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# Mutational Comparison and Structural Analysis of Omicron with Variants of SARS CoV Spike Protein

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**ABSTRACT**

For the past two years, the world has been devastated by COVID-19. Many people have died because of the SARS COVID-2 coronavirus. Research from South Africa has revealed the discovery of a new variant called Omicron (B.1.1.529). Because of the high number of mutations, this variant becomes an enormous threat to each country. This paper focuses on the comparison of omicron with several mutated SARS CoV-2. To recognize the transformation of the omicron variant, we took the few mutated SARS CoV 2 grouping data from NCBI database and correlate with the Omicron variant using the CLUSTAL OMEGA tool.

Keywords: Omicron, Corona virus, Delta variant, Alpha variant, Beta variant, Gamma variant, Clustal Omega.

## 1. Introduction

Human living standards around the world are being disrupted by a pandemic of severe acute respiratory syndrome (SARS-CoV-2). SARS-CoV-2 is a single-stranded RNA virus that is rapidly developing and constantly causing genomic transformations as it is communicated. Since the first human SARS-CoV-2 contamination in Wuhan in December 2019 a number of sub unitary protein antibodies were introduced to be used in humans. Corona virus is mutated into alpha, beta, gamma, delta. Contrasting with alpha, beta, gamma delta variant is rapidly spreading. The sensational inflow of Covid instances in India overpowered clinics and crematoriums and has been determined in atleast ninety-six nations. It has been classified as 55% more contagious than alpha. Significant genomic alterations that give rise to new variations represent one of the most challenging circumstances in the global management of this pandemic. Researchers from South Africa have published a new variant called Omicron (B.1.1.529). This mutation becomes a danger to all nations due to its sheer number of mutations. Omicron has many spike protein alterations. Confirmation indicates a high risk of re-infection with this variant. It is currently unknown how the Omicron variant spreads from one individual to another.

The substitution of Delta by Omicron as the variation in South Africa raises worries that the Omicron variation might be more contagious than Delta, however because of the low number of cases in South Africa were identified. Examination of spike protein indicates that omicron variants is probably going to have expanded transmission in contrast to initial SARS-CoV-2 infection. The risk can be minimized by wearing very suitable cloaks, keeping hands clean, physical distancing, maintaining indoor ventilation, avoiding crushing, and immunizations.

## 2. Symptoms:

So far, the Omicron symptoms are mild compared to those of the Delta variant. Loss of smell and taste are the symptoms of COVID-19 (particularly Delta), is unknown in Omicron's case. A strange symptom of the Omicron variant is inappropriate night sweats. Patients infected with the new variant have additionally mentioned to have “scratchy” throats alternatively of “sore” throat.

## 3. Different types of variants of SARS-CoV 2:

### *3.1 Alpha (B.1.1.7)*

The alpha variant was first being observed on Sep 2020 and the alpha variant of the Covid emerged in southeast England, and is regularly known as B.1.1.7. The variation is 1.5 times more infectious than earlier Coronavirus. The alpha variation has 12 mutations contrasted with the first SARS-CoV-2 infection. Eight of these change the state of the infection's external spike protein. They are N501Y, 69del, 70del, 144del, E484K, S494P, A570D, D614G, P681H, T716l, D1118H, and S982A.Out of these three are deletions and remaining are non-synonymous. The remarkable qualities of this variation of concern incorporate a 50 percent expanded transmission and there is a possible increase in seriousness.

### *3.2 Beta (B.1.351)*

The beta variant was first distinguished in South Africa. This variant is normally arisen with enormous number of transformations. As the variation spreads quicker than other earlier variations and consequently it led to the pandemic in the country. This variation is spreading globally more than 48 distinctive countries the variation was identified in at least 23 states. There are 9 pointable mutations specifically 18L→F, 80D→A, 215D→G, 246R→I, 417K→N, 484E→K, 501N→Y, 614D→G, 701A→V and one deletion LAL 242−244 del.

