestinal and Liver Physiology*, 318 (6), pp

- 138) Mukherjee, S., Tworowski, D., Detroja, R., Mukherjee, S.B., Frenkel-Morgenstern, M.

**Immunoinformatics and structural analysis for identification of immunodominant epitopes and potential vaccine targets**

(2020) *Vaccines*, 8 (2), art. no. 290, pp. 1-17.

- 139) Gu, Q.-H., Huynh, M., Shi, Y., Jia, X.-Y., Luo, J.-J., Jiang, T.-J., Cui, Z., Ooi, J.D., Kitching, .

**Experimental antiglomerular basement membrane GN induced by a peptide from actin**

(2020) *Journal of the American Society of Nephrology*, 31 (6), pp. 1282-1295.

- 140) Shahid, F., Ashfaq, U.A., Javaid, A., Khalid, H.

**Immunoinformatics guided rational design of a next generation multi epitope based vaccine exploring Zika virus proteome**

(2020) *Infection, Genetics and Evolution*, 80, art. no. 104199, .

- 141) Ong, E., Wang, H., Wong, M.U., Seetharaman, M., Valdez, N., He, Y.

**Vaxign-ML: Supervised machine learning reverse vaccinology model for improved prediction of vaccine antigens**

(2020) *Bioinformatics*, 36 (10), pp. 3185-3191.

- 142) Yazdani, Z., Rafiei, A., Valadan, R., Ashrafi, H., Pasandi, M., Kardan, M.

**Designing a potent L1 protein-based HPV peptide vaccine: A bioinformatics approach**

(2020) *Computational Biology and Chemistry*, 85, art. no. 107209, .

- 143)

Benedé, S., Ramos-Soriano, J., Palomares, F., Losada, J., Mascaraque, A., López-Rodríguez, J., Villalba, M., Batanero, E.

**Peptide Glycodendrimers as Potential Vaccines for Olive Pollen Allergy**

(2020) *Molecular Pharmaceutics*, 17 (3), pp. 827-836.

144) Saylor, K., Gillam, F., Lohneis, T., Zhang, C.

**Designs of Antigen Structure and Composition for Improved Protein-Based Vaccine**

(2020) *Frontiers in Immunology*, 11, art. no. 283, .

145) Bunsuz, A., Serçinoğlu, O., Ozbek, P.

**Computational investigation of peptide binding stabilities of HLA-B\*27 and HLA-B\*4**

(2020) *Computational Biology and Chemistry*, 84, art. no. 107195, .

146) Bhattacharya, M., Malick, R.C., Mondal, N., Patra, P., Pal, B.B., Patra, B.C., Kumar Das, B

**Computational characterization of epitopic region within the outer membrane protein columnare for vaccine development**

(2020) *Journal of Biomolecular Structure and Dynamics*, 38 (2), pp. 450-459.

147) Elhag, M., Alaagib, R.M., Ahmed, N.M., Abubaker, M., Haroun, E.M., Albagi, S.O.A., Hassa

**Design of Epitope-Based Peptide Vaccine against Pseudomonas aeruginosa Fructose Protein Using Immunoinformatics**

(2020) *Journal of Immunology Research*, 2020, art. no. 9475058, .

148) Sankar, P., Venugopal, S.

**Immuno-informatics approach based epitopes prediction for vaccine design against syndrome coronavirus-2**

(2020) *International Journal of Pharmaceutical Research*, 12, pp. 2459-2472.

149) Karwal, P., Vats, I.D., Sinha, N., Singhal, A., Sehgal, T., Kumari, P.

**Therapeutic applications of peptides against zika virus: A review**

(2020) *Current Medicinal Chemistry*, 27 (23), pp. 3906-3923.

150) Lima, E.N.C., Lima, R.S.A., Arif, M.S., Piqueira, J.R.C., Diaz, R.S.

**Evolutionary temporal footprint of an HIV-1 envelope protein in an epidemiologically linked c**  
(2020) *Open AIDS Journal*, 14 (1), pp. 41-49.

151) Jadoon, M.H., Rehman, Z., Khan, A., Rizwan, M., Khan, S., Mehmood, A., Munir, A.

**In silico t-cell and b-cell epitope based vaccine design against alphavi-rus strain of c**  
(2020) *Infectious Disorders - Drug Targets*, 20 (4), pp. 523-530.

152) Abdelmageed, M.I., Abdelmoneim, A.H., Mustafa, M.I., Elfadol, N.M., Murshed, N.S., Shan

**Design of a Multiepitope-Based Peptide Vaccine against the e Protein of Human COV**  
**Approach**  
(2020) *BioMed Research International*, 2020, art. no. 2683286, .

