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Estimations of Ferets and Three dimensions on Two Dimensional Plane of COVID-19 SEMwith Image J Nano-Particles Software.

Olabimtan O.H*[1], Sherice Malagon .K[2],Batari Musa .L[3], Muhammad Aliyu[4], Orijajogun Omohu.J[5]&Agboni Mercy.O[6]

[1]National Research Institute for Chemical Technology, Department of Industrial and Environmental Pollution Zaria Kaduna State, Nigeria.
[2]Western Governors University 4001-700E, 700Salt Lake City UT 84107, USA.
[3]National Research for Chemical Technology, Department of Scientific and Industrial research Zaria Kaduna State, Nigeria
[4]Zamfara College of Arts and Science, Department of Computer Science and Information Technology, Gasau Zamfara State, Nigeria.
[5]Sheda Science and Technology, Chemistry Advanced Research Center Abuja, Nigeria.
[6]Ogel Research and Services, Zaria Kaduna State, Nigeria.

Corresponding author email: Olabode4angel@gmail.com.

Abstract: *Nanoscale Image J java software was successfully applied for estimating the ferret, (2 and 3) dimensional sizes of COVID-19. These were coordinated with 100nm scale magnifications with Scanning electron microscopy (SEM) and at 155.2028 pixels/nm in distance with the software. Three distinct cells of the virus with protein spikes (A, B, C) and without protein spikes (1, 2, and 3) were analyzed for areas (2D), volumes (3D) and the standard mean of the structures.*
The ferets against the non-protein spiked area (R^2=0.6540), protein spiked area (R^2=0.9724), non-protein spiked volume (R^2=0.9996) and protein spiked volume (R^2=0.9881) show remarkable and significant interactions.
These conclusively characterized the virus concerning the selected dimensions at Nanoscale level; giving an empirical basis to the inhibition and deactivation of the virus with synthetic Nanoparticles.

Keywords: COVID-19;Nano-image J software; 2 & 3dimensions; ferret and SEM**.**

1.0 INTRODUCTION

Human coronaviruses were initially recognized at the end of the 1960s [1]. The most former ones found were an irresistible bronchitis infection in chickens and two in human patients with the normal cold which was later named human coronavirus 229E OC43, as different species from this family have since been distinguished as SARS-CoV(2003), HCV NL63(2004), HKU1(2005), MERS-CoV(2012),nCoV(2019) and SARS-CoV(2019)[2]. The name "coronavirus" is gotten from Latin crown, signifying "crown" or "wreath", alluding to the trademark appearance of virions which is the infective type of the infection defined by electron microscopy with an edge of huge, bulbous surface projections making an image indicative of a crown or sunshine based crown. This morphology is made by the viral spike peplomers, which are proteins surrounding the virus [3]. Coronaviruses are vast pleomorphic round particles with globular surface projections. The scale of the infection particles is around 120 nm despite an undisclosed amplification with the scanning electron microscopy [3].

The envelope of the infection in electron micrographs shows up as a specific pair of electron-thick shells. The viral envelope comprises a lipid bilayer where the membrane layer (M), envelope (E) and spike where (S) auxiliary proteins are secured. A subset of coronaviruses explicitly the beta coronavirus subgroup A additionally has a shorter spike-like surface protein called hemagglutinin esterase (HE) [3].

Inside the envelope, there is the nucleocapsid, which is framed from different duplicates of the nucleocapsid (N) protein, which are bound to the positive-sense single-stranded RNA genome in a nonstop string type networks [4].The genome size for coronaviruses ranges from roughly 27 to 34 kilobases [5].The lipid bilayer envelope, layer proteins, and nucleocapsid secure the infection when it is outside the host cell. [6]

Human to human transmission of coronaviruses is fundamentally thought to happen among close contacts through respiratory droplets produced by sneezing and coughing. [7] The connection of the coronavirus spike protein with its supplement has cell receptor is focal in deciding the tissue tropism, infectivity, and species scope of the virus.[3] .The SARS coronavirus, for instance, contaminates human cells by appending to the angiotensin-changing over catalyst 2 (ACE2) receptor.[8] They are a cluster of infections that assault the upper and lower respiratory tracts in people and cause a scope of ailments to increasingly serious intense respiratory disorder (SARS) and the Middle East respiratory disorder (MERS) which are dangerous and lethal to health [9]. These infections can be transmitted by various types of creatures, including camels, felines, and presumably bats [10].In December 2019, a

