Criteria - III (Research, Innovation and Extension)

C3_DVV-2

3.7.1	Number of functional MoUs /linkagewith institutions/ industries in India and abroad for internship, on-the-job training, project work, student / faculty exchange and collaborative research during the last five years (10)

3.7.1.1: Number of functional MoUs with institutions/ industries in India and abroad for internship, on-the-job training, project work, student / faculty exchange and collaborative research during the last five years

Year of signing MoU	Name of the organization with whom MOU/Collaboration being signed	Duration	Purpose of MOU/Collaboration	List the actual activities under each MOU year-wise
2021	Dr. Rakesh K Mishra, Centre for Cellular and Molecular Biology, Hydrabad	Six monts	Six Months Project/Internship	MSc. Dissertation (Annexure 1)
2021	D. Manish Jaiswal, Tata Institute of Fundamental Research, Hydrabad	Six Months	Six Months Project/Internship	MSc. Dissertation (Annexure 2)
2022	Prof. Raghavan Varadarajan, MBU, Indian Institute of Science, Bangalore.	Six Months	Six Months Project/Internship	MSc. Dissertation (Annxure 3)
2022	Dr. Mahipal Ganj, Dept. of Biochemistry, Indian Institute of Science, Bangalore	Six months	Six Months Project/Internship	MSc. Dissertation (Annxure 4)
2022	Dr. Nitin Tupperwar, Centre for Cellular and Molecular Biology	Six months	Six Months Project/Internship	MSc. Dissertation (Annxure 4)

Annexure-I

Certificate

This is to certify that the M.Sc. dissertation entitled "Role of conserved non-coding regions in gene regulation in zebrafish" submitted by Bilal Ahmad Shah to the Department of Biotechnology, University of Kashmir, Hazratbal Srinagar J&K in the partial fulfilment of the requirement of the degree of Master of Science (Biotechnology), is a record of the original bonafide work carried out by him under my guidance and supervision. The report has reached the requisite standards for submission to the best of my knowledge, understanding, and belief. Moreover, the results contained in this report have not been submitted in part or full to any other university or institute for the award of any degree or diploma.

Dr. Rakesh Kumar Mishra

Distinguished Professor (AcSIR)

J.C. Bose Fellow

Centre for Cellular and Molecular Biology

Uppal Road

Hyderabad 500007

Dr. Rakesh K Mishra
Distinguished Emeritus Professor
Academy of Scientific and Innovative Research
CSIR-Centre for Cellular and Molecular Biology
Hyderabad-500 007, India.

Annex-7

टाटा मूलभूत अनुसंधान संस्थान
TATA INSTITUTE OF FUNDAMENTAL RESEARCH
भारत सरकार के परमाणु ऊर्जा विभाग की स्वायत्त संस्था एवं समविश्वविद्यालय
(An autonomous institute of the Department of Atomic Energy,
Government of India, and a Deemed University)
सर्वेक्षण संख्या 36 / पी, गोपनपल्ली गांव, सेरिलिंगमपल्ली मंडल, रंगारेड्डी जिला, हैदराबाद - 500 046
Survey No.36/P, Gopanpally Village, Serilingampally Mandal, Ranga Reddy District,
Hyderabad - 500 046
दूरभाष / Telephone: 040 - 20203078
फैक्स / Fax: 040 - 20203105
वेबसाइट / Website : www.tifrh.res.in

CERTIFICATE

I certify that **Mr. Bilal Ahmad Naikoo** (Regd. No. TIFR-H/2021-21/003) has worked on this project titled **'Identification of the novel regulators of mitochondrial biogenesis using *Drosophila melanogaster* as the model system'** under my supervision and in collaboration with my PhD student Mr. Aravind H. All the experiments presented in this thesis were carried out by Mr. Bilal. He has written this report by himself. The experimental data presented in this report belong to TIFR, Hyderabad. The work presented in this thesis is part of a long term project and hence cannot be published or presented in a conference without my knowledge.

Dr. Manish Jaiswal 16/02/2022
Principal Investigator

Annex -3

TO WHOM IT MAY CONCERN

This is to certify that Bakshi Navid is a bonafide student of the Department of Biotechnology under Roll No.: 20058119006, Batch 2020. He has carried out his Master's thesis project titled **'Aspartate Scanning Mutagenesis as a tool for epitope mapping'** under the supervision of Prof. Raghavan Varadarajan at the Molecular Biophysics Unit, Indian Institute of Science, Bangalore, India, during the period of six-months.