153) Alkaff, A.H., Saragih, M., Fardiansyah, M.A., Tambunan, U.S.F.

**Role of immunoinformatics in accelerating epitope-based vaccine development agai**  
(2020) *Open Biochemistry Journal*, 14 (1), pp. 9-18.

154) Lata, K.S., Vaghasia, V., Bhairappanvar, S., Patel, S., Das, J.

**Vaccine design against leptospirosis using an immunoinformatic approach**  
(2020) *Methods in Molecular Biology*, 2131, pp. 173-184.

155) Nosrati, M., Hajizade, A., Nazarian, S., Amani, J., Namvar Vansofla, A., Tarverdizadeh, Y.

**Designing a multi-epitope vaccine for cross-protection against Shigella spp: An immr**  
**vaccinology study**  
(2019) *Molecular Immunology*, 116, pp. 106-116.

156) Rahmani, A., Baee, M., Rostamtabar, M., Karkhah, A., Alizadeh, S., Tourani, M., Nouri, H.F

**Development of a conserved chimeric vaccine based on helper T-cell and CTL epitope**  
**immune response against Schistosoma mansoni using immunoinformatics approach**  
(2019) *International Journal of Biological Macromolecules*, 141, pp. 125-136.

157) Safavi, A., Kefayat, A., Sotoodehnejadnematalahi, F., Salehi, M., Modarressi, M.H.

**In Silico Analysis of Synaptonemal Complex Protein 1 (SYCP1) and Acrosin Binding**  
**Design Novel Multiepitope Peptide Cancer Vaccine Against Breast Cancer**  
(2019) *International Journal of Peptide Research and Therapeutics*, 25 (4), pp. 1343-1359.

158) Bahrami, A.A., Payandeh, Z., Khalili, S., Zakeri, A., Bandehpour, M.

**Immunoinformatics: In Silico Approaches and Computational Design of a Multi-epitope vaccine**  
(2019) *International Reviews of Immunology*, 38 (6), pp. 307-322.

159) Munteanu, C.R., Gesta, M., Martínez-Acevedo, Y.G., Pedreira, N., Pazos, A., Dorado, J.

**Improvement of epitope prediction using peptide sequence descriptors and machine learning**  
(2019) *International Journal of Molecular Sciences*, 20 (18), art. no. 4362, .

160) Bazmara, S., Shadmani, M., Ghasemnejad, A., Aghazadeh, H., Pooshang Bagheri, K.

**In silico rational design of a novel tetra-epitope tetanus vaccine with complete population coverage**  
(2019) *Medical Hypotheses*, 130, art. no. 109267, .

161) Slathia, P.S., Sharma, P.

**A common conserved peptide harboring predicted T and B cell epitopes in domain II of Japanese Encephalitis Virus and West Nile Virus for potential use in epitope based vaccine**  
(2019) *Comparative Immunology, Microbiology and Infectious Diseases*, 65, pp. 238-245.

162) Singh, S., Chiu, J.-R., Sun, K.-L., Su, E.C.-Y.

**Improving Allergenic Protein Prediction Using Physicochemical Features on Non-Redundant Protein Sequences**  
(2019) *Proceedings - International Conference on Machine Learning and Cybernetics*, 2019, pp. 104-110.

163) Ahmad, B., Ashfaq, U.A., Rahman, M.-U., Masoud, M.S., Yousaf, M.Z.

**Conserved B and T cell epitopes prediction of ebola virus glycoprotein for vaccine design using immunoinformatics approach**  
(2019) *Microbial Pathogenesis*, 132, pp. 243-253.

164) Khatoon, N., Pandey, R.K., Ojha, R., Aathmanathan, V.S., Krishnan, M., Prajapati, V.K.

**Exploratory algorithm to devise multi-epitope subunit vaccine by investigating Leishmania proteins**  
(2019) *Journal of Biomolecular Structure and Dynamics*, 37 (9), pp. 2381-2393.

165) Keshewani, V., Tarang, S.

**An immunoinformatic approach to universal therapeutic vaccine design against BK**  
(2019) *Vaccine*, 37 (26), pp. 3457-3463.

166) Hossain, F., Andreana, P.R.

**Developments in carbohydrate-based cancer therapeutics**  
(2019) *Pharmaceuticals*, 12 (2), art. no. 84, .

167) Qiu, X., Duvvuri, V.R., Bahl, J.

**Computational approaches and challenges to developing universal influenza vaccine**  
(2019) *Vaccines*, 7 (2), art. no. 45, .

168) Hajissa, K., Zakaria, R., Suppian, R., Mohamed, Z.

