Delta plus variant with neutral mutation is less virulent compared to wild type SARS-CoV2

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Abstract

Background

With the start of the Coronavirus disease19 (COVID19) pandemic, the Coronavirus has mutated constantly. Recently a new variant called Delta plus has been reported in few countries, including South Africa, Brazil and India. The Delta plus variant contains an additional mutation called K417N on the coronavirus spike. The present study aims to determine the virulence and transmissibility of the Delta plus variant and to check the efficiency of different antibodies on its neutralization.

Materials and Methods

Different computational tools such as PROVEAN, an online tool, HOPE server, simulation using CABS Flex, Clus pro, an online docking tool, were used to predict the structure and function of Delta plus variant by performing a comparative study with wild type protein. Also, to find an effective antibody against Delta plus variant, antigen-antibody docking studies were conducted through Clus pro server. Furthermore, we performed a 2D interaction diagram analysis to find the amino acid residue's interaction against antibodies.

Results

PROVEAN and HOPE showed the mutation (K417N) in the S-glycoprotein of Delta plus as NEUTRAL mutation. This mutation causes the loss of cysteine bonds leading to the destabilization of the 3D structure of spike protein. Furthermore, the RMSF plot emphasizing the 17th amino acid position of wild and Delta plus mutant revealed the high fluctuation of mutant protein structure compared to the wild protein structure. Further, a comparative docking study against hACE2 shows higher binding energy of wild-type RBD (-751.7 kcal/mol) than mutant RBD (-750.1 kcal/mol). Moreover, antigen-antibody docking study revealed higher affinity of BD-23 Fab antibodies with greater interaction energy (-997 kcal/mol) compared to other antibodies and thus may prove to be a promising therapeutic against Delta plus variant.

Conclusion

Delta plus variant is less stable, has a lower binding affinity to hACE2 and has less virulence than wild type. However, the BD-23 Fab antibody has shown a more significant association for this variant and can be used in its treatment.

Introduction

COVID-19, coronavirus disease 2019, is a new infectious disease caused by a previously unknown virus called SARS-CoV-2. Coronavirus badly destroys the respiratory system and lungs. Coronaviruses are large, roughly spherical particles with unique surface projections. Their size is highly variable, with average diameters of 80 to 120. The total molecular mass is on average 40,000 [kDa](#). They are enclosed

in an envelope embedded with many protein molecules ^[1]. The lipid bilayer envelope, membrane proteins, and nucleocapsid protect the virus outside the host cell. Being primarily a respiratory disease, it is highly transmissible through both direct and indirect contact. It displays a range of symptoms in different individuals and thus has been grouped into mild, moderate, and severe diseases. The virus utilizes spike proteins on its surface to recognize ACE-2 receptors present on the host cells to enter the cell cytoplasm and replicate. The viral invasion of cells induces damage response, pyroptosis, infiltration of immune cells, expression of pro-inflammatory cytokines (cytokine storm), and activation of the adaptive immune system. Depending on viral load and host factors like age and underlying medical conditions, the immune responses against SARS-cov-2 may cause acute respiratory distress syndrome (ARDS).

A novel coronavirus (SARS-CoV-2), the cause of Coronavirus Disease 2019 (COVID-19), was discovered. Until February 18, 2020, there were 72 533 confirmed COVID-19 cases (including 10 644 severe cases) and 1872 deaths in China. SARS-CoV-2 is spreading among the public and causing a substantial burden due to its human-to-human transmission. However, the intermediate host of SARS-CoV-2 is still unclear. Finding the possible intermediate host of SARS-CoV-2 is imperative to prevent the further spread of the epidemic. There have been over seven million cases and almost 413 372 deaths globally due to the novel Coronavirus (2019-nCoV) associated disease COVID-19, as of June 11, 2020. Phylogenetic analysis suggests that there is a common source for these infections. The overall sequence similarities between the spike protein of 2019-nCoV and that of SARS-CoV are known to be around 76% to 78% and 73% to 76% for the whole protein and receptor-binding domain (RBD), respectively. Thus, they have the potential to serve as the drug and/or vaccine candidate. However, the individual response against 2019-nCoV differs due to genetic variations in the human population. Understanding the variations in angiotensin-converting enzyme 2 (ACE2) and human leukocyte antigen (HLA) that may affect the severity of 2019-nCoV infection could help identify individuals at a higher risk from the COVID-19. The new Delta plus variant has been formed due to a Delta or B.1.617.2 variant mutation. There is no indication yet of the severity of the disease due to the new variant. Delta Plus (AY.1) is resistant to monoclonal antibody cocktails. It is not yet a variant of concern (VoC) in India due to low incidence. One of the emerging variants is B.1.617.2.1, or AY.1 is characterized by the acquisition of K417N mutation ^[2].