Date: 21/12/22

Prof. Raies A. Qadri

Head of the Department,
Department of Biotechnology,
University of Kashmir.

Annex- 4

Department of Biochemistry
Indian Insutute of Science
Bangalore, 560012

TO WHOM IT MAY CONCERN

It is certified that the Dissertation Report entitled **"Single-molecule Investigations of Plectoneme Dynamics and Transcription"** which is being submitted by Mr. Faheem Farooq in partial fulfilment of the requirements for the award of the degree of Master of Science in Biotechnology at the Department of Biotechnology, University of Kashmir is a record of candidate's own work carried out by him under my supervision and guidance. The matter embodied in this report has not been submitted for award of any other degree.

G. Mahipal
Dr. Mahipal Ganji
(Research Supervisor)

Date: 13/12/2022

Dr. MAHIPAL GANJI
Assistant Professor
Department of Biochemistry
Indian Institute of Science
Bangalore - 560 012

Faheem Farooq
(Candidate)

सीएसआईआर-कोशिकीय एवं आणविक जीवविज्ञान केन्द्र
CSIR-CENTRE FOR CELLULAR AND MOLECULAR BIOLOGY
(वैज्ञानिक तथा औद्योगिक अनुसंधान परिषद)
(Council of Scientific & Industrial Research)
(विज्ञान एवं प्रौद्योगिकी मंत्रालय, भारत सरकार / Ministry of Science & Technology, Govt. of India)
उप्पल रोड, हब्सीगुडा, हैदराबाद - 500 007 तेलंगाना भारत
Uppal Road, Habsiguda, Hyderabad - 500 007, Telangana, India

TO WHOMSOEVER IT MAY CONCERN

This is to certify that **Ms. Nishi Singh** from University of Kashmir, Department of biotechnology (session 2020-2022), has carried out her dissertation project work on "**Understanding the role of LdBPK_350140.1 in regulation of cap binding activity of leishIF4E-4 in *Leishmania***" under my supervision at the Centre for Cellular and Molecular Biology, Uppal Road, Hyderabad during 20th July to 15th December 2022. This work is original and has not been submitted for any degree or diploma to any other Institute or University.

[Dr. Nitin Tupperwar]

Supervisor

Dr. Nitin Tupperwar
Scientist
Centre for Cellular and Molecular Biology
Council of Scientific and Industrial Research
Habsiguda, Uppal Road, HYDERABAD - 500 007.

फैक्स Fax
अंतर्राष्ट्रीय भारत International India
+91-40-27160591, 27160311
040-27160591, 27160311
+91-40-27160591, 27160311
040-27160591, 27160311
दूरभाष Telephone +91-
वेब साइट Website http://

SCIENTIFIC REPORTS
nature research

Check for updates

OPEN

Aggregation of M3 (E376D) variant of alpha1- antitrypsin

Arif Bashir[1]✉, Younis Hazari[1,5], Debnath Pal[2], Dibyajyoti Maity[2], Samirul Bashir[1], Laishram Rajendrakumar Singh[3], Naveed Nazir Shah[4] & Khalid Majid Fazili[1]✉

Alpha1-antitrypsin (α1AT) is an abundant serine-protease inhibitor in circulation. It has an important role in neutralizing the neutrophil elastase activity. Different pathogenic point mutations like Z$^{(E342K)}$-α1AT have been implicated in the development of liver cirrhosis and Chronic Obstructive Pulmonary Disease (COPD), the latter being a cluster of progressive lung diseases including chronic bronchitis and emphysema. M3-α1AT (376Glu > Asp) is another variant of α1AT which so far is largely being considered as normal though increased frequency of the variant has been reported in many human diseases including COPD. We also observed increased frequency of M3-α1AT in COPD cases in Kashmiri population. The frequency of heterozygous (AC) genotype in cases and controls was 58.57% and 27.61% (odds-ratio 6.53 (2.27–15.21); $p < 0.0001$) respectively, while homozygous CC genotype was found to be 21.42% and 6.66% (odds-ratio 10.56 (3.63–18.64); $p < 0.0001$) respectively. Comparative *in vitro* investigations that include trypsin–antitrypsin assay, Circular Dichroism spectroscopy and dynamic light scattering performed on wild-type (M-α1AT), M3-α1AT, and Z-α1AT proteins along with the molecular dynamics simulations revealed that M3-α1AT has properties similar to Z-α1AT capable of forming aggregates of varied size. Our maiden observations suggest that M3-α1AT may contribute to the pathogenesis of COPD and other disorders by mechanisms that warrant further investigations.