**Epitope-based vaccine as a universal vaccination strategy against *Toxoplasma gondii***  
(2019) *Journal of Advanced Veterinary and Animal Research*, 6 (2), pp. 174-182.

169) Thakkar, N., Bailey-Kellogg, C.

**Balancing sensitivity and specificity in distinguishing TCR groups by CDR sequence**  
(2019) *BMC Bioinformatics*, 20 (1), art. no. 241, .

170) Martins, J., Magalhães, C., Rocha, M., Osório, N.S.

**Machine Learning-Enhanced T Cell Neoepitope Discovery for Immunotherapy Design**  
(2019) *Cancer Informatics*, 18, .

171) Nosrati, M., Behbahani, M., Mohabtkar, H.

**Towards the first multi-epitope recombinant vaccine against Crimean-Congo hemorrhagic fever: a bioinformatics aided vaccine design approach**  
(2019) *Journal of Biomedical Informatics*, 93, art. no. 103160, .

172) Salvador, E.A., Pires de Souza, G.A., Cotta Malaquias, L.C., Wang, T., Leomil Coelho, L.F.

**Identification of relevant regions on structural and nonstructural proteins of Zika virus**



**test development: an in silico approach**

(2019) *New Microbes and New Infections*, 29, art. no. 100506, .

173) Criscitiello, C., Viale, G., Curigliano, G.

**Peptide vaccines in early breast cancer**

(2019) *Breast*, 44, pp. 128-134.

174) Charlton Hume, H.K., Vidigal, J., Carrondo, M.J.T., Middelberg, A.P.J., Roldão, A., Lua, L.F

**Synthetic biology for bioengineering virus-like particle vaccines**

(2019) *Biotechnology and Bioengineering*, 116 (4), pp. 919-935.

175) Jain, S., Baranwal, M.

**Computational analysis in designing T cell epitopes enriched peptides of Ebola glycoprotein binding interaction with HLA molecules**

(2019) *Journal of Theoretical Biology*, 465, pp. 34-44.

176) Rahman, M.S., Rahman, M.K., Saha, S., Kaykobad, M., Rahman, M.S.

**Antigenic: An improved prediction model of protective antigens**

(2019) *Artificial Intelligence in Medicine*, 94, pp. 28-41.

177) Ivanov, S.M., Huber, R.G., Alibay, I., Warwicker, J., Bond, P.J.

**Energetic Fingerprinting of Ligand Binding to Paralogous Proteins: The Case of the**

(2019) *Journal of Chemical Information and Modeling*, 59 (1), pp. 245-261.

178) Bi, J., Zheng, Y., Yan, F., Hou, S., Li, C.

**Prediction of Epitope-Associated TCR by Using Network Topological Similarity Base**

(2019) *IEEE Access*, 7, art. no. 8876604, pp. 151273-151281.

179) Mohammadi, E., Pirkhezranian, Z., Monhemi, H., Razmyar, J., Tahmoorespur, M., Sekhavat

**Epitope characterization, docking and molecular dynamic simulation studies on two virus proteins**

(2019) *Biotechnologia Aplicada*, 36 (1), pp. 1211-1218.

180) Gaafar, B.B.M., Ali, S.A., Abd-Elrahman, K.A., Almofti, Y.A., Fridkis-Hareli, M.

**Immunoinformatics Approach for Multiepitope Vaccine Prediction from H, M, F, and I Ruminants Virus**

(2019) *Journal of Immunology Research*, 2019, art. no. 6124030, .

181) Ghorbanpour, R., Nikbakht, G., Jalali, A.H.

**Immuno-bioinformatics study of autotransporter protein, antigen 43, in enterotoxigenic *E. coli* O157:H7**

(2019) *Journal of Veterinary Research*, 74 (1), pp. 128-141.

182) Chaudhary, R., Balhara, M., Jangir, D.K., Dangi, M., Dangi, M., Chhillar, A.K.

**In silico protein interaction network analysis of virulence proteins associated with *Salmonella enterica* serovar Typhimurium**

(2019) *Current Topics in Medicinal Chemistry*, 19 (2), pp. 146-155.

183) Mohammadi, E., Dashty, S.

**Epitope prediction, modeling, and docking studies for H3L protein as an agent of swine influenza virus**

(2019) *Biotechnologia*, 100 (1), pp. 69-80.

184) Ali, S.A., Almofti, Y.A., Abd-Elrahman, K.A.

**Immunoinformatics Approach for Multiepitopes Vaccine Prediction against Glycoprotein GP54 of Laryngotracheitis Virus**

(2019) *Advances in Bioinformatics*, 2019, art. no. 1270485, .

185) Jabbar, B., Rafique, S., Salo-Ahen, O.M.H., Ali, A., Munir, M., Idrees, M., Mirza, M.U., Van Rana, M.A.

