पेटेंट कार्यालय
शासकीय जर्नल

OFFICIAL JOURNAL
OF
THE PATENT OFFICE

निर्गमन सं. 35/2021	शुक्रवार	दिनांक: 27/08/2021
ISSUE NO. 35/2021	FRIDAY	DATE: 27/08/2021

पेटेंट कार्यालय का एक प्रकाशन
PUBLICATION OF THE PATENT OFFICE

(12) PATENT APPLICATION PUBLICATION
(19) INDIA
(22) Date of filing of Application :04/08/2021

(21) Application No.202121035051 A
(43) Publication Date : 27/08/2021

(54) Title of the invention : DISCOVERY OF THE DIPIVEPRINE A MAIN PROTEASE INHIBITOR AS ANTI-SARS-COV-2 AGENT •

(51) International classification	:G16C0020500000, G16C0020600000, G16B0035000000, G16B0015000000, G16C0020400000
(31) Priority Document No	:NA
(32) Priority Date	:NA
(33) Name of priority country	:NA
(86) International Application No Filing Date	:NA :NA
(87) International Publication No	: NA
(61) Patent of Addition to Application Number Filing Date	:NA :NA
(62) Divisional to Application Number Filing Date	:NA :NA

(71)**Name of Applicant :**
1)Dr Nitin Ghanshamdas Haswani
Address of Applicant :R C Patel Institute of Pharmacy, Shirpur Dist Dhule MS Maharashtra India
2)Dr. Vishal M. Balaramnavar
(72)**Name of Inventor :**
1)Dr Pritam Sharad Jain
2)Dr. Vishal M. Balaramnavar
3)Dr Nitin Ghanshamdas Haswani
4)Dr Kapil Madhavprasad Agrawal
5)Dr Saurabh Chandrashekhar Khadse

(57) Abstract :
A method (300) for identifying a binding site of a Dipivefrin drug, the method comprising: developing pharmacophore models to extract features from the Dipivefrin drug; validating the developed pharmacophore models by comparing with pre-defined models of existing coronavirus drugs; performing a virtual screening of a database of drugs with the validated pharmacophore models; performing a structure-based virtual screening of the validated pharmacophore models by structural docking of a target protein into the validated pharmacophore models; assigning a score to each pharmacophore model of the Dipivefrin drug in order to identify the validated pharmacophore models with a high binding affinity and efficiency; and comparing the score obtained from the virtual screening and the structure based virtual screening for classifying the scored pharmacophore models based on the target protein binding affinity and efficiency for the coronaviridae family of virus.

No. of Pages : 24 No. of Claims : 10