

Documents

- 1) Gupta, S., Mohan, S., Somani, V.K., Aggarwal, S., Bhatnagar, R.
Simultaneous immunization with omp25 and I7/I12 provides protection against brucella
(2020) *Pathogens*, 9 (2), art. no. 152, .
- 2) Can, H., Erkunt Alak, S., Köseoğlu, A.E., Döşkaya, M., Ün, C.
Do Toxoplasma gondii apicoplast proteins have antigenic potential? An in silico study
(2020) *Computational Biology and Chemistry*, 84, art. no. 107158, .
- 3) 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 c columnare for vaccine development
(2020) *Journal of Biomolecular Structure and Dynamics*, 38 (2), pp. 450-459.
- 4) Abbas, G., Zafar, I., Ahmad, S., Azam, S.S.
Immunoinformatics design of a novel multi-epitope peptide vaccine to combat multi-drug resistance caused by Vibrio vulnificus
(2020) *European Journal of Pharmaceutical Sciences*, 142, art. no. 105160, .
- 5) Bidmeshki, T., Ahadi, A.M., Ayat, H.
A new design and epitopes analysis for recombinant vaccine against salmonella typhi
(2020) *Trends in Immunotherapy*, 4 (2), art. no. 891, pp. 47-54.
- 6) Srivastava, S., Verma, S., Kamthania, M., Kaur, R., Badyal, R.K., Saxena, A.K., Shin, H.-J., K
Structural Basis for Designing Multiepitope Vaccines Against COVID-19 Infection: In Silico Validation
(2020) *JMIR Bioinformatics and Biotechnology*, 1 (1), art. no. e19371, .

7) Slathia, P.S., Sharma, P.

In Silico Designing of Vaccines: Methods, Tools, and Their Limitations
(2020) *Computer-Aided Drug Design*, pp. 245-277.

8) Oli, A.N., Obialor, W.O., Ositadimma, M., Ifeanyichukwu, Odimegwu, D.C., Okoyeh, J.N., Emuibeonu, G.C.

Immunoinformatics and vaccine development: An overview
(2020) *ImmunoTargets and Therapy*, 9, pp. 13-30.

9) Dagur, H.S., Dhakar, S.S., Gupta, A.

Epitope-Based Vaccine Design against Novel Coronavirus SARS-CoV-2 Envelope Protein
(2020) *Eurasian Journal of Medicine and Oncology*, 4 (3), pp. 201-208.

10) Azam, F.M., Zamri-Saad, M., Rahim, R.A., Chumnantpoen, P., E-Kobon, T., Othman, S.

Antigenic outer membrane proteins prediction of *Pasteurella multocida* serotype b:2
(2020) *Asia-Pacific Journal of Molecular Biology and Biotechnology*, 28 (4), pp. 102-116.

11) Mahdizadeh, H., Salimian, J., Noormohammadi, Z., Amani, J., Halabian, R., Panahi, Y.

Structure prediction and expression of modified RCTLA4-ig as a blocker for B7 molecule
(2020) *Iranian Journal of Pharmaceutical Research*, 19 (3), pp. 329-348.

12) Jakhar, R., Gakhar, S.K.

An immunoinformatics study to predict epitopes in the envelope protein of SARS-CoV-2
(2020) *Canadian Journal of Infectious Diseases and Medical Microbiology*, 2020, art. no. 70

13) Dar, H.A., Waheed, Y., Najmi, M.H., Ismail, S., Hetta, H.F., Ali, A., Muhammad, K.

Multiepitope Subunit Vaccine Design against COVID-19 Based on the Spike Protein of SARS-CoV-2: A Molecular Dynamics Simulation Analysis
(2020) *Journal of Immunology Research*, 2020, art. no. 8893483, .

14) Author, M.N., Author, Á.D.O.C., Charry, O.J.P.

Comparison of machine learning models for the prediction of cancer cells using MHC class II epitopes
(2020) *Proceedings of SPIE - The International Society for Optical Engineering*, 11583, art. no. 1158301.

15) Sarkar, B., Ullah, M.A., Araf, Y., Rahman, M.S.

Engineering a novel subunit vaccine against SARS-CoV-2 by exploring immunoinformatics
(2020) *Informatics in Medicine Unlocked*, 21, art. no. 100478, .

16) Dai, Y., Chen, H., Zhuang, S., Feng, X., Fang, Y., Tang, H., Dai, R., Tang, L., Liu, J., Ma, T., .

Immunodominant regions prediction of nucleocapsid protein for SARS-CoV-2 early diagnosis
(2020) *Pathogens and Global Health*, 114 (8), pp. 463-470.

17) Oladipo, E.K., Ajayi, A.F., Ariyo, O.E., Onile, S.O., Jimah, E.M., Ezediuno, L.O., Adebayo, O. A.N., Oyeleke, M.O., Oyewole, M.P., Oguntomi, A.S., Akindiya, O.E., Olamoyegun, B.O., Aremu, D.O., Bello, H.B., Senbadejo, T.Y., Awoyelu, E.H., Oladipo, A.A., Oladipo, B.B., Aji, Oyawoye, O.M., Oloke, J.K.

Exploration of surface glycoprotein to design multi-epitope vaccine for the prevention of COVID-19
(2020) *Informatics in Medicine Unlocked*, 21, art. no. 100438, .

18) Islam, R., Parvez, M.S.A., Anwar, S., Hosen, M.J.

Delineating blueprint of an epitope-based peptide vaccine against the multiple serotypes of COVID-19 using a hierarchical reverse vaccinology approach
(2020) *Informatics in Medicine Unlocked*, 20, art. no. 100430, .

19) Sankar, P., Venugopal, S.

Immuno-informatics approach based epitopes prediction for vaccine design against severe acute respiratory syndrome coronavirus-2
(2020) *International Journal of Pharmaceutical Research*, 12, pp. 2459-2472.

20) Dehbarez, F.M., Nezafat, N., Mahmoodi, S.

In silico design of a novel multi-epitope peptide vaccine against hepatocellular carcinoma
(2020) *Letters in Drug Design and Discovery*, 17 (9), pp. 1164-1176.

21) Mahmud, S.M.N., Rahman, M., Kar, A., Jahan, N., Khan, A.

Designing of an epitope-based universal peptide vaccine against highly conserved region of polymerase protein of human marburg virus: A computational assay
(2020) *Anti-Infective Agents*, 18 (3), pp. 294-305.

- 22) Zaheer, T., Waseem, M., Waqar, W., Dar, H.A., Shehroz, M., Naz, K., Ishaq, Z., Ahmad, T., Ullah, Muhammad, S.A., Ali, A.

Anti-COVID-19 multi-epitope vaccine designs employing global viral genome sequences
(2020) *PeerJ*, 8, art. no. 9541, .

- 23) Akbar, S., Hayat, M., Tahir, M., Chong, K.T.

CACP-2LFS: Classification of Anticancer Peptides Using Sequential Discriminative Machine Learning Feature Selection Approach
(2020) *IEEE Access*, 8, art. no. 9139980, pp. 131939-131948.

- 24) Yazdi, M., Kolahi, M., Foroghmand, A.M., Tabandeh, M.R.