Alpha1-antitrypsin (α1AT) is one of the most abundant circulating antiproteases. The serum levels of α1AT are raised secondary to activation of inflammatory-immune processes in humans[1]. α1AT is coded by a serine-protease inhibitor (*SERPIN*) A1. It is primarily expressed in hepatocytes and to some extent by lung tissue, macrophages, and monocytes. Among the different variants of α1AT, Z-α1AT (Glu342Lys) is the most pathogenic variant of α1AT and has been extensively studied. This variant has a distinctive capacity to form loop-sheet polymers due to the conformational change. The gain-of-toxic function of Z-α1AT in the hepatocytes leads to the manifestation of cirrhosis and hepatocellular carcinoma. On the contrary, reduced levels of serum α1AT lead to unregulated neutrophil elastase activity leading to the pathogenesis of a host of diseases including emphysema[1]. Owing to its pathogenicity, Z-α1AT is considered as a double-edged sword whose aggregation, on one hand leads to a pathological state of liver and loss-of-function on the other side results in emphysema[2]. The X-ray crystallography, *in silico* analysis, and kinetics of α1AT have provided valuable insights to understand its folding mechanism[3,4]. The conformational plasticity of serpins is not only important in terms of inhibitory activity but also unfolds a mechanistic understanding of their susceptibility towards misfolding and aggregation. During the folding process, α1AT is kinetically trapped in a metastable state. In this state, a patch of 15 amino acid residues (345–360) located near the C-terminus of α1AT, protruding out of its main body, is exposed to the polar solvent as a flexible loop connected between β-s5A and β-s1C that is called as reactive center loop (RCL). Native fold of α1AT is composed of three β-sheets (A–C) surrounded by 8–9 α-helices (hA–hI). The interaction of protease with the metastable α1AT gives rise to a marked conformational transition driven upon cleavage at P1′–P1 site in the RCL.

The 342 $Glu^{-} \rightarrow Lys^{+}$ substitution just above the top of s5A strand in Z-α1AT removes a salt bridge between Glu342 and Lys290, thereby driving an electrostatic repulsion between them. This promotes polymerization by delaying the already slow insertion of s5A that prolong the exposure of the C-terminal domain of Z-α1AT[4]. Z-α1AT is the commonest of all the deficient variant observed with serum levels 0.06–0.2 g/L among

[1]UPR Signalling Laboratory, Department of Biotechnology, University of Kashmir, Srinagar, 190006, Jammu and Kashmir, India. [2]Department of Computational and Data Sciences (CDS), Indian Institute of Sciences, Bengaluru, 560012, India. [3]Dr. B. R. Ambedkar Center for Biomedical Research (ACBR), University of Delhi, Delhi, 110007, India. [4]Department of Chest Medicine, Govt. Medical College, Srinagar, 190001, Jammu and Kashmir, India. [5]Present address: Laboratory of Proteostasis Control and Biomedicine, Faculty of Medicine, University of Chile, Av. Independencia, 1027, Santiago, Chile. ✉e-mail: bashir.aarif@gmail.com; fazili@kashmiruniversity.ac.in

diagnostics

MDPI

Article

Ensemble Machine Learning Model to Predict SARS-CoV-2 T-Cell Epitopes as Potential Vaccine Targets

Syed Nisar Hussain Bukhari [1,*], Amit Jain [1], Ehtishamul Haq [2], Abolfazl Mehbodniya [3] and Julian Webber [4]

[1] University Institute of Computing, Chandigarh University, NH-95, Chandigarh-Ludhiana Highway, Mohali 140413, India; amit_jainci@yahoo.com
[2] Department of Biotechnology, University of Kashmir, Srinagar 190006, India; haq@uok.edu.in
[3] Department of Electronics and Communication Engineering, Kuwait College of Science and Technology, Kuwait City 13133, Kuwait; a.niya@kcst.edu.kw
[4] Graduate School of Engineering Science, Osaka University, Toyonaka, Osaka 560-8531, Japan; jwebber@ieee.org
* Correspondence: nisar.bukhari@gmail.com