pneumonia episode was accounted for in Wuhan, China on 31 December 2019, where the epidemic was linked to a novel strain of coronavirus, which was given the temporary name 2019-nCoV by the World Health Organization (WHO) and later renamed SARS-CoV-2 by the International Committee on Taxonomy of Viruses [11]. As of the 21st of March 2020, twenty-two (22) cases have been affirmed, two cases have been released from COVID-19 in Nigeria cases in the coronavirus pneumonia pandemic [12]. The Wuhan strain has been distinguished as another strain of Beta coronavirus from bunch 2B with around 70% hereditary closeness to the SARS-CoV [12]. The infection has a 96% closeness to a bat coronavirus, so it is generally suspected to start from bats also [13]. Given their high explicit surface structure and the chance of being functionalized with a wide scope of principal natural groups of nanomaterials like gold nanoparticles and carbon quantum dabs (CQDs) are potential antidotes for interfacing with infections and inhibiting their entrance into cells[9]. Lately, a gathering of specialists from the University of Lille, France, and Ruhr-University Bochum, Germany, demonstrated that the CQDs fictionalized with boronic acid ligands meddled with the capacity of coronavirus' S protein and altogether restrained its connection with the host cells [9]. Their examinations exhibited that the expansion of these nanomaterials to the phone culture medium, previously and during disease with coronavirus, impressively diminished the contamination rates with the cells. Amazingly, after one viral life cycle of 5.5 hours with coronavirus, an incredible inhibitory performance was observed at the viral replication step [9].The carbon quantum specks CQDs with a regular distance of 10 nm and phenomenal solvency in water can be an ideal contender for winning the fight against coronavirus, because they effectively enter the cell through endocytosis and cooperate with the infection's protein, accordingly forestalling viral genome replication [14]. Different nanomaterial has likewise been found with a similar antiviral impact. For example, a Chinese research group has built up a novel class of peptide inhibitors dependent on gold Nanorods, which specifically focus on coronavirus' S protein and upset its activities [15]. Moreover, the coronavirus immunization has as of late been set up by methods in nanotechnology where the analysts of Shizuoka University, Japan, prevailed with regards to the integrating infection like particles (VLPs) as Nano vesicles utilizing bug cells. These particles are fundamentally the same as coronavirus, then again, actually they don't have the infection genome; when they go into the host's cells, they animate the cells' insusceptible framework to battle the contamination brought about by this infection type [16]. To build up the coronavirus immunization in the referenced examination, the group communicated the auxiliary proteins of MERS coronavirus in silkworm hatchlings and Bm5 cells. The S protein of MERS coronavirus – without its transmembrane and cytoplasmic spaces was infused into the hemolymph of silkworm hatchlings and afterward sanitized through affinity chromatography. A short time later, the decontaminated proteins shaped the nanoparticles that had the option to append to the receptor of coronavirus called dipeptidyl peptidase 4 on the outside of the host cells. The E and M proteins were additionally communicated also, however, a significant point to consider was the way that the S protein could be activated given that it was completely shown on the VLPs; henceforth, the specialists utilized surfactant treatment and mechanical expulsion techniques to create S-protein-showing Nano vesicles with distances across of around 100 to 200 nm. Eventually, the arranged VLP mimetic Nano vesicles end up being viable against MERS coronavirus, and to be sure it can be utilized as a nanoparticle-based immunization to battle the coronavirus outburst [9].ImageJ is a Java-based image program that was designed at the National Institutes of Health and the Laboratory for Optical and Computational Instrumentation (LOCI, University of Wisconsin) [17]. ImageJ was structured with open engineering that gives extensibility through Java modules and recordable macros [18]. Custom securing, investigation and handling modules can be achieved with Image J software with Java compiler. Client composed modules make it conceivable to tackle many pictures preparing and examining issues, from three-dimensional live-cell imaging to radiological picture handling and various imaging framework information correlations with mechanized hematology frameworks. Image J module engineering and implicit advancement condition have made it a well-known stage for training image dimensions. [18] Hence, the two (Specific area) and three (Specific volume) dimensional estimations of COVID-19 with image J nanoparticles analyzer were explored and established with a clear objective of tailoring synthesized nanomaterial with specified conditions against the activities and potencies of this virus within the host cells.