In silico assessment of plant L-asparaginase and estimating its allergenicity in comparison with human L-asparaginase
(2020) *Pediatric Hematology/Oncology and Immunopathology*, 19 (1), pp. 35-46.

- 25) Wang, D., Mai, J., Zhou, W., Yu, W., Zhan, Y., Wang, N., Epstein, N.D., Yang, Y.

Immunoinformatic analysis of T-and B-cell epitopes for SARS-CoV-2 vaccine design
(2020) *Vaccines*, 8 (3), art. no. 355, pp. 1-15.

- 26) Afzali, F., Ghahremanifard, P., Ranjbar, M.M., Salimi, M.

Exploring plac1 structure and underlying mechanisms to design a derivative vaccine against COVID-19; in-silico study
(2020) *Current Proteomics*, 17 (5), pp. 379-391.

- 27) Goumari, M.M., Farhani, I., Nezafat, N., Mahmoodi, S.

Multi-epitope vaccines (MEVs), as a novel strategy against infectious diseases
(2020) *Current Proteomics*, 17 (5), pp. 354-364.

- 28) Abdelmoneim, A.H., Mustafa, M.I., Abdelmageed, M.I., Murshed, N.S., Dawoud, E.D., Ahmed, Elfadl, N.M., Sati, A.O.M., Makhawi, A.M.

Immunoinformatics design of multi-epitopes peptide-based universal cancer vaccine against COVID-19

metalloproteinase-9 protein as a target
(2020) *Immunological Medicine*, pp. 1-18.

29) Russo, G., Reche, P., Pennisi, M., Pappalardo, F.

The combination of artificial intelligence and systems biology for intelligent vaccine c
(2020) *Expert Opinion on Drug Discovery*, pp. 1267-1281.

30) Samad, A., Ahammad, F., Nain, Z., Alam, R., Imon, R.R., Hasan, M., Rahman, M.S.

Designing a multi-epitope vaccine against SARS-CoV-2: an immunoinformatics appro
(2020) *Journal of Biomolecular Structure and Dynamics*, pp. 1-17.

31) Kardani, K., Bolhassani, A., Namvar, A.

An overview of in silico vaccine design against different pathogens and cancer
(2020) *Expert Review of Vaccines*, .

32) Yan, F., Gao, F.

A systematic strategy for the investigation of vaccines and drugs targeting bacteria
(2020) *Computational and Structural Biotechnology Journal*, 18, pp. 1525-1538.

33) Mima, K.A., Katorkina, E.I., Katorkin, S.A., Tsybanov, S.Zh., Malogolovkin, A.S.

In silico prediction of B- And T-cell epitopes in the CD2v protein of african swine fever virus, Asfivirus, Asfarviridae) [In silico идентификация В- и Т-клеточных эпитопов (африканской чумы свиней (African swine fever virus, Asfivirus, Asfarviridae)]
(2020) *Voprosy Virusologii*, 65 (2), pp. 103-112.

34) Arianzad, S.A., Zeinoddini, M., Haddadi, A., Nazarian, S., Sajedi, R.H.

In silico design of chimeric and immunogenic protein-containing IpaB and IpaD as a v shigella dysenteriae
(2020) *Current Proteomics*, 17 (4), pp. 333-341.

35) 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 cl
(2020) *Infectious Disorders - Drug Targets*, 20 (4), pp. 523-530.

36) Sarkar, B., Ullah, M.A., Araf, Y.

A systematic and reverse vaccinology approach to design novel subunit vaccines against DENV-1 and human Papillomavirus-16 (HPV-16)

(2020) *Informatics in Medicine Unlocked*, 19, art. no. 100343, .

37) Abdelmageed, M.I., Abdelmoneim, A.H., Mustafa, M.I., Elfadol, N.M., Murshed, N.S., Shanti

Design of a Multiepitope-Based Peptide Vaccine against the e Protein of Human COVID-19: A Systematic Approach

(2020) *BioMed Research International*, 2020, art. no. 2683286, .

38) Mobarak Qamsari, M., Rasooli, I., Darvish Alipour Astaneh, S.

Identification and immunogenic properties of recombinant ZnuD protein loops of *Acinetobacter baumannii*: Immunogenicity of ZnuD loops of *A. baumannii*

(2020) *Informatics in Medicine Unlocked*, 19, art. no. 100342, .

39) Karimah, N., Pambudi, S.

Prediction of B-cell epitope by in silico analysis of mycobacterium tuberculosis Ag85

(2020) *Asia-Pacific Journal of Molecular Biology and Biotechnology*, 28 (1), pp. 101-109.

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

Role of immunoinformatics in accelerating epitope-based vaccine development against COVID-19

(2020) *Open Biochemistry Journal*, 14 (1), pp. 9-18.

41) Joshi, A., Joshi, B.C., Mannan, M.A.-U., Kaushik, V.

Epitope based vaccine prediction for SARS-COV-2 by deploying immuno-informatics

(2020) *Informatics in Medicine Unlocked*, 19, art. no. 100338, .

42) Bobby, N., Abbas, M.A., Lee, E.-B., Park, S.-C.

Pharmacodynamics of Ceftiofur Selected by Genomic and Proteomic Approaches of *Paralichthys olivaceus* Isolated from the Flounder, *Paralichthys olivaceus*

(2020) *International Journal of Genomics*, 2020, art. no. 4850290, .

43) Shiragannavar, S., Madagi, S.

In silico vaccine design against mycoplasma hominis infections

(2020) *Biomedical and Pharmacology Journal*, 13 (1), pp. 457-468.

44) Anwar, S., Mouroso, J.T., Khan, M.F., Hosen, M.J.

Prediction of epitope-based peptide vaccine against the Chikungunya virus by immu

(2020) *Current Pharmaceutical Biotechnology*, 21 (4), pp. 325-340.

45) Taheri-Anganeh, M., Amiri, A., Movahedpour, A., Khatami, S.H., Ghasemi, Y., Savardashtaki

In silico evaluation of PLAC1-flic as a chimeric vaccine against breast cancer

(2020) *Iranian Biomedical Journal*, 24 (3), pp. 173-182.

46) 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.

47) Desai, P., Tarwadi, D., Pandya, B., Yagnik, B.

Immunoinformatic identification of potential epitopes

(2020) *Methods in Molecular Biology*, 2131, pp. 265-275.

48) Ramana, J., Mehla, K.

Immunoinformatics and epitope prediction

(2020) *Methods in Molecular Biology*, 2131, pp. 155-171.

49) Ibrahim, H.S., Kafi, S.K.

A computational vaccine designing approach for MERS-CoV infections

(2020) *Methods in Molecular Biology*, 2131, pp. 39-145.

50) Leow, C.Y., Kazi, A., Ismail, C.M.K.H., Chuah, C., Lim, B.H., Leow, C.H., Singh, K.K.B.

Reverse vaccinology approach for the identification and characterization of outer membrane proteins of *Shigella flexneri* as potential cellular- and antibody-dependent vaccine candidates

(2020) *Clinical and Experimental Vaccine Research*, 9 (1), pp. 15-25.