Abstract: An ongoing outbreak of coronavirus disease 2019 (COVID-19), caused by a single-stranded RNA virus called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has caused a worldwide pandemic that continues to date. Vaccination has proven to be the most effective technique, by far, for the treatment of COVID-19 and to combat the outbreak. Among all vaccine types, epitope-based peptide vaccines have received less attention and hold a large untapped potential for boosting vaccine safety and immunogenicity. Peptides used in such vaccine technology are chemically synthesized based on the amino acid sequences of antigenic proteins (T-cell epitopes) of the target pathogen. Using wet-lab experiments to identify antigenic proteins is very difficult, expensive, and time-consuming. We hereby propose an ensemble machine learning (ML) model for the prediction of T-cell epitopes (also known as immune relevant determinants or antigenic determinants) against SARS-CoV-2, utilizing physicochemical properties of amino acids. To train the model, we retrieved the experimentally determined SARS-CoV-2 T-cell epitopes from Immune Epitope Database and Analysis Resource (IEDB) repository. The model so developed achieved accuracy, AUC (Area under the ROC curve), Gini, specificity, sensitivity, F-score, and precision of 98.20%, 0.991, 0.994, 0.971, 0.982, 0.990, and 0.981, respectively, using a test set consisting of SARS-CoV-2 peptides (T-cell epitopes and non-epitopes) obtained from IEDB. The average accuracy of 97.98% was recorded in repeated 5-fold cross validation. Its comparison with 05 robust machine learning classifiers and existing T-cell epitope prediction techniques, such as NetMHC and CTLpred, suggest the proposed work as a better model. The predicted epitopes from the current model could possess a high probability to act as potential peptide vaccine candidates subjected to in vitro and in vivo scientific assessments. The model developed would help scientific community working in vaccine development save time to screen the active T-cell epitope candidates of SARS-CoV-2 against the inactive ones.

Keywords: COVID-19; SARS-CoV-2; T-cell epitope; peptide-based vaccines; machine learning; random forest; ensemble learning; voting ensemble

Citation: Bukhari, S.N.H.; Jain, A.; Haq, E.; Mehbodniya, A.; Webber, J. Ensemble Machine Learning Model to Predict SARS-CoV-2 T-Cell Epitopes as Potential Vaccine Targets. *Diagnostics* **2021**, *11*, 1990. https://doi.org/10.3390/diagnostics11111990

Academic Editor: Tim Duong

Received: 13 September 2021
Accepted: 21 October 2021
Published: 26 October 2021

1. Introduction

An infection outbreak caused by a novel coronavirus has proliferated rapidly around the world. The World Health Organization (WHO) designated the disease as COVID-19 [1,2]. The pathogen was named SARS-CoV-2 by the Coronaviridae Study Group (CSG) [3]. The pathogen has resulted in 225,488,491 COVID-19 cases and 4,644,376 deaths worldwide as of September 13, 2021, posing a significant challenge to public health worldwide [4]. Furthermore, because SARS-CoV-2 keeps on circulating, the chances of mutations in the virus also increases. The recent delta variant with *Pango lineage* as AY.1, AY.2, AY.3,

diagnostics

MDPI

Article

Ensemble Machine Learning Model to Predict SARS-CoV-2 T-Cell Epitopes as Potential Vaccine Targets

Syed Nisar Hussain Bukhari [1,*], Amit Jain [1], Ehtishamul Haq [2], Abolfazl Mehbodniya [3] and Julian Webber [4]

[1] University Institute of Computing, Chandigarh University, NH-95, Chandigarh-Ludhiana Highway, Mohali 140413, India; amit_jainci@yahoo.com
[2] Department of Biotechnology, University of Kashmir, Srinagar 190006, India; haq@uok.edu.in
[3] Department of Electronics and Communication Engineering, Kuwait College of Science and Technology, Kuwait City 13133, Kuwait; a.niya@kcst.edu.kw
[4] Graduate School of Engineering Science, Osaka University, Toyonaka, Osaka 560-8531, Japan; jwebber@ieee.org
* Correspondence: nisar.bukhari@gmail.com