2.0 MATERIAL AND METHODS

The SEM picture of COVID-19 as captured by CDC/Fred Murphy. [19]

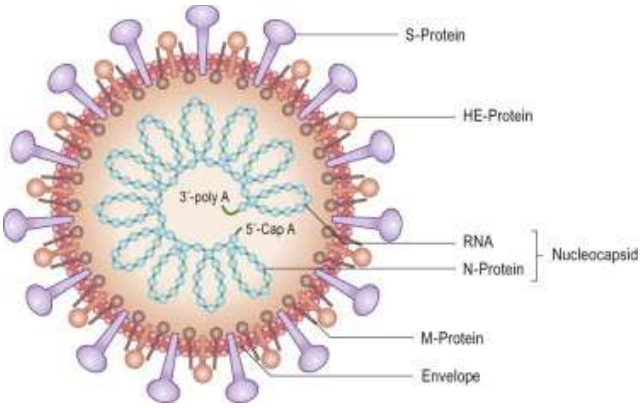
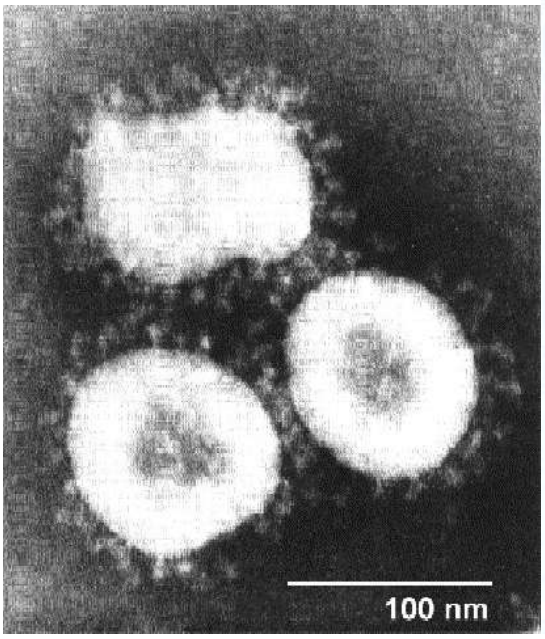


Figure 1.structure of COVID-19



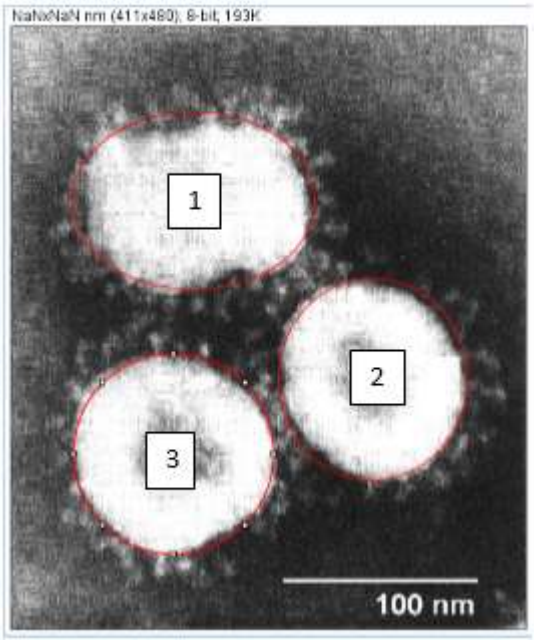


Figure 2. SEM of COVID-19.Figure 3. Image J highlights of COVID-19 specimen

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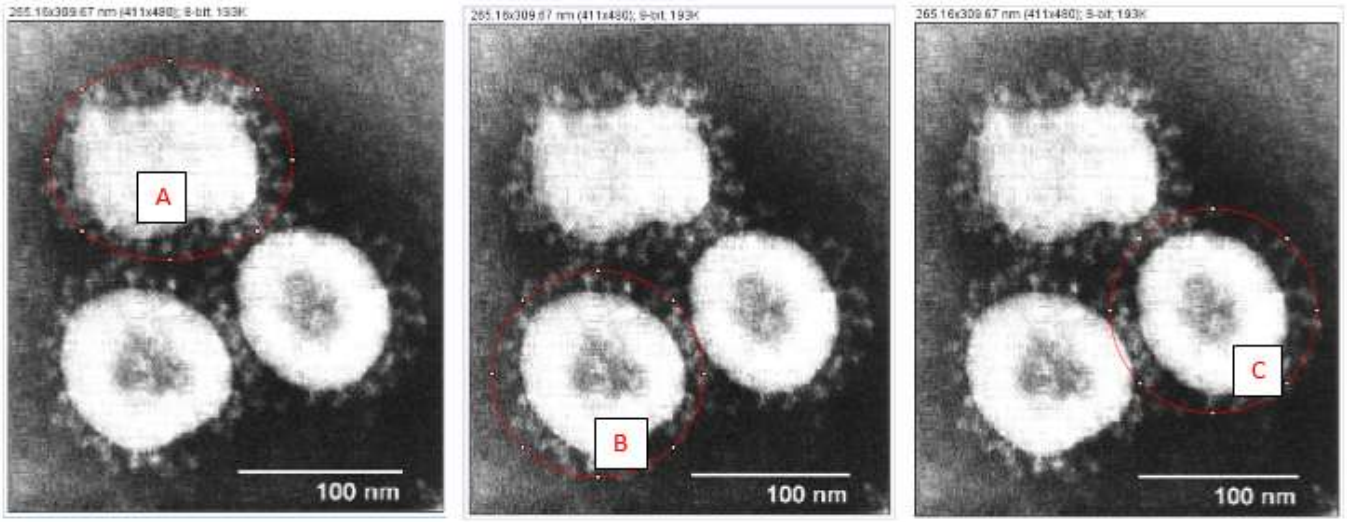