- 51) Zarei, M., Rahbar, M.R., Nezafat, N., Negahdaripour, M., Morowvat, M.H., Ghasemi, Y.
Computational analysis of arginine deiminase sequences to provide a guideline for pi
(2020) *Current Proteomics*, 17 (2), pp. 132-146.
- 52) Zarei, M., Rahbar, M.R., Negahdaripour, M., Morowvat, M.H., Nezafat, N., Ghasemi, Y.
Cell penetrating peptide: Sequence-based computational prediction for intercellular d
(2020) *Current Proteomics*, 17 (2), pp. 117-131.
- 53) Dana, H., Chalbatani, G.M., Gharagouzloo, E., Miri, S.R., Memari, F., Rasoolzadeh, R., Zina
Marmari, V.
In silico analysis, molecular docking, molecular dynamic, cloning, expression and pu
in colorectal cancer treatment
(2020) *Drug Design, Development and Therapy*, 14, pp. 309-329.
- 54) Nosrati, M., Mohabatkar, H., Behbahani, M.
Introducing of an integrated artificial neural network and Chou's pseudo amino acid c
computational epitope-mapping of Crimean-Congo haemorrhagic fever virus antigens
(2020) *International Immunopharmacology*, 78, art. no. 106020, .
- 55) Sajjad, R., Ahmad, S., Azam, S.S.
In silico screening of antigenic B-cell derived T-cell epitopes and designing of a multi
Acinetobacter nosocomialis
(2020) *Journal of Molecular Graphics and Modelling*, 94, art. no. 107477, .
- 56) Guleria, V., Jaiswal, V.
Comparative transcriptome analysis of different stages of Plasmodium falciparum to
candidates
(2020) *Genomics*, 112 (1), pp. 796-804.
- 57) Xie, L., Yang, W., Fan, X., Xie, J.
Comprehensive analysis of protein acetyltransferases of human pathogen Mycobacte
(2019) *Bioscience Reports*, 39 (12), art. no. BSR20191661, .

58) D'Mello, A., Ahearn, C.P., Murphy, T.F., Tettelin, H.

ReVac: A reverse vaccinology computational pipeline for prioritization of prokaryotic
(2019) *BMC Genomics*, 20 (1), art. no. 981, .

59) De Paiva Conte, F., Tinoco, B.C., Chaves, T.S., De Oliveira, R.C., Mansur, J.F., Mohana-Bor
Costa Neves, P.C., Rodrigues-Da-Silva, R.N.

**Identification and validation of specific B-cell epitopes of hantaviruses associated to
syndrome**
(2019) *PLoS Neglected Tropical Diseases*, 13 (12), art. no. e0007915, .

60) Evander Emeltan Tjoa, S., Maria Vianney, Y., Emantoko Dwi Putra, S.

In silico mutagenesis: decreasing the immunogenicity of botulinum toxin type A
(2019) *Journal of Biomolecular Structure and Dynamics*, 37 (18), pp. 4767-4778.

61) Majid, M., Andleeb, S.

**Designing a multi-epitopic vaccine against the enterotoxigenic *Bacteroides fragilis* by
approach**
(2019) *Scientific Reports*, 9 (1), art. no. 19780, .

62) Barbosa, M.S., de Sousa, I.B.A., Simionatto, S., Borsuk, S., Marchioro, S.B.

Recombinant polypeptide of *Mycobacterium leprae* as a potential tool for serological
(2019) *AMB Express*, 9 (1), art. no. 201, .

63) Petitdidier, E., Pagniez, J., Pissarra, J., Holzmüller, P., Papierok, G., Vincendeau, P., Lemes

**Peptide-based vaccine successfully induces protective immunity against canine visceral
leishmaniasis**
(2019) *npj Vaccines*, 4 (1), art. no. 49, .

64) Zhu, T., McClure, R., Harrison, O.B., Genco, C., Massari, P.

**Integrated bioinformatic analyses and immune characterization of new *Neisseria gonorrhoeae*
expressed during natural mucosal infection**
(2019) *Vaccines*, 7 (4), art. no. 153, .

65)

Namvar, A., Bolhassani, A., Javadi, G., Noormohammadi, Z.

In silico/In vivo analysis of high-risk papillomavirus L1 and L2 conserved sequences for a subtype prophylactic vaccine

(2019) *Scientific Reports*, 9 (1), art. no. 15225, .

66) Sanasam, B.D., Kumar, S.

In-silico structural modeling and epitope prediction of highly conserved Plasmodium

(2019) *Molecular Immunology*, 116, pp. 131-139.

67) Abdulla, F., Adhikari, U.K., Uddin, M.K.

Exploring T & B-cell epitopes and designing multi-epitope subunit vaccine targeting the lifecycle using immunoinformatics approach

(2019) *Microbial Pathogenesis*, 137, art. no. 103791, .

68) Rodrigues, R.L., Menezes, G.D.L., Saivish, M.V., Costa, V.G.D., Pereira, M., Moreli, M.L., S

Prediction of MAYV peptide antigens for immunodiagnostic tests by immunoinformatic simulations

(2019) *Scientific Reports*, 9 (1), art. no. 13339, .

69) Khan, M., Khan, S., Ali, A., Akbar, H., Sayaf, A.M., Khan, A., Wei, D.-Q.

Immunoinformatics approaches to explore Helicobacter Pylori proteome (Virulence Factors) for multi-epitope subunit vaccine

(2019) *Scientific Reports*, 9 (1), art. no. 13321, .

70) Dorosti, H., Eslami, M., Nezafat, N., Fadaei, F., Ghasemi, Y.

Designing self-assembled peptide nanovaccine against Streptococcus pneumoniae: A

(2019) *Molecular and Cellular Probes*, 48, art. no. 101446, .

71) Beltrán Lissabet, J.F., Herrera Belén, L., Farias, J.G.

TTAgP 1.0: A computational tool for the specific prediction of tumor T cell antigens

(2019) *Computational Biology and Chemistry*, 83, art. no. 107103, .

72) Solanki, V., Tiwari, M., Tiwari, V.

Prioritization of potential vaccine targets using comparative proteomics and designing of epitope vaccine against *Pseudomonas aeruginosa*

(2019) *Scientific Reports*, 9 (1), art. no. 5240, .

- 73) Shey, R.A., Ghogomu, S.M., Esoh, K.K., Nebangwa, N.D., Shintouo, C.M., Nongley, N.F., As Vanhamme, L., Souopgui, J.

In-silico design of a multi-epitope vaccine candidate against onchocerciasis and relat

(2019) *Scientific Reports*, 9 (1), art. no. 4409, .

- 74) Chauhan, V., Rungta, T., Goyal, K., Singh, M.P.

Designing a multi-epitope based vaccine to combat Kaposi Sarcoma utilizing immunc

(2019) *Scientific Reports*, 9 (1), art. no. 2517, .

- 75) Kamthania, M., Srivastava, S., Desai, M., Jain, A., Shrivastav, A., Sharma, D.K.

Immunoinformatics Approach to Design T-cell Epitope-Based Vaccine Against Hendra

(2019) *International Journal of Peptide Research and Therapeutics*, 25 (4), pp. 1627-1637.

- 76) Sefid, F., Alagheband Bahrami, A., Darvish, M., Nazarpour, R., Payandeh, Z.