This entire genome sequencing demonstrated that, during the review time frame, the beta lineage addressed 95% of all heredities containing transformations are at positions 417 and 484 in the Spike glycoprotein. Next the viability of the BNT162b2 mRNA immunization against contamination with the beta variation and serious illness were done and it produces effective results.

### *3.3 Gamma (P.1)*

The gamma VOC was first identified in the city of Manaus and has been a mutated version of Covid-19 resurgence in Brazil and across South America in January 2021.Here there are 12 mutations namely L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, D614G, H655Y, T1027I, V1176F in the receptor binding domain of the spike protein. This variation contains the potential invulnerable departure transformation (E484K).

The variation has demonstrated to be moderately impervious to balance by recuperating plasma and vaccine sera later Moderna or Pfizer immunization. In any case, the size of the loss was small. The review was led among almost 70,000 medical care laborers in Manaus, which was the focal point for the development of the P.1 variation. Corona Vac (inactivated immunization) was demonstrated to be half viable in preventing disease 14 days from the date of first dose.

### *3.4 Delta (B.1.617.2)*

The Delta variety, in any case called B.1.617.2, can spread even more successfully, according to WHO. The strain has changes on the spike protein that simplify it for it to corrupt human cells. That suggests people may be more irresistible accepting they contract the contamination and even more viably spread it to others. The Delta variety is around half more irresistible than the Alpha variety, which was first perceived in the U.K and Alpha, in any case called B.1.1.7, was by then half more irresistible than the primary Covid initially recognized in China in 2019.

The Delta Plus variation, otherwise called B.1.617.2.1 or AY.1, is viewed as a "subvariant" of the Delta rendition. It has a transformation that permits the infection to attack the lung cells. The Delta genome has 17 transformations four mutations in the NTD (T19R, G142D, Δ156–157 and R158G), two in the RBD (L452R and T478K), one mutation close to the furin-cleavage site (P681R) and one in the S2 region (D950N). The only preventive measure is getting vaccinated.

## 4. Spike protein(S) –The structure and its Function:

The S proteins are clove-shaped single-stranded RNA-enveloped virus performs a vital part in the receptor recognition and cell layer combination process, and is made out of two subunits, S1 and S2. The SARS-CoV-2 contains 1273 amino acids and comprises of a signal peptide situated at the N-end, the S1 subunit, and the S2 subunit. The S1 subunit contains N-terminal and a receptor-binding domain; the S2 subunit includes the Fusion peptide (FP), hepta peptide repeat sequence1 (HR1), HR2, TM space and cytoplasm domain.

The virus particles ties on the outer layer of the host cell and that is the initial step of virus infection. RBD binds to ACE2. ACE2 is a sort I indispensable film protein that works as a carboxy peptidase, separating angiotensin II to angiotensin controlling pulse. The infection ties to ACE2 on the host cell (lungs, heart, and so forth) for infection passage and ensuing pathogenesis, results in serious respiratory disease. The Sprotein-ACE2 association is an obvious objective for immunizations.

First it is injected at the surface and can be perceived straight by the host safe system. Second, it intercedes the cooperation with the host cell restricting to the ACE2 receptor, which is fundamental for resulting infection passage into target cells resulting pathogenicity. The anatomical parts inside the S2 subunit incorporate three long α -helices, various α -helical sections, expanded turned C -sheets, layer traversing α -helix, and an intracellular cysteine-rich section. The shape of the SARS-CoV-2 S protein has been identified using cryo-electron microscopy.

# *5.Tools and Methods:*

### *5.1 Clustal Omega:*

Clustal is a PC program utilized in bioinformatics for adjusting different nucleotide or protein arrangements in an effective way. Clustal omega has most wide variety of operating systems out of all the tools. Clustal Omega is consistency based and is broadly considered to be one of the quickest online executions of all numerous arrangement tools and still position high in precision.

### *5.2 Multiple Sequence alignment:*

- The program requires at least three arrangements to compute the different grouping arrangement for two successions use pairwise arrangement

devices.