Figure 4. Image J highlights of COVID-19 protein spikes.

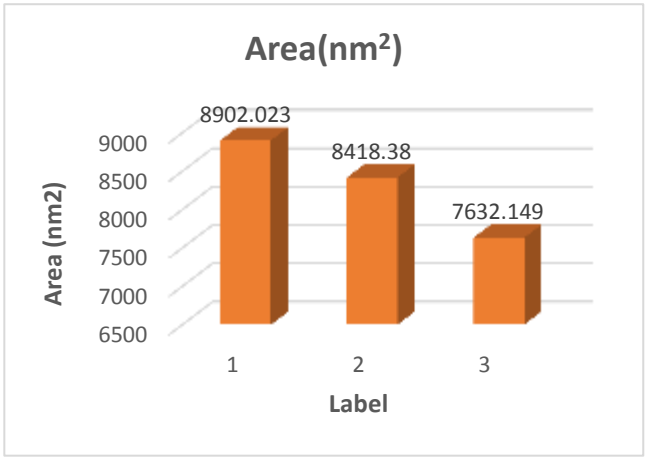

Figure 5.Area (2D) histogram of COVID-19 specimens Without protein spikes.

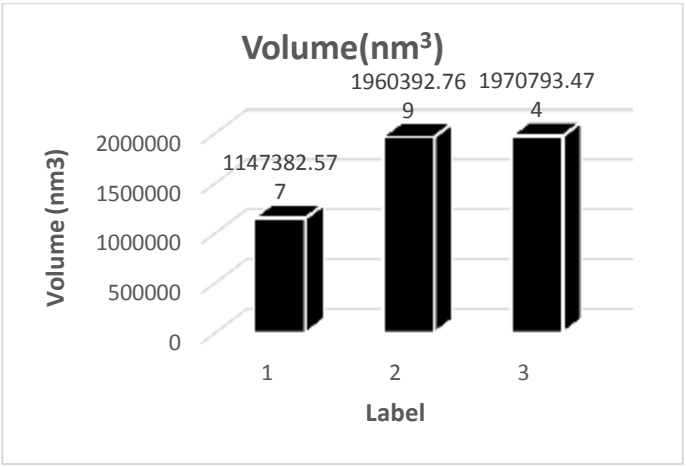

Figure 6. Volume (3D) histogram of COVID-19 Specimens without protein spikes.

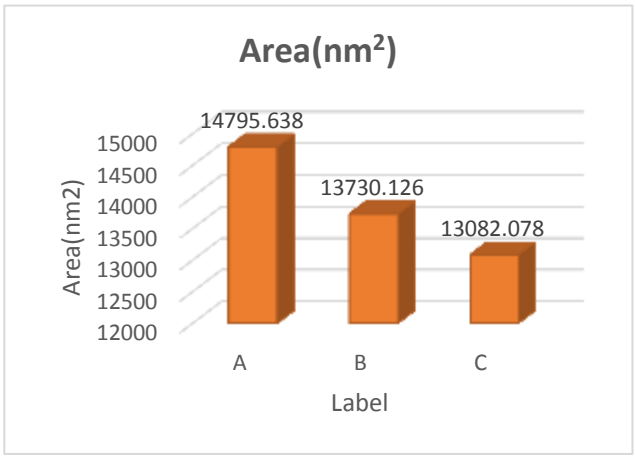

Figure 7.Area (2D) definitions with COVID-19 protein spikes.