In Silico Analysis for Determination and Validation of Iron-Regulated Protein from Esc

(2019) *International Journal of Peptide Research and Therapeutics*, 25 (4), pp. 1523-1537.

- 77) Behzadipour, Y., Hemmati, S.

Considerations on the rational design of covalently conjugated cell-penetrating pepti delivery of proteins: A guide to CPP selection using glucarpidase as the model cargo

(2019) *Molecules*, 24 (23), art. no. 4318, .

- 78) Michel-Todó, L., Reche, P.A., Bigey, P., Pinazo, M.-J., Gascón, J., Alonso-Padilla, J.

In silico Design of an Epitope-Based Vaccine Ensemble for Chagas Disease

(2019) *Frontiers in Immunology*, 10, art. no. 2698, .

- 79) Tahir Ul Qamar, M., Saleem, S., Ashfaq, U.A., Bari, A., Anwar, F., Alqahtani, S.

Epitope-based peptide vaccine design and target site depiction against Middle East R Coronavirus: An immune-informatics study

(2019) *Journal of Translational Medicine*, 17 (1), art. no. 362, .

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

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

81) Vianney, Y.M., Tjoa, S.E.E., Aditama, R., Dwi Putra, S.E.

Designing a less immunogenic nattokinase from *Bacillus subtilis* subsp. natto: a computational approach
(2019) *Journal of Molecular Modeling*, 25 (11), art. no. 337, .

82) Rostamtabar, M., Rahmani, A., Baee, M., Karkhah, A., Prajapati, V.K., Ebrahimpour, S., Nou

Development a multi-epitope driven subunit vaccine for immune response reinforcement against *Neisseria meningitidis* using comprehensive immunoinformatics approaches
(2019) *Infection, Genetics and Evolution*, 75, art. no. 103992, .

83) Coronado, L., Rios, L., Frías, M.T., Amarán, L., Naranjo, P., Percedo, M.I., Perera, C.L., Prieto, L.J.

Positive selection pressure on E2 protein of classical swine fever virus drives variability and antigenicity: Implication for epidemiological surveillance in endemic areas
(2019) *Transboundary and Emerging Diseases*, 66 (6), pp. 2362-2382.

84) Pérez-Sánchez, R., Manzano-Román, R., Obolo-Mvoulouga, P., Oleaga, A.

In silico selection of functionally important proteins from the malarial parasite *Plasmodium falciparum*: assessment of their protective efficacy as vaccine targets
(2019) *Parasites and Vectors*, 12 (1), art. no. 508, .

85) Kalita, P., Lyngdoh, D.L., Padhi, A.K., Shukla, H., Tripathi, T.

Development of multi-epitope driven subunit vaccine against *Fasciola gigantica* using immunoinformatics approach
(2019) *International Journal of Biological Macromolecules*, 138, pp. 224-233.

86) Ahmadi, K., Pouladfar, G., Kalani, M., Faezi, S., Pourmand, M.R., Hasanzadeh, S., Mafakhe

Epitope-based immunoinformatics study of a novel Hla-MntC-SACOL0723 fusion protein from *Staphylococcus aureus*: Induction of multi-pattern immune responses
(2019) *Molecular Immunology*, 114, pp. 88-99.

- 87) Nirwati, H., Donato, C.M., Ikram, A., Aman, A.T., Wibawa, T., Kirkwood, C.D., Soenarto, Y., F
Phylogenetic and immunoinformatic analysis of VP4, VP7, and NSP4 genes of rotavirus children with acute gastroenteritis in Indonesia
 (2019) *Journal of Medical Virology*, 91 (10), pp. 1776-1787.
- 88) Azim, K.F., Hasan, M., Hossain, M.N., Somana, S.R., Hoque, S.F., Bappy, M.N.I., Chowdhuri
Immunoinformatics approaches for designing a novel multi epitope peptide vaccine against Norwalk virus
 (2019) *Infection, Genetics and Evolution*, 74, art. no. 103936, .
- 89) Singh, M., Bhatt, P., Sharma, M., Varma-Basil, M., Chaudhry, A., Sharma, S.
Immunogenicity of late stage specific peptide antigens of Mycobacterium tuberculosis
 (2019) *Infection, Genetics and Evolution*, 74, art. no. 103930, .
- 90) Pasala, C., Chilamakuri, C.S.R., Katari, S.K., Nalamolu, R.M., Bitla, A.R., Amineni, U.
Epitope-driven common subunit vaccine design against H. pylori strains
 (2019) *Journal of Biomolecular Structure and Dynamics*, 37 (14), pp. 3740-3750.
- 91) Matos, A.D.S., Rodrigues-da-Silva, R.N., Soares, I.F., Baptista, B.D.O., Souza, R.M.D., Bites P.R.R., Sánchez-Arcila, J.C., Daniel-Ribeiro, C.T., López-Camacho, C., Reyes-Sandoval, A. J.D.C.
Antibody Responses Against Plasmodium vivax TRAP Recombinant and Synthetic Antigen in Individuals From the Brazilian Amazon
 (2019) *Frontiers in Immunology*, 10, art. no. 2230, .
- 92) Dar, H.A., Zaheer, T., Shehroz, M., Ullah, N., Naz, K., Muhammad, S.A., Zhang, T., Ali, A.
Immunoinformatics-aided design and evaluation of a potential multi-epitope vaccine against dengue virus
 (2019) *Vaccines*, 7 (3), art. no. 88, .
- 93) Jain, R., Singh, S., Verma, S., Jain, A.
Genome-Wide Prediction of Potential Vaccine Candidates for Campylobacter jejuni Using Machine Learning
 (2019) *Interdisciplinary Sciences – Computational Life Sciences*, 11 (3), pp. 337-347.

94) Gupta, N., Khan, F., Kumar, A.

Exploring Highly Antigenic Protein of Campylobacter jejuni for Designing Epitope Based Immunoinformatics Approach

(2019) *International Journal of Peptide Research and Therapeutics*, 25 (3), pp. 1159-1172.

95) Manivel, G., Meyyazhagan, A., Durairaj D, R., Piramanayagam, S.

Genome-wide analysis of Excretory/Secretory proteins in Trypanosoma brucei brucei characteristics and identification of potential targets by immunoinformatics approach

(2019) *Genomics*, 111 (5), pp. 1124-1133.

96) Atapour, A., Mokarram, P., MostafaviPour, Z., Hosseini, S.Y., Ghasemi, Y., Mohammadi, S.,

Designing a Fusion Protein Vaccine Against HCV: An In Silico Approach

(2019) *International Journal of Peptide Research and Therapeutics*, 25 (3), pp. 861-872.

97) Ojha, R., Pareek, A., Pandey, R.K., Prusty, D., Prajapati, V.K.

Strategic Development of a Next-Generation Multi-Epitope Vaccine to Prevent Nipah Virus

(2019) *ACS Omega*, 4 (8), pp. 13069-13079.

98) Pérez-Sánchez, R., Manzano-Román, R., Obolo-Mvoulouga, P., Oleaga, A.

Function-guided selection of midgut antigens from Ornithodoros erraticus ticks and its protective efficacy in rabbits

(2019) *Veterinary Parasitology*, 272, pp. 1-12.