- Look at all arrangements in pair insightful.
- Performs bunch examination on pairwise to produce order for arrangement. This might be in a twofold tree or a straightforward requesting.
- Assemble the various arrangement by first adjusting the most comparative pair of successions then the following most comparative pair, etc.

***5.3 RASMOL:***

The product used to inspect and show structure data of biomolecules like aminoacids and proteins are called perception apparatuses. Rasmol is one of the protein structure representation instruments. Rasmol is a molecular illustrations program proposed for the perception of proteins, nucleic acids and little atoms. The program is pointed toward display, teaching and age of distribution quality pictures. The program peruses in sub-atomic direction documents and intelligently shows the particle on the screen in an assortment of portrayals and shading plans. It tt in the takes input as protein information bank, Mol2 design, MDL organization and Charm design. It gives the result of atoms bond development [34].

***5.4 NCBI:***

NCBI, National Center for Biotechnology Information. It is a piece of public library of medication at public establishment of wellbeing. It is the improvement of programming apparatuses for arrangement examination and disperse biomedical data. Its job is to keep up with natural data sets whether essential or auxiliary. It incorporates GENEBANK. NCBI gives the information recovery frameworks like ENTREZ. It gives the computational sources to the examination of the GENEBANK information and other organic information [35].

***5.5PDB:***

Protein data bank is a data set for the three-dimensional design information of enormous natural atoms like proteins and nucleic acids. The information ordinarily got by X beam crystallography, NMR Spectroscopy and cryo-electron microscopy. The information is uninhibitedly open on the web by means of the sites of its part associations. The PDB is supervised by an association called the Worldwide Protein Data Bank or wwPDB .