**Antigenic Peptide Prediction From E6 and E7 Oncoproteins of HPV Types 16 and 18 Using Immunoinformatics and MD Simulation Analysis**

(2018) *Frontiers in Immunology*, 9, art. no. 3000, .

186) Tahir, R.A., Wu, H., Rizwan, M.A., Jafar, T.H., Saleem, S., Sehgal, S.A.

**Immunoinformatics and molecular docking studies reveal potential epitope-based protein for the detection of NS3 protein**

(2018) *Journal of Theoretical Biology*, 459, pp. 162-170.

187) Khairkhah, N., Namvar, A., Kardani, K., Bolhassani, A.

**Prediction of cross-clade HIV-1 T-cell epitopes using immunoinformatics analysis**  
(2018) *Proteins: Structure, Function and Bioinformatics*, 86 (12), pp. 1284-1293.

188) Slathia, P.S., Sharma, P.

**Conserved epitopes in variants of amastin protein of *Trypanosoma cruzi* for vaccine approach**  
(2018) *Microbial Pathogenesis*, 125, pp. 423-430.

189) Vakili, B., Eslami, M., Hatam, G.R., Zare, B., Erfani, N., Nezafat, N., Ghasemi, Y.

**Immunoinformatics-aided design of a potential multi-epitope peptide vaccine against**  
(2018) *International Journal of Biological Macromolecules*, 120, pp. 1127-1139.

190) Asbach, B., Meier, J.P., Pfeifer, M., Köstler, J., Wagner, R.

**Computational Design of Epitope-Enriched HIV-1 Gag Antigens with Preserved Struc**  
**Induction of Broad CD8+ T Cell Responses**  
(2018) *Scientific Reports*, 8 (1), art. no. 11264, .

191) Lata, K.S., Kumar, S., Vaghasia, V., Sharma, P., Bhairappanvar, S.B., Soni, S., Das, J.

**Exploring Leptospiral proteomes to identify potential candidates for vaccine design immunoinformatics approach**  
(2018) *Scientific Reports*, 8 (1), art. no. 6935, .

192) Suryani, Y., Taupiqurrohman, O., Aryanti, S., Subkhi, M.N., Paujiah, E.

**Development of Ebola Vaccine Candidate by in Silico from Glikoprotein (GP) Gene o**  
(2018) *Journal of Physics: Conference Series*, 1090 (1), art. no. 012081, .

193) Santoni, D.

**Viral peptides-MHC interaction: Binding probability and distance from human peptid**  
(2018) *Journal of Immunological Methods*, 459, pp. 35-43.

194)

Das, S., Mohakud, N.K., Suar, M., Sahu, B.R.

**Vaccine development for enteric bacterial pathogens: Where do we stand?**

(2018) *Pathogens and Disease*, 76 (5), art. no. fty057, .

195) Degoot, A.M., Chirove, F., Ndifon, W.

**Trans-allelic model for prediction of peptide:MHC-II interactions**

(2018) *Frontiers in Immunology*, 9 (JUN), art. no. 1410, .

196) Fanuel, S., Tabesh, S., Mokhtarian, K., Saroddiny, E., Fazlollahi, M.R., Pourpak, Z., Falak,

**Construction of a recombinant B-cell epitope vaccine based on a der p1-derived hyp approach**

(2018) *Immunotherapy*, 10 (7), pp. 537-553.

197) Sabah, S.N., Gazi, M.A., Sthity, R.A., Husain, A.B., Quyyum, S.A., Rahman, M., Islam, M.F

**Designing of Epitope-Focused Vaccine by Targeting E6 and E7 Conserved Protein S Informatics Approach in Human Papillomavirus 58 Isolates**

(2018) *Interdisciplinary Sciences – Computational Life Sciences*, 10 (2), pp. 251-260.

198) Kim, S., Kim, H.S., Kim, E., Lee, M.G., Shin, E.-C., Paik, S., Kim, S.

**Neopepsee: Accurate genome-level prediction of neoantigens by harnessing sequer immunogenicity information**

(2018) *Annals of Oncology*, 29 (4), pp. 1030-1036.

199) Kar, P., Ruiz-Perez, L., Arooj, M., Mancera, R.L.

**Current methods for the prediction of T-cell epitopes**

(2018) *Peptide Science*, 110 (2), art. no. e24046, .

200) Yao, Y., Shen, Y., Zhu, L., Ni, Y., Wang, H., Shao, S.

**Preliminary study and bioinformatics analysis on the potential role of CagQ in type I**

(2018) *Microbial Pathogenesis*, 116, pp. 1-7.

---