99) Hajighahramani, N., Eslami, M., Negahdaripour, M., Ghoshoon, M.B., Dehshahri, A., Erfani, Nezafat, N., Ghasemi, Y.

Computational design of a chimeric epitope-based vaccine to protect against Staphylococcus aureus

(2019) *Molecular and Cellular Probes*, 46, art. no. 101414, .

100) Bagno, F.F., Godoi, L.C., Salazar, N., Pereira, G.D.C., Figueiredo, M.M., Fonseca, F.G.D.

Development of an enzyme-linked immunosorbent assay using recombinant protein Chikungunya virus

(2019) *Data in Brief*, 25, art. no. 104015, .

101) Marchan, J.

In silico identification of epitopes present in human heat shock proteins (HSPs) over
(2019) *Journal of Immunological Methods*, 471, pp. 34-45.

102) Prisilla, A., Chellapandi, P.

Cloning and expression of immunogenic Clostridium botulinum C2I mutant proteins evolutionary imprints
(2019) *Comparative Immunology, Microbiology and Infectious Diseases*, 65, pp. 207-212.

103) Abdul-Jalil, A.A., Khalaf, S.N.

Protein kinases a (PknA), a good target for vaccine design against tuberculosis
(2019) *Indian Journal of Public Health Research and Development*, 10 (6), pp. 668-673.

104) Ding, C., Liu, Q., Li, J., Ma, J., Wang, S., Dong, Q., Xu, D., Qiu, J., Wang, X.

Attenuated Listeria monocytogenes protecting zebrafish (Danio rerio) against Vibrio
(2019) *Microbial Pathogenesis*, 132, pp. 38-44.

105) Dodangeh, S., Fasihi-Ramandi, M., Daryani, A., Valadan, R., Sarvi, S.

In silico analysis and expression of a novel chimeric antigen as a vaccine candidate
(2019) *Microbial Pathogenesis*, 132, pp. 275-281.

106) Möller, J., Kraner, M.E., Burkovski, A.

More than a toxin: Protein inventory of Clostridium tetani toxoid vaccines
(2019) *Proteomes*, 7 (2), art. no. 15, .

107) Hasan, M., Azim, K.F., Begum, A., Khan, N.A., Shammi, T.S., Imran, A.S., Chowdhury, I.M.

Vaccinomics strategy for developing a unique multi-epitope monovalent vaccine against
(2019) *Infection, Genetics and Evolution*, 70, pp. 140-157.

108) Faezi, S., Bahrmand, A.R., Sardari, S., Nikokar, I., Khanaki, K., Siadat, S.D., Goudarzi, G.,

Epitope-based immunoinformatics study of a novel PilQ380–706-PilA fusion protein
(2019) *Gene Reports*, 15, art. no. 100385, .

109) Pandey, R.K., Ojha, R., Chatterjee, N., Upadhyay, N., Mishra, A., Prajapati, V.K.

Combinatorial screening algorithm to engineer multiepitope subunit vaccine targeting HIV-1 infection

(2019) *Journal of Cellular Physiology*, 234 (6), pp. 8717-8726.

110) Farhani, I., Nezafat, N., Mahmoodi, S.

Designing a Novel Multi-epitope Peptide Vaccine Against Pathogenic Shigella spp. B Approaches

(2019) *International Journal of Peptide Research and Therapeutics*, 25 (2), pp. 541-553.

111) Kumar, N., Singh, A., Grover, S., Kumari, A., Kumar Dhar, P., Chandra, R., Grover, A.

HHV-5 epitope: A potential vaccine candidate with high antigenicity and large coverage

(2019) *Journal of Biomolecular Structure and Dynamics*, 37 (8), pp. 2098-2109.

112) Möller, J., Kraner, M., Sonnewald, U., Sangal, V., Tittlbach, H., Winkler, J., Winkler, T.H., Mattos-Guaraldi, A.L., Burkovski, A.

Proteomics of diphtheria toxoid vaccines reveals multiple proteins that are immunogenic and contribute to protection of humans against *Corynebacterium diphtheriae*

(2019) *Vaccine*, 37 (23), pp. 3061-3070.

113) Hasan, M., Ghosh, P.P., Azim, K.F., Mukta, S., Abir, R.A., Nahar, J., Hasan Khan, M.M.

Reverse vaccinology approach to design a novel multi-epitope subunit vaccine against Zika virus

(2019) *Microbial Pathogenesis*, 130, pp. 19-37.

114) 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 for diagnostic test development: an in silico approach

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

115) Ravichandran, L., Venkatesan, A., Febin Prabhu Dass, J.

Epitope-based immunoinformatics approach on RNA-dependent RNA polymerase (RdRp) of Zika virus

virus (NiV)

(2019) *Journal of Cellular Biochemistry*, 120 (5), pp. 7082-7095.

116) Ojha, R., Nandani, R., Prajapati, V.K.

Contriving multiepitope subunit vaccine by exploiting structural and nonstructural v Epstein–Barr virus-associated malignancy

(2019) *Journal of Cellular Physiology*, 234 (5), pp. 6437-6448.

117) Ahmad, S., Ranaghan, K.E., Azam, S.S.

Combating tigecycline resistant *Acinetobacter baumannii*: A leap forward towards m discovery

(2019) *European Journal of Pharmaceutical Sciences*, 132, pp. 1-17.

118) Sanasam, B.D., Kumar, S.

PRE-binding protein of *Plasmodium falciparum* is a potential candidate for vaccine c silico evaluation of the hypothesis

(2019) *Medical Hypotheses*, 125, pp. 119-123.

119) Khan, F., Srivastava, V., Kumar, A.

Computational Identification and Characterization of Potential T-Cell Epitope for the Against Enterotoxigenic *Escherichia coli*

(2019) *International Journal of Peptide Research and Therapeutics*, 25 (1), pp. 289-302.

120) Bazmara, H., Rasooli, I., Jahangiri, A., Sefid, F., Astaneh, S.D.A., Payandeh, Z.

Antigenic Properties of Iron Regulated Proteins in *Acinetobacter baumannii*: An In S

(2019) *International Journal of Peptide Research and Therapeutics*, 25 (1), pp. 205-213.

121) Naz, K., Naz, A., Ashraf, S.T., Rizwan, M., Ahmad, J., Baumbach, J., Ali, A.

PanRV: Pangenome-reverse vaccinology approach for identifications of potential va pangenome

(2019) *BMC Bioinformatics*, 20 (1), art. no. 123, .

122) Kaliamurthi, S., Selvaraj, G., Chinnasamy, S., Wang, Q., Nangraj, A.S., Cho, W.C., Gu, K.,

Immunomics datasets and tools: To identify potential epitope segments for designin

to cervix papilloma

(2019) *Data*, 4 (1), art. no. 31, .

123) 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.

124) Farahmand, B., Taheri, N., Shokouhi, H., Soleimanjahi, H., Fotouhi, F.

Chimeric protein consisting of 3M2e and HSP as a universal influenza vaccine candi preliminary evaluation

(2019) *Virus Genes*, 55 (1), pp. 22-32.

125) Martínez, L., Milanič, M., Malaina, I., Álvarez, C., Pérez, M.-B., De La Fuente, I.M.

Weighted lambda superstrings applied to vaccine design

(2019) *PLoS ONE*, 14 (2), art. no. e0211714, .