## 6.Result and Discussion:

***6.1 Mutated variants in their region:***

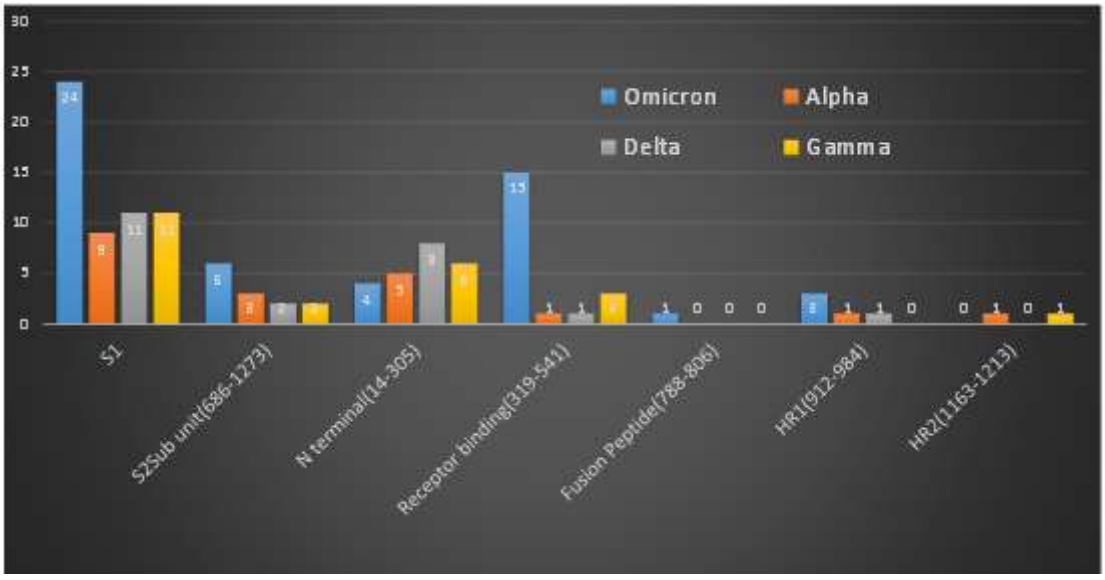


**Fig 2-No of Mutated variants in Spike Protein region**

This graph represents the majority of CoV-2 mutational variants (omicron, alpha, delta, gamma) in specific parts of the spike protein region. The S protein is composed of the S1 and S2 subunits. For omicron, there are 24 mutations in the S1 subunit and approximately 11 mutations in delta and gamma. The S1 subunit consists of an N-terminal domain and a receptor binding domain. In the N-terminal domain, the delta variant has multiple mutations. Similarly, for RBD, the omicron mutations are larger. The S2 unit (686-1273) has several subdivisions: fusion peptides, HR1, HR2, CH, CT, TM, and CT. Here we mainly concentrate on the fusion peptides, HR1 and HR2. There are no mutations in the gamma variant in the HR1 portion and no changes in the omicron and delta variants in the HR2 portion. In fusion peptides, the modification occurs only at the omicron

***6.2 Comparison of omicron with mutated variants in SARS CoV-2 using CLUSTAL OMEGA***

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UFO69279.1        MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS   60
UFL16569.1        MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS   60
UFP15886.1        MFVFLVLLPLVSSQCVNLRTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS   60
YP_009724390.1    MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS   60
UFJ45321.1        MFVFLVLLPLVSSQCVNFTNRTQLPSAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS   60
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UFO69279.1        NVTWFHVI--SGTNGTKRFDNPVLPFNDGVYFASIEKSNIIRGWIFGTTLDSKTQSLLIV   118
UFL16569.1        NVTWFHAI--SGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIV   118
UFP15886.1        NVTWFHAIHVSGTNGTTRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIV   120
YP_009724390.1    NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIV   120
UFJ45321.1        NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIV   120
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UFO69279.1        NNATNVVIKVCEFQFCNDPFLD---HKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLE   175
UFL16569.1        NNATNVVIKVCEFQFCNDPFLGVY-HKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLE   177
UFP15886.1        NNATNVVIKVCEFQFCNDPFLDVYYHKNNKSWMES--GVYSSANNCTFEYVSQPFLMDLE   178
YP_009724390.1    NNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLE   180
UFJ45321.1        NNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLE   180
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UFO69279.1        GKQGNFKNLREFVFKNIDGYFKIYSKHTPIIVREPEDLPQGFSALEPLVDLPIGINITRF 235
UFL16569.1        GKQGNFKNLREFVFKNIDGYFKIYSKHTPINL--VRDLPQGFSALEPLVDLPIGINITRF  235
UFP15886.1        GKQGNFKNLREFVFKNIDGYFKIYSKHTPINL--VRDLPQGFSALEPLVDLPIGINITRF  236
YP_009724390.1    GKQGNFKNLREFVFKNIDGYFKIYSKHTPINL--VRDLPQGFSALEPLVDLPIGINITRF  238
UFJ45321.1        GKQGNFKNLSEFVFKNIDGYFKIYSKHTPINL--VRDLPQGFSALEPLVDLPIGINITRF  238
                  ********* ********************* :  .************************