Sixty-three genomes of Delta (B.1.617.2) with the new K417N mutation have been identified by the GISAID so far. Delta plus was present in six genomes from India as of June 7, as per Public Health England (PHE). The variant frequency for K417N is not much in India at this point. The sequences are mainly from Europe, Asia and America. The earliest sequence of this genome was found in Europe in late March this year^[3]. The Delta plus variant contains an additional mutation called K417N on the coronavirus spike, which has been found in the Beta and Gamma variants, first seen in South Africa and Brazil, respectively (Beta was linked to increased hospitalization and deaths during South Africa's first wave of infections, while Gamma was estimated to be highly transmissible).

Even with 166 examples of Delta plus shared on GISAID, a global open sharing database, "we don't have much reason to believe this is any more dangerous than the original Delta," according to Dr. Jeremy Kamil, a virologist at Louisiana State University Health Sciences Center in Shreveport^[4]. Coronaviruses

(CoVs) classified in the Coronaviridae family infect a vast spectrum of vertebrate groups. Seven CoVs that cause human disease to consist of Alpha-CoVs, which are HCoV-229E, and NL63 and beta-CoVs, which are MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-HKU1, and SARS-CoV-2. SARS-CoV-2 is an enveloped, positive-polarity, single-stranded RNA virus responsible for a new Coronavirus disease 2019 (COVID-19). The mutagenic ability of the SARS-CoV-2 directs its evolution and genome variability, thus allowing viruses to escape from host immunity and develop drug resistance^[5]. Tracing viral mutations is also essential for developing new vaccines, antiviral drugs, and diagnostic systems. During replication in the host cell, genomic mutations occur in the virus, and these mutations are transferred to new generations. In the current scenario, where immunization programs have already commenced in nations highly affected by COVID-19, the advent of new variants has raised global public health concerns worldwide on the possible role in disease severity and antibody responses. An important question that raises the alarm is what if these new variants are "immune escape" variants, which means people who have had SARS-CoV-2 infection are susceptible to re-infection, and therefore, the current vaccines probably need redesigning to be effective against the variants^[6].

Thus, to design a novel therapeutic against the Delta plus variant, we applied an in silico approach to first analyze the structure and function of the Delta plus variant and, using the protein-protein docking approach, the identification of potent antibodies which would provide a therapeutic inhibitor against this viral infection. Our present work includes structural analysis of the DELTA plus variant through mutational analysis and simulation studies and comparative protein-protein docking studies against ACE2 receptors to analyze its functional role. Furthermore, against six different monoclonal antibodies, protein-protein docking studies were also performed to find the promising therapeutic against DELTA plus variant. The selection was based upon binding score and hydrogen bonding interactions.

Materials And Methods

Retrieval of Protein Structures

SARS CoV2 spike RBD protein (PDB ID: 7CWO) ^[7] was retrieved from RCSB PDB. Further, different antibody-spike protein complexes with heavy and light chain fragments were retrieved from PDB, as shown in Table 1. Moreover, the hACE2 receptor crystal structure was also retrieved (PDB ID: 7A97) ^[8].

Table 1: Different monoclonal antibodies complex structures retrieved from PDB.

Monoclonal antibodies name	PDB ID	Structure	Reference
CR3022	6W41		[⁹]
B38	7BZ5		[¹⁰]
CB6	7C01		[¹¹]
P2B-2F6	7BWJ		[¹²]
REGN	6XDG		[¹³]

Creation of Delta plus variant in spike RBD protein

The Delta plus variant K417N was created using Pymol software [15], an open-source molecular visualization system in the Schrodinger suite Figure 1.