126) Samykannu, G., Vijayababu, P., Antonyraj, C.B., Perumal, P., Narayanan, S., Basheer Aha

In Silico Characterization of B Cell and T Cell Epitopes for Subunit Vaccine Design o Molecular Dynamics Simulation Approach

(2019) *Journal of Computational Biology*, 26 (2), pp. 105-116.

127) Mahmood, M.S., Asad-Ullah, M., Batool, H., Batool, S., Ashraf, N.M.

Prediction of epitopes of Neisseria Gonorrhoeae against USA human leukocyte antiq immunoinformatic approach towards development of future vaccines for USA popul

(2019) *Molecular and Cellular Probes*, 43, pp. 40-44.

128) Jebastin, T., Narayanan, S.

In silico epitope identification of unique multidrug resistance proteins from Salmone development

(2019) *Computational Biology and Chemistry*, 78, pp. 74-80.

129) Unni, P.A., Ali, A.M.M.T., Rout, M., Thabitha, A., Vino, S., Lulu, S.S.

Designing of an epitope-based peptide vaccine against walking pneumonia: an immi

(2019) *Molecular Biology Reports*, 46 (1), pp. 511-527.

130) Momtaz, F., Foysal, J., Rahman, M., Fotedar, R.

Design of epitope based vaccine against shrimp white spot syndrome virus (WSSV) proteins: An immunoinformatic approach

(2019) *Turkish Journal of Fisheries and Aquatic Sciences*, 19 (2), pp. 59-69.

131) Zarei, M., Nezafat, N., Rahbar, M.R., Negahdaripour, M., Sabetian, S., Morowvat, M.H., Gh

Decreasing the immunogenicity of arginine deiminase enzyme via structure-based c

(2019) *Journal of Biomolecular Structure and Dynamics*, 37 (2), pp. 523-536.

132) Ebrahimi, S., Mohabatkar, H., Behbahani, M.

Predicting Promiscuous T Cell Epitopes for Designing a Vaccine Against Streptococ

(2019) *Applied Biochemistry and Biotechnology*, 187 (1), pp. 90-100.

133) Guthrie, N.L., Berman, M.A., Edwards, K.L., Appelbaum, K.J., Dey, S., Carpenter, J., Eisen

Achieving rapid blood pressure control with digital therapeutics: Retrospective coh

(2019) *JMIR Cardio*, 3 (1), art. no. e13030, .

134) Singh, Y.

Comparative in silico analyses reveal crucial factors for virulence, antigenicity, and i

(2019) *Mycobacterium Tuberculosis: Molecular Infection Biology, Pathogenesis, Diagnostic Interventions*, pp. 171-188.

135) Zhang, D., Guan, Z.-X., Zhang, Z.-M., Li, S.-H., Dao, F.-Y., Tang, H., Lin, H.

Recent development of computational predicting bioluminescent proteins

(2019) *Current Pharmaceutical Design*, 25 (40), pp. 4264-4273.

136) Rashid, M.I., Rehman, S., Ali, A., Andleeb, S.

Fishing for vaccines against *Vibrio cholerae* using in silico pan-proteomic reverse v

(2019) *PeerJ*, 2019 (6), art. no. 6223, .

137)

Ahearn, C.P., Kirkham, C., Chaves, L.D., Kong, Y., Pettigrew, M.M., Murphy, T.F.

Discovery and contribution of nontypeable haemophilus influenzae NTHI1441 to human r invasion

(2019) *Infection and Immunity*, 87 (11), art. no. e00462-19, .

138) Guthrie, N.L., Carpenter, J., Edwards, K.L., Appelbaum, K.J., Dey, S., Eisenberg, D.M., Ka

Emergence of digital biomarkers to predict and modify treatment efficacy: machine l

(2019) *BMJ Open*, 9 (7), art. no. e030710, .

139) Brodzik, K., Krysztopa-Grzybowska, K., Polak, M., Lach, J., Strapagiel, D., Zasada, A.A.

Analysis of the amino acid sequence variation of the 67-72p protein and the structur corynebacterium diphtheriae for their suitability as potential vaccine antigens

(2019) *Polish Journal of Microbiology*, 68 (2), pp. 233-246.

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

Immuno-bioinformatics study of autotransporter protein, antigen 43, in enterotoxige from calves

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

141) Mahmoodi, S., Nezafat, N.

In silico designing a novel multi-epitope DNA vaccine against anti-apoptotic proteins

(2019) *Current Proteomics*, 16 (3), pp. 222-230.

142) Mohammadi, E., Dashty, S.

Epitope prediction, modeling, and docking studies for H3L protein as an agent of sr

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

143) Hoggarth, A., Weaver, A., Pu, Q., Huang, T., Schettler, J., Chen, F., Yuan, X., Wu, M.

Mechanistic research holds promise for bacterial vaccines and phage therapies for l

(2019) *Drug Design, Development and Therapy*, 13, pp. 909-924.

144) Kong, M., Zhang, Y., Chen, W.

APGC: Universal protein prediction based on compositional, physico-chemical and structural features
(2019) *Match*, 81 (1), pp. 193-207.

145) Rezaei, M., Rabbani-Khorasgani, M., Zarkesh-Esfahani, S.H., Emamzadeh, R., Abtahi, H.

Prediction of the Omp16 epitopes for the development of an epitope-based vaccine against *Shigella flexneri*
(2019) *Infectious Disorders - Drug Targets*, 19 (1), pp. 36-45.

146) Dalsass, M., Brozzi, A., Medini, D., Rappuoli, R.

Comparison of open-source reverse vaccinology programs for bacterial vaccine antigen prediction
(2019) *Frontiers in Immunology*, 10 (FEB), art. no. 113, .

147) Srivastava, S., Kamthania, M., Kumar Pandey, R., Kumar Saxena, A., Saxena, V., Kumar Saxena, N.

Design of novel multi-epitope vaccines against severe acute respiratory syndrome virus using molecular interaction and dynamics
(2019) *Journal of Biomolecular Structure and Dynamics*, 37 (16), pp. 4345-4360.

148) Kaliamurthi, S., Selvaraj, G., Chinnasamy, S., Wang, Q., Nangraj, A.S., Cho, W.C.S., Gu, H.

Exploring the papillomaviral proteome to identify potential candidates for a chimeric papilloma using immunomics and computational structural vaccinology
(2019) *Viruses*, 11 (1), art. no. 63, .

149) Liu, J., Parrish, J.R., Hines, J., Mansfield, L., Finley, R.L., Jr.

A proteome-wide screen of *Campylobacter jejuni* using protein microarrays identifies novel antigens
(2019) *PLoS ONE*, 14 (1), art. no. e0210351, .

150) Validi, M., Karkhah, A., Prajapati, V.K., Nouri, H.R.

Immuno-informatics based approaches to design a novel multi epitope-based vaccine for the reinforcement against Leptospirosis
(2018) *Molecular Immunology*, 104, pp. 128-138.

151) Ikram, A., Zaheer, T., Awan, F.M., Obaid, A., Naz, A., Hanif, R., Paracha, R.Z., Ali, A., Naveed, A.