UFO69279.1        QTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSE   295
UFL16569.1        QTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSE   295
UFP15886.1        QTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSE   296
YP_009724390.1    QTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSE   298
UFJ45321.1        QTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSE   298
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UFO69279.1        TKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFDEVFNATRFASVYAWNRKRI   355
UFL16569.1        TKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRI   355
UFP15886.1        TKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRI   356
YP_009724390.1    TKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRI   358
UFJ45321.1        TKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRI   358
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UFO69279.1        SNCVADYSVLYNLAPFFTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGNI   415
UFL16569.1        SNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGKI   415
UFP15886.1        SNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGKI   416
YP_009724390.1    SNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGKI   418
UFJ45321.1        SNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGTI   418
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UFO69279.1        ADYNYKLPDDFTGCVIAWNSNKLDSKVSGNYNYLYRLFRKSNLKPFERDISTEIYQAGNK   475
UFL16569.1        ADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGST   475
UFP15886.1        ADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYRYRLFRKSNLKPFERDISTEIYQAGSK   476
YP_009724390.1    ADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGST   478
UFJ45321.1        ADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGST   478
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UFO69279.1        PCNGVAGFNCYFPLRSYSFRPTYGVGHQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKC   535
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UFL16569.1        PCNGVEGFNCYFPLQSYGFQPTYGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKC  535
UFP15886.1        PCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKC  536
YP_009724390.1    PCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKC  538
UFJ45321.1        PCNGVKGFNCYFPLQSYGFQPTYGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKC  538
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UFO69279.1        VNFNFNGLKGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVI  595
UFL16569.1        VNFNFNGLTGTGVLTESNKKFLPFQQFGRDIDDTTDAVRDPQTLEILDITPCSFGGVSVI  595
UFP15886.1        VNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVI  596
YP_009724390.1    VNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVI  598
UFJ45321.1        VNFNFNGLTGIGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVI  598
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UFO69279.1        TPGTNTSNQVAVLYQGVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEYVNN  655
UFL16569.1        TPGTNTSNQVAVLYQGVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNN  655
UFP15886.1        TPGTNTSNQVAVLYQGVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNN  656
YP_009724390.1    TPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNN  658
UFJ45321.1        TPGTNTSNQVAVLYQGVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEYVNN  658
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UFO69279.1        SYECDIPIGAGICASYQTQTKSHRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNF  715
UFL16569.1        SYECDIPIGAGICASYQTQTNSHRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPINF  715
UFP15886.1        SYECDIPIGAGICASYQTQTNSRRRVRSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNF  716
YP_009724390.1    SYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNF  718
UFJ45321.1        SYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNF  718
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UFO69279.1        TISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLKRALTGIAVEQDKNT  775
UFL16569.1        TISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNT  775
UFP15886.1        TISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNT  776
YP_009724390.1    TISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNT  778
UFJ45321.1        TISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNT  778
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UFO69279.1        QEVFAQVKQIYKTPPIKYFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYG  835
UFL16569.1        QEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYG  835
UFP15886.1        QEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYG  836
YP_009724390.1    QEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYG  838
UFJ45321.1        QEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYG  838
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UFO69279.1        DCLGDIAARDLICAQKFKGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPF  895
UFL16569.1        DCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPF  895
UFP15886.1        DCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPF  896
YP_009724390.1    DCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPF  898
UFJ45321.1        DCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPF  898
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UFO69279.1        AMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNHNAQA  955
UFL16569.1        AMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQA  955
UFP15886.1        AMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQNVVNQNAQA  956
YP_009724390.1    AMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQA  958
UFJ45321.1        AMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQA  958
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UFO69279.1        LNTLVKQLSSKFGAISSVLNDIFSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI  1015
UFL16569.1        LNTLVKQLSSNFGAISSVLNDILARLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI  1015
UFP15886.1        LNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI  1016
YP_009724390.1    LNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI  1018
UFJ45321.1        LNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI  1018
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UFO69279.1          RASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTA 1075
UFL16569.1          RASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTA 1075
UFP15886.1          RASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTA 1076
YP_009724390.1      RASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTA 1078
UFJ45321.1          RASANLAAIKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTA 1078
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UFO69279.1          PAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVY 1135
UFL16569.1          PAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTHNTFVSGNCDVVIGIVNNTVY 1135
UFP15886.1          PAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVY 1136
YP_009724390.1      PAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVY 1138
UFJ45321.1          PAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVY 1138
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UFO69279.1          DPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLI 1195
UFL16569.1          DPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLI 1195
UFP15886.1          DPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLI 1196
YP_009724390.1      DPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLI 1198
UFJ45321.1          DPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASFVNIQKEIDRLNEVAKNLNESLI 1198
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UFO69279.1          DLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDE 1255
UFL16569.1          DLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDE 1255
UFP15886.1          DLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDE 1256
YP_009724390.1      DLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDE 1258
UFJ45321.1          DLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDE 1258
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UFO69279.1          DDSEPVLKGVKLHYT 1270
UFL16569.1          DDSEPVLKGVKLHYT 1270
UFP15886.1          DDSEPVLKGVKLHYT 1271
YP_009724390.1      DDSEPVLKGVKLHYT 1273
UFJ45321.1          DDSEPVLKGVKLHYT 1273
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The above data represent alpha, beta, gamma, reference, and omicron sequences. Sequences were placed in the Clustal Omega tool where multiple sequence alignments were performed. Mutated ones are highlighted in red. This comparison reveals that the omicron variant has more mutations in the spike region.