Protein variation effect analyzer (PROVEAN)

PROVEAN [16] is an open-source tool that helps speculate whether an amino acid substitution, insertion, or deletion has resulted in a protein's biological properties depending upon the similarity and alignment between protein and variant sequence and protein sequence homology. This tool holds the perspective at three levels: PROVEAN protein, PROVEAN protein batch, and PROVEAN genome variants. The PROVEAN genome variant function was applied for the prognosis, showing input formats such as a catalog of genomic coordinates and variations. Furthermore, the PROVEAN provides a delta alignment score depending upon the variants and reference version of protein query concerning protein sequence homolog retrieved from NCBI protein database through BLAST [17]. The threshold is set at -2.5 as default for binary categorization system, which indicates PROVEAN score above threshold as 'Neutral' and value below or equal to a threshold value as 'Deleterious'.

Structural effect prediction of Delta plus mutant protein

We used the HOPE server to find an amino acid substitution effect on the protein structure [18]. HOPE is an online server that finds the structural impact of the point mutation in a protein sequence.

Molecular dynamic simulation

Using CABS Flex 2.0 [19] software, the molecular simulation was performed for 100 trajectory frames, 10 ns for 100 cycles applying some additional distance restraints along with the global weight of 1.0 and Blues, established on the Poisson-Boltzmann/Generalized Born (PB/GB) molecular mechanics, with salt radius 2Å, ionic strength 0.15, minimum atomic radius 1Å and 1.4Å solvent probe radius at 298 K, to find

the protein complex conformational stability. The RMSF values of each amino acid residue of the protein complex were predicted values through CABS Flex 2.0, to search for protein conformational stability within a nanosecond time scale. The highest RMSF score reveals more flexibility and the lowest score confirms the system's limited movement all over the simulation process.

Protein protein docking

Protein structure preparation

The RBD region of spike glycoprotein (chain A) was retrieved through the CHIMERA tool [20]. Also, different crystal structures of antibodies containing both heavy and light chains were extracted by removing the spike glycoprotein structure using the edit parameter present in the CHIMERA tool. Similarly, The structure of the ACE2 receptor was also extracted in a similar manner from its complex. Further using Cluspro [21], an online tool, protein-protein docking was performed by taking each antibody complex as ligand against wild and (K417N) variant of spike glycoprotein as protein structure. Moreover, protein-protein docking was also performed against the ACE2 receptor to find the change in the binding ability of spike glycoprotein (both wild and mutant type).

Protein structure preprocessing

Spike glycoprotein structure was preprocessed by removing all nonstandard residues, including water molecules, adding hydrogen atoms through the Chimera tool. Moreover, the protein structure was considered for further studies in monomeric form. Different antibodies based complex structure was retrieved by removing the spike glycoprotein chain from the complex and other nonstandard residues by using the CHIMERA tool. ACE2 receptor structure was also prepared and preprocessed similarly.

Molecular Docking

Cluspro is web-based protein-protein docking that is fully automated and is a worldwide experiment dedicated to protein interaction and energy calculation. It is based upon the Fast Fourier Transform associated approach, making it realistic to evaluate and initiate billions of docked configurations by basic scoring parameters. It executes a multilevel procedure: rigid-body protein docking, energy-dependent filtering, scoring the maintained structures depending upon the clustering attribute, and ultimately refining a confined number of complexes through energy minimization. The server provides the top structures based on cluster size and lowest energy. We screened one of the compatible models after reviewing the size and energy of the cluster – considering lower energies and more cluster sizes.

2D interaction diagram

Protein-protein and protein- antibody interactions were visualized through LigPlot plus v2.2D interactions of ACE2 receptor and different antibodies with RBD variants were performed by antibody

script available in antibody loop numbering scheme (KABAT Scheme) and DIMPLOT script algorithm package available into LigPlot plus v2.2 [22].

Results

The RBD region is vital for interactions with the ACE2 receptor and antibody. Therefore, we have performed structural and functional analysis of Delta plus mutant variant. In comparison with the wild type, it was revealed that structural modification in the RBD region would affect its function, which was analyzed through binding energy between RBD (wild and variant) against ACE2 receptor and antibody.

Comparative structural prediction of the wild and mutant protein

Using PROVEAN and HOPE server, the retrieved RBD region of Spike Glycoprotein fasta sequence from NCBI was provided as input, along with K417N was provided as residue to generate mutation. The PROVEAN result indicated the PROVEAN score =0.27, above the threshold value indicating NEUTRAL mutation. The HOPE server also revealed that the mutant residue is smaller in size as compared to the wild type. Moreover, wild-type structure interpreted in UNIPROT was involved in cysteine bridge formation, which is essential for protein stability. Since, after mutation, the loss of cysteine bond would lead to a severe effect in the 3D structure of the protein, leading to destabilization (Figure 2).