Exploring NS3/4A, NS5A and NS5B proteins to design conserved subunit multi-epitope vaccine against Hepatitis C virus

utilizing immunoinformatics approaches

(2018) *Scientific Reports*, 8 (1), art. no. 16107, .

152) Ain, Q.U., Ahmad, S., Azam, S.S.

Subtractive proteomics and immunoinformatics revealed novel B-cell derived T-cell enterocolitica: An etiological agent of Yersiniosis

(2018) *Microbial Pathogenesis*, 125, pp. 336-348.

153) Hizbullah, Nazir, Z., Afridi, S.G., Shah, M., Shams, S., Khan, A.

Reverse vaccinology and subtractive genomics-based putative vaccine targets identified in *Pseudomonas pseudomallei* Bp1651

(2018) *Microbial Pathogenesis*, 125, pp. 219-229.

154) Satyam, R., Janahi, E.M., Bhardwaj, T., Somvanshi, P., Haque, S., Najm, M.Z.

In silico identification of immunodominant B-cell and T-cell epitopes of non-structural proteins of *Leishmania donovani*

(2018) *Microbial Pathogenesis*, 125, pp. 129-143.

155) 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 *Leishmania donovani*

(2018) *International Journal of Biological Macromolecules*, 120, pp. 1127-1139.

156) Solanki, V., Tiwari, V.

Subtractive proteomics to identify novel drug targets and reverse vaccinology for the development of a vaccine against *Acinetobacter baumannii*

(2018) *Scientific Reports*, 8 (1), art. no. 9044, .

157) Aathmanathan, V.S., Jothi, N., Prajapati, V.K., Krishnan, M.

Investigation of immunogenic properties of Hemolin from silkworm, *Bombyx mori* as a vaccine adjuvant: An immunoinformatic approach

(2018) *Scientific Reports*, 8 (1), art. no. 6957, .

158) Panda, C., Mahapatra, R.K.

Identification of novel therapeutic candidates in *Cryptosporidium parvum*: An in silico approach

(2018) *Parasitology*, 145 (14), pp. 1907-1916.

159) Raja, V., Sobana, S., Mercy, C.S.A., Cotto, B., Bora, D.P., Natarajaseenivasan, K.

Heterologous DNA prime-protein boost immunization with RecA and FliD offers cross-leptospiral infection

(2018) *Scientific Reports*, 8 (1), art. no. 6447, .

160) Kar, P.P., Srivastava, A.

Immuno-informatics analysis to identify novel vaccine candidates and design of a m candidate against Theileria parasites

(2018) *Frontiers in Immunology*, 9 (OCT), art. no. 2213, .

161) Ojha, R., Khatoon, N., Prajapati, V.K.

Conglomeration of novel Culex quinquefasciatus salivary proteins to contrive multi-against infections caused by blood imbibing transmitter

(2018) *International Journal of Biological Macromolecules*, 118, pp. 834-843.

162) Vijayababu, P., Samykannu, G., Antonyraj, C.B., Narayanan, S., Basheer Ahamed, S.I., Pe

B-cell and T-cell epitope identification with stability analysis of AI-2 import ATP-bind –In silico approach

(2018) *Microbial Pathogenesis*, 123, pp. 487-495.

163) Chirani, A.S., Ghazi, M., Goudarzi, M., Peerayeh, S.N., Soleimanjahi, H., Dadashi, M., Haji

A survey on chimeric UreB229-561-HpaA protein targeting Helicobacter pylori: Comp activity valuation

(2018) *Computational Biology and Chemistry*, 76, pp. 42-52.

164) Mohanty, E., Dehury, B., Satapathy, A.K., Dwibedi, B.

Design and testing of a highly conserved human rotavirus VP8* immunogenic peptic development

(2018) *Journal of Biotechnology*, 281, pp. 48-60.

165) Bano, T., Janahi, E.M., Dhasmana, A., Lohani, M., Haque, S., Mandal, R.K., Dar, S.A., Jaw Areeshi, M.Y.

In silico CD4+, CD8+ & humoral immunity associated antigenic epitope prediction ar

HTLV-I

(2018) *Journal of B.U.ON.*, 23 (5), pp. 1514-1527.

166) Kumar Pandey, R., Ojha, R., Mishra, A., Kumar Prajapati, V.

Designing B- and T-cell multi-epitope based subunit vaccine using immunoinformatic approach against HIV-1 virus infection

(2018) *Journal of Cellular Biochemistry*, 119 (9), pp. 7631-7642.

167) Ehsan, N., Ahmad, S., Azam, S.S., Rungrotmongkol, T., Uddin, R.

Proteome-wide identification of epitope-based vaccine candidates against multi-drug resistant tuberculosis

(2018) *Biologicals*, 55, pp. 27-37.

168) Qureshi, S., Saxena, H.M., Imam, N., Kashoo, Z., Sharief Banday, M., Alam, A., Malik, M.Z

Isolation and genome analysis of a lytic *Pasteurella multocida* Bacteriophage PMP-C

(2018) *Letters in Applied Microbiology*, 67 (3), pp. 244-253.

169) Pasala, C., Chilamakuri, C.S.R., Katari, S.K., Nalamolu, R.M., Bitla, A.R., Umamaheswari,

An in silico study: Novel targets for potential drug and vaccine design against drug resistant tuberculosis

(2018) *Microbial Pathogenesis*, 122, pp. 156-161.

170) Goodswen, S.J., Kennedy, P.J., Ellis, J.T.

A gene-based positive selection detection approach to identify vaccine candidates against a test case protozoan pathogen

(2018) *Frontiers in Genetics*, 9 (AUG), art. no. 332, .

171) Ikram, A., Hakim, M.S., Zhou, J.-H., Wang, W., Peppelenbosch, M.P., Pan, Q.

Genotype-specific acquisition, evolution and adaptation of characteristic mutations in *Acinetobacter baumannii*

(2018) *Virulence*, 9 (1), pp. 121-132.

172) Ahmad, S., Azam, S.S.

A novel approach of virulome based reverse vaccinology for exploring and validating vaccine candidates against the most troublesome nosocomial pathogen: *Acinetobacter baumannii*

(2018) *Journal of Molecular Graphics and Modelling*, 83, pp. 1-11.

173) Foroutan, M., Ghaffarifar, F., Sharifi, Z., Dalimi, A., Pirestani, M.

Bioinformatics analysis of ROP8 protein to improve vaccine design against Toxoplasma gondii
(2018) *Infection, Genetics and Evolution*, 62, pp. 193-204.

174) Pandey, R.K., Ali, M., Ojha, R., Bhatt, T.K., Prajapati, V.K.

Development of multi-epitope driven subunit vaccine in secretory and membrane proteins of Plasmodium falciparum to convey protection against malaria infection
(2018) *Vaccine*, 36 (30), pp. 4555-4565.

175) Obolo-Mvoulouga, P., Oleaga, A., Manzano-Román, R., Pérez-Sánchez, R.

Evaluation of the protective efficacy of Ornithodoros moubata midgut membrane antigens and in silico prediction algorithms
(2018) *Ticks and Tick-borne Diseases*, 9 (5), pp. 1158-1172.

176) Narula, A., Pandey, R.K., Khatoon, N., Mishra, A., Prajapati, V.K.