## 7. Interpretation:

The sequence (omicron, alpha, delta, and gamma) containing 1273 amino acids S proteins of SARS-CoV-2 is taken from NCBI website. The variants of corona virus sequences are compared to the reference sequence (YP_009724390.1) shifted from 99.7 to 100%, showing consequently a serious level of preservation. In omicron, nearly 40% of these sequences were identical to the reference sequence, while the remaining 60% indicates a single transformation. There are around 30 mutations namely 67A→V, 95T→I, 142G→D, 212L→I, 339G→D, 373S→P, 375S→F, 417K→N, 440N→K, 446G→S,477S→N,478T→K,484E→A,493Q→R,496G→S,498Q→R,501N→Y,505Y→H,547T→K,614D→G,655H→Y,679N→K,681P→H,764N→K,796D→Y,856N→K,954Q→H,969N→k and 981L→F.

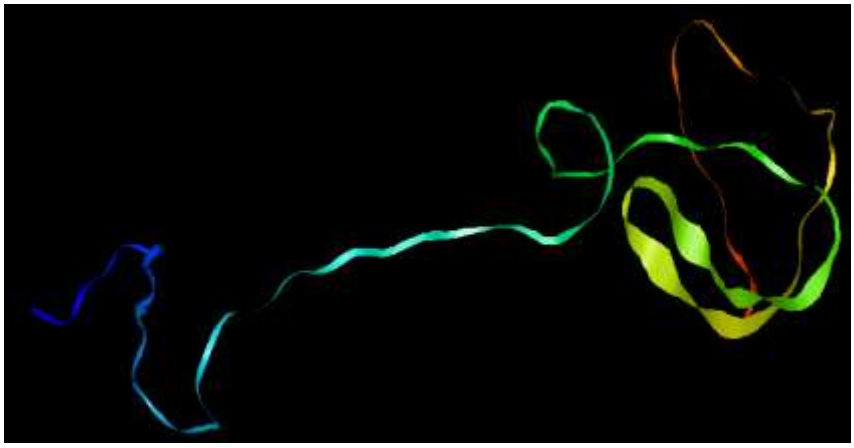

Fig 2. Structural visualization of mutated variant using RASMOL

In comparison with omicron two mutations are common in alpha and gamma (D614G, N501H). In Omicron five mutations matches with delta (T95I, G142D, K417N, T478K, D614G). Numerous mutations were found to occur in the S1 subunit (14-685). S1-NTD of SARS-CoV-2 is very similar to the Omicron (although it generally shares 5% changes and 95% similarities with SARS-CoV). Residues of the RBD bind tightly to the peptidase space of ACE2 and this region is a key determinant of viral-receptor interactions, where approximately 15 residues are mutated. Variation of the fusion peptide occurred at 796. Hepta peptide the repeated sequence HR1 and HR2 only few changes were happened. In HR1 and HR2, it was evident that only minor changes occurred. From fig 2 we might predict that the omicron variant is a β-turn structure using Rasmol.

## 8. Conclusion:

We compiled the NCBI protein database of different variants of SARS CoV 2. From this analysis, we found that omicron variant contains a large number of mutations, but its cause of seriousness was low compared to Delta variants. According to reports, the Omicron variant has 4.2 times more transfer potential than Delta variant. Currently, due to lack of data there are no confirmed reports of the severity of Omicron.

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