Simulation analysis of protein structures (wild vs. mutant)

The protein dynamic fluctuation (native vs. mutant) was performed using molecular dynamic simulation, indicated through the fluctuation plot (Figure 3A, 3B) .The RMSF scores of each protein residue were provided (supplementary file 1). Emphasizing the position 17 of both (wild and mutant) residues (table 2) of the RMSF plot, we can identify that the mutant type of protein structure revealed very high fluctuation compared to the wild protein structure. The RMSF result indicated that the wild protein structure is more stable than the mutant type structure. Therefore, the K417N mutation in the RBD region of the SARS COV2 gene causes an overall elevation of the protein structure in comparison to the wild type.

Table 2: RMSF scores of mutant and wild-type structures for comparative analysis.

Native Protein	Mutant Protein (K417N)
RMSF:0.8210Å	RMSF:1.15 Å

Docking studies analysis

Novel variant Delta plus, one of the highly transmissible variants, was modeled by mutating the reported position of amino acid residues of spike glycoprotein complex using Pymol software. Mutagenesis was carried out in a wild-type RBD region of complex structure. Further, the mutant structure was used for docking studies against hACE2 receptor protein and also in the identification of antibodies as therapeutic through binding score analysis.

Protein-Protein docking analysis

A comparative docking study was performed between the RBD region of spike protein (wild and mutant type) and hACE2 receptor through ClusPro program. RBD (wild type) 's binding energy against hACE2 receptor is -751.7 kcal/mol whereas RBD (mutant type) binding against hACE2 receptor is -750.1 kcal/mol. It was investigated through binding scores with slightly lower binding affinity as observed in the Delta plus mutant strain against the hACE2 receptor.

Moreover, Delta plus variant and wild type hydrogen bond interactions with hACE2 receptor (Figure 4A and B) were also retrieved as detailed along with distances in (table 3A and B).

Table 3A: Hydrogen bond interactions of wild type structure against hACE2

Amino acid residues of Wild type	hACE2 receptor amino acid residues	Distance of hydrogen bonding
ARG (466)	ASN (159)	2.65 Å
ASN (450)	ILE (151)	3.17 Å

Table 3B: Hydrogen bond interactions of Delta plus variant structure against hACE2

Amino acid residues of Delta plus variant type	hACE2 receptor amino acid residues	Distance of hydrogen bonding
SER (349)	GLU (160)	3.02 Å
LYS (444)	PRO (146)	2.71 Å
ARG (346)	GLU (150)	2.80Å

Antigen-antibodies docking study

Moreover, to gain insights of Delta plus variants into different antibody binding the ClusPro server was used for antigen-antibody docking study. Mutant and wild RBD type structure was taken as a protein structure and various reported antibodies complex as ligands for docking. As shown in Tables 4a and 4b, the result revealed the lowest cluster energy of the variant and wild-type RBD spike protein against each antibody complex (Figure 5). The result indicated that Delta plus variants showed very effective binding against CR3022, CB6 and BD-23 Fab (Figure 6) in comparison to wild type. However, BD-23 Fab antibodies showed more interaction energy (-997 kcal/mol) from other antibodies, indicating a promising therapeutic against Delta plus variant. BD-23 Fab antibody heavy chain[ARG(107),TRP(105),GLY (56),GLN (62),TYR (106), THR (65) and TYR (60)] hydrogen bonding interactions against amino acid residues of Delta plus variant [(LEU (390),GLY (381),ASP (428) and HIS(519)] was also retrieved through DIMPLOT interaction diagram (Figure 7).

Table 4a and 4b: Protein-Protein docking scores of wild type and mutant (K417N) against hACE2 receptor and different antibodies.

Effect of RBD region against hACE2	Effect of Delta plus region against hACE2
-751.7	-750.1 (slightly lower affinity)

Antibodies name	Binding energy against RBD	Binding energy against Delta plus	Effect of mutation on antibodies
CR3022	-880.5	-884.0	Higher affinity
B38	-918.0	-912.6	Lower affinity
CB6	-789.4	-804.4	Higher affinity
P2B-2F6	-724.7	-724.4	Lower affinity
REGN	-878.1	-866.4	Lower affinity
BD-23 Fab	-996.9	-997.0	Higher affinity

Discussion

SARS -CoV2 an outbreak on March 11, 2020 was declared officially by the World Health Organization. The SARS -CoV2 prevalence is increasingly posing a serious threat worldwide. With the deepening

analysis to COVID 19, the former optimistic belief has been slowly returned by expectations against the virus for a long-term fight. To curb pandemics, prophylactic drugs and effective vaccines are needed urgently [23].

Based on the different published articles, SARS-CoV-2 recognizes the ACE2, a human receptor, confirmed through our docking study. Thus, the Spike protein, mainly its RBD, which is essential for hACE2 binding, is the most promising target for SARS-CoV-2 vaccines development and antibody-based formulations and drugs [24,25] Depending on the novel disclosed functional analysis and structural details, we described the antigenic features and receptor recognition of Delta Plus variant (SARS-COV2 mutant).

Mutagenesis in SARS-CoV-2 structure during the pandemic is leading to another region of concern. The mutation in SARS-CoV-2 is recognized to be more rapid, and it is still increasing [25]. For the viral genome, the intervention of the human immune system for such rapid mutation is one reason. Furthermore, due to such fast occurring mutation, there is high variance in the genome, hence challenging researchers to find a suitable vaccine or drug.

It is a matter of concern that the mutations in the virus can provide sequence changes and structural variations, which can decrease the vaccine's efficacy on the coronaviruses by evading the immune system of the host cell through antibody escape [26]. Mutational analysis of the residues at the surface of the Receptor binding motif and ACE2 has a vital role in potent pharmacophores for therapeutic drug development. At present, the spike protein has been considered a potent immunogen since it is found as the most significant accessible region of the virus. This protein is mainly seen for the high contagion rate of the virus [27].

Amino acid modifications in a protein can lead to numerous impacts, beginning from folding issues to converting intermolecular interactions with protein or ligands partners. Many specific structural properties like the type of amino acid substitution (conservative or nonconservative replacement), the position in the structural protein (e.g., the modification takes place in secondary structure elements or the loop, the solvent-exposed or residue is buried), the residue is within protein-ligand complex, or within a catalytic site, the replaced amino acid residue is in a rigid or flexible areas are among the various others that were suggested through different findings [28].

In the present work, we have singled out a novel mutation, the K417N, which is present within the RBD region of SARS CoV2 protein. Further, in the structural analysis, we found that the mutant structure is neutral mutation as compared to RBD region of wild type. Thus, the replacement of K417 by N (South African strain) seems relatively neutral in protein expression level while not very favorable for the interaction with ACE2. Moreover, it was also found unstable due to loss of cysteine bridge. Cysteine bridge is used to initiate a basic element in the molecular construction of peptides and proteins required, e.g., in acting as toxins or in basic biological procedures[29]. Thus, it was found missing in mutant structure, which results in instability.

Further, for comparative analysis of RBD (mutant vs. wild type), molecular dynamic simulation was also performed to study the protein dynamic and structural flexibility. In dynamics posture, protein reveals various conformational modifications for a particular function, where correlative movement provides an essential role in binding and recognizing different biological macromolecules, and this movement is mainly hampered by the mutation [30]. The RMSF scores of C-alpha chain atoms of RBD wild type revealed the critical fluctuations in flexibility and stability compared to mutant type. In addition, some findings revealed the instability of the spike protein structure before ACE2 receptor binding by investigating the framed mutations' effect. We found that the RMSF values of wild-type protein structure are lower than variant and certifies the compressed nature of spike protein trajectory.

The RBD is present in the spike glycoprotein (S1 subunit) and is essential for interconnecting with the SARS-CoV-2 cellular receptor angiotensin-converting enzyme-2 (ACE2) [31]. The ACE2 interaction region of the RBD is a remarkably small 25-amino-acid area present at the tip of the RBD [32], and due to its pivotal role in the attachment of virus, it is also the area for various potential neutralizing antibodies binding [33]. Thus, inhibiting RBD-ACE2 interaction plays the main role in natural and induced vaccine protection from SARS-CoV-2 contagion. Furthermore, various such mAbs (monoclonal antibodies) have been found to form cocktails that are being processed in advanced clinical trials of SARS-CoV-2 prophylaxis and treatment [34].

Moreover, efficient binding with the ACE2 receptor was also carried out in the present study using the protein-protein docking mechanism. It was found that wild type can bind with the hACE2 receptor more efficiently than the Delta plus variant, which signifies that wild type spike protein is more virulent compared to Delta plus variant both structurally and functionally. Further, to find the therapeutics against Delta plus variant, antigen-antibody related docking studies revealed BD-23 Fab was more effective against Delta plus variant.

Some studies related to superimposition of SARS-CoV-2 RBD/ACE2 structural complex and SARS-CoV-2 RBD/BD-23 structural complex revealed that BD-23 could conflict with ACE2 to obstruct the RBD-ACE2 binding, providing the neutralizing effect of BD-23 with the SARS-CoV-2 [35]. Research is still ongoing in India and worldwide to find the efficacy of vaccines against this variant. The Delta variant has mutated to establish the Delta plus or AY.1 variant (B.1.617.2.1). Recent findings indicate the evidence of resistance of antiSARS-CoV-2 therapeutic such as monoclonal antibody cocktail Casirivimab and Imdevimab against Delta plus variant, formulated by Regeneron and Roche[36], which was indicated by our findings also.

Conclusion

Using multiple computational tools Delta plus variant was analyzed structurally, which revealed that this type of mutation is neutral, with cysteine bond loss that causes a severe effect on the 3D structure of protein. Moreover, compared with the wild type, the K417N variant structure is also unstable. Moreover, functional analysis revealed that K417N variant structure binding affinity against hACE2 receptor is

slightly lower than wild type. Lastly, we performed antigen-antibody docking studies where BD-23 Fab monoclonal antibody was found to be therapeutic against Delta plus variant as revealed through its binding energy. The promising lead we recognized can also contribute information to vaccine development for the Delta plus variant protein.

Declarations

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Competing interests

The authors declare that they have no any conflict of interest.

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Figures

Figure 1

Mutagenesis creation of Delta plus variant: Using PYMOL software mutation was created in RBD sequence (K417N).

Figure 2

Cysteine bond loss observed after mutation: Using HOPE server disulphide bond loss was observed leading to instability of mutant structure.

Figure 3

A. Fluctuation plot of wild type structure: Using CABS-FLEX server RMSF values of each residues of wild type protein structure as fluctuation plot was retrieved. B. Fluctuation plot of mutant type structure: Using CABS-FLEX server RMSF values of each residues of mutant type protein structure as fluctuation plot was retrieved.

A.

Diagram illustrating the structure of a protein complex, showing various residues and their interactions. The structure is divided into two main regions by a dashed line.

Top Region (Green and Pink Residues):

- Asp157(E)** (Green)
- Asn159(E)** (Green)
- Ile151(E)** (Green)
- Leu156(E)** (Pink)
- Leu143(E)** (Pink)
- Cys141(E)** (Pink)
- Cys133(E)** (Pink)
- Gly147(E)** (Pink)

Bottom Region (Blue and Pink Residues):

- Asn354(A)** (Pink)
- Ser494(A)** (Pink)
- Ile468(A)** (Pink)
- Tyr449(A)** (Pink)
- Tyr451(A)** (Pink)
- Arg466(A)** (Blue)
- Asn450(A)** (Blue)

Key interactions and distances are highlighted:

- A green dashed line indicates a distance of **2.65** Å between the side chain of **Asn159(E)** and the side chain of **Asn450(A)**.
- A red dashed line indicates a distance of **3.17** Å between the side chain of **Asp157(E)** and the side chain of **Asn450(A)**.

A. Hydrogen bond interaction of wild type structure: Using DIMPLOT server hydrogen bond interaction was observed of wild type structure against hACE2 receptor. B. Hydrogen bond interaction of mutant type structure: Using DIMPLOT server hydrogen bond interaction was observed of mutant type structure against hACE2 receptor.

Figure 5

Antigen -Antibody complex structure: Complex structure of delta plus variant against each antibody complex after docking was retrieved.

Figure 6

Graphical representation of antigen – antibodies binding scores: Different binding scores of Delta plus variant against different antibodies was represented.

Figure 7

Interaction diagram of Delta plus variant against BD-23 Fab antibody: Different amino acid residues involved in antigen antibody interaction was retrieved through DIMPLLOT server.