Excavating chikungunya genome to design B and T cell multi-epitope subunit vaccine: An immunoinformatics approach to control chikungunya infection
(2018) *Infection, Genetics and Evolution*, 61, pp. 4-15.

177) Chauhan, V., Goyal, K., Singh, M.P.

Identification of broadly reactive epitopes targeting major glycoproteins of Herpes simplex virus-1 using immunoinformatics analysis
(2018) *Infection, Genetics and Evolution*, 61, pp. 24-35.

178) Hossain, M.U., Omar, T.M., Alam, I., Das, K.C., Mohiuddin, A.K.M., Keya, C.A., Salimullah, M.

Pathway based therapeutic targets identification and development of an interactive vaccine against Campylobacter jejuni rm1221 through non-redundant protein dataset
(2018) *PLoS ONE*, 13 (6), art. no. e0198170., .

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

Construction of a recombinant B-cell epitope vaccine based on a der p1-derived hypodermic approach
(2018) *Immunotherapy*, 10 (7), pp. 537-553.

180) Chirani, A.S., Majidzadeh, R., Pouriran, R., Heidary, M., Nasiri, M.J., Gholami, M., Goudarz

The effect of in silico targeting Pseudomonas aeruginosa patatin-like protein D, for i
(2018) *Computational Biology and Chemistry*, 74, pp. 12-19.

181) Khan, F., Srivastava, V., Kumar, A.

Epitope Based Peptide Prediction from Proteome of Enterotoxigenic E.coli
(2018) *International Journal of Peptide Research and Therapeutics*, 24 (2), pp. 323-336.

182) Antunes, S., Couto, J., Ferrolho, J., Rodrigues, F., Nobre, J., Santos, A.S., Margarida Sant
Domingos, A.

**Rhipicephalus bursa sialotranscriptomic response to blood feeding and babesia ovi
candidate protective antigens**
(2018) *Frontiers in Cellular and Infection Microbiology*, 8 (MAY), art. no. 116, .

183) Ding, C., Ma, J., Dong, Q., Liu, Q.

Live bacterial vaccine vector and delivery strategies of heterologous antigen: A review
(2018) *Immunology Letters*, 197, pp. 70-77.

184) Abdollahi, S., Rasooli, I., Mousavi Gargari, S.L.

An in silico structural and physicochemical characterization of TonB-dependent cop
(2018) *Microbial Pathogenesis*, 118, pp. 18-31.

185) Chauhan, V., Singh, M.P., Ratho, R.K.

**Identification of T cell and B cell epitopes against Indian HCV-genotype-3a for vaccine
analysis**
(2018) *Biologicals*, 53, pp. 63-71.

186) Pandey, R.K., Ojha, R., Aathmanathan, V.S., Krishnan, M., Prajapati, V.K.

Immunoinformatics approaches to design a novel multi-epitope subunit vaccine aga
(2018) *Vaccine*, 36 (17), pp. 2262-2272.

187)

Hossain, R., Yasmin, T., Hosen, M.I., Nabi, A.H.M.N.

In silico identification of potential epitopes present in human adenovirus proteins for vac putative drugs for treatment against viral infection
(2018) *Journal of Immunological Methods*, 455, pp. 55-70.

188) Ebrahimi, S., Mohabatkar, H.

Prediction of T-cell epitopes for designing a reverse vaccine against streptococcal b
(2018) *Molecular Biology Research Communications*, 7 (1), pp. 35-41.

189) Bragazzi, N.L., Gianfredi, V., Villarini, M., Rosselli, R., Nasr, A., Hussein, A., Martini, M., Be

Vaccines meet big data: State-ofthe- Art and future prospects. From the classical 3is vaccinology 1.0 to vaccinology 3.0, vaccinomics, and Beyond: A historical overview
(2018) *Frontiers in Public Health*, 6, art. no. 62, .

190) Asad, Y., Ahmad, S., Rungrotmongkol, T., Ranaghan, K.E., Azam, S.S.

Immuno-informatics driven proteome-wide investigation revealed novel peptide-bas emerging multiple drug resistant Providencia stuartii
(2018) *Journal of Molecular Graphics and Modelling*, 80, pp. 238-250.

191) Baliga, P., Shekar, M., Venugopal, M.N.

Potential Outer Membrane Protein Candidates for Vaccine Development Against the Reverse Vaccinology Based Identification
(2018) *Current Microbiology*, 75 (3), pp. 368-377.

192) Hossain, M.U., Omar, T.M., Oany, A.R., Kibria, K.M.K., Shibly, A.Z., Moniruzzaman, M., Ali,

Design of peptide-based epitope vaccine and further binding site scrutiny led to gro against Lassa virus
(2018) *3 Biotech*, 8 (2), art. no. 81, .

193) Vakili, B., Nezafat, N., Hatam, G.R., Zare, B., Erfani, N., Ghasemi, Y.

Proteome-scale identification of Leishmania infantum for novel vaccine candidates: approach
(2018) *Computational Biology and Chemistry*, 72, pp. 16-25.

194) Yousefi, S., Abbassi-Dalooi, T., Sekhavati, M.H., Tahmoorespur, M.

Evaluation of immune responses induced by polymeric OMP25-BLS Brucella antigen
(2018) *Microbial Pathogenesis*, 115, pp. 50-56.

195) Cravo, P., Machado, R.B., Leite, J.A., Leda, T., Suwanarusk, R., Bittencourt, N., Albrecht, L., Lacerda, M.V.G., Ferreira, M.U., Soares, I.S., Goh, Y.S., Bargieri, D.Y., Nosten, F., Russell,

In silico epitope mapping and experimental evaluation of the Merozoite Adhesive Er (MAEBL) as a malaria vaccine candidate
(2018) *Malaria Journal*, 17 (1), art. no. 20, .

196) Dangi, M., Kumari, R., Singh, B., Chhillar, A.K.

Advanced In Silico Tools for Designing of Antigenic Epitope as Potential Vaccine Candidate
(2018) *Bioinformatics: Sequences, Structures, Phylogeny*, pp. 329-357.

197) Rana, A., Thakur, S., Kumar, G., Akhter, Y.

Recent trends in system-scale integrative approaches for discovering protective antigens
(2018) *Frontiers in Genetics*, 9, art. no. 572, .

198) Larijani, M.S., Sadat, S.M., Bolhassani, A., Pouriayeali, M.H., Bahramali, G., Ramezani, A.

In silico design and immunologic evaluation of HIV-1 p24-nef fusion protein to approach candidate services
(2018) *Current HIV Research*, 16 (5), pp. 322-337.

199) Kalamurthi, S., Selvaraj, G., Kaushik, A.C., Gu, K.-R., Wei, D.-Q.

Designing of CD8 + and CD8 + -overlapped CD4 + epitope vaccine by targeting late antigen of papillomavirus
(2018) *Biologics: Targets and Therapy*, 12, pp. 107-125.

200) Kalamurthi, S., Selvaraj, G., Junaid, M., Khan, A., Gu, K., Wei, D.-Q.

Cancer immunoinformatics: A promising era in the development of peptide vaccines against induced cervical cancer
(2018) *Current Pharmaceutical Design*, 24 (32), pp. 3791-3817.