Abstract: An ongoing outbreak of coronavirus disease 2019 (COVID-19), caused by a single-stranded RNA virus called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has caused a worldwide pandemic that continues to date. Vaccination has proven to be the most effective technique, by far, for the treatment of COVID-19 and to combat the outbreak. Among all vaccine types, epitope-based peptide vaccines have received less attention and hold a large untapped potential for boosting vaccine safety and immunogenicity. Peptides used in such vaccine technology are chemically synthesized based on the amino acid sequences of antigenic proteins (T-cell epitopes) of the target pathogen. Using wet-lab experiments to identify antigenic proteins is very difficult, expensive, and time-consuming. We hereby propose an ensemble machine learning (ML) model for the prediction of T-cell epitopes (also known as immune relevant determinants or antigenic determinants) against SARS-CoV-2, utilizing physicochemical properties of amino acids. To train the model, we retrieved the experimentally determined SARS-CoV-2 T-cell epitopes from Immune Epitope Database and Analysis Resource (IEDB) repository. The model so developed achieved accuracy, AUC (Area under the ROC curve), Gini, specificity, sensitivity, F-score, and precision of 98.20%, 0.991, 0.994, 0.971, 0.982, 0.990, and 0.981, respectively, using a test set consisting of SARS-CoV-2 peptides (T-cell epitopes and non-epitopes) obtained from IEDB. The average accuracy of 97.98% was recorded in repeated 5-fold cross validation. Its comparison with 05 robust machine learning classifiers and existing T-cell epitope prediction techniques, such as NetMHC and CTLpred, suggest the proposed work as a better model. The predicted epitopes from the current model could possess a high probability to act as potential peptide vaccine candidates subjected to in vitro and in vivo scientific assessments. The model developed would help scientific community working in vaccine development save time to screen the active T-cell epitope candidates of SARS-CoV-2 against the inactive ones.

Keywords: COVID-19; SARS-CoV-2; T-cell epitope; peptide-based vaccines; machine learning; random forest; ensemble learning; voting ensemble

Citation: Bukhari, S.N.H.; Jain, A.; Haq, E.; Mehbodniya, A.; Webber, J. Ensemble Machine Learning Model to Predict SARS-CoV-2 T-Cell Epitopes as Potential Vaccine Targets. *Diagnostics* **2021**, *11*, 1990. https://doi.org/10.3390/diagnostics11111990

Academic Editor: Tim Duong

Received: 13 September 2021
Accepted: 21 October 2021
Published: 26 October 2021

1. Introduction

An infection outbreak caused by a novel coronavirus has proliferated rapidly around the world. The World Health Organization (WHO) designated the disease as COVID-19 [1,2]. The pathogen was named SARS-CoV-2 by the Coronaviridae Study Group (CSG) [3]. The pathogen has resulted in 225,488,491 COVID-19 cases and 4,644,376 deaths worldwide as of September 13, 2021, posing a significant challenge to public health worldwide [4]. Furthermore, because SARS-CoV-2 keeps on circulating, the chances of mutations in the virus also increases. The recent delta variant with *Pango lineage* as AY.1, AY.2, AY.3,

Journal of Cellular Biochemistry

RESEARCH ARTICLE

Lung cancer cell-derived EDA-containing fibronectin induces an inflammatory response from monocytes and promotes metastatic tumor microenvironment

Asif Amin, Taseem A. Mokhdomi, Shoiab Bukhari, Zubair Wani, Naveed A. Chikan, Basit A. Shah, Aabid M. Koul, Umer Majeed, Faizah Farooq, Ayub Qadri, Raies A. Qadri

First published: 04 January 2021 | https://doi.org/10.1002/jcb.29883 | Citations: 8

CELL BIOCHEMISTRY & FUNCTION

RESEARCH ARTICLE

Ala307Thr variation modulates FSHR structure and impairs its binding affinity for FSH: Implications in polycystic ovarian syndrome

Asif Amin, Asif Lone, Umer Majeed Wani, Faizah Farooq, Ruchi Shah, Rakesh Kumar, Raies A. Qadri

First published: 07 June 2023 | https://doi.org/10.1002/cbf.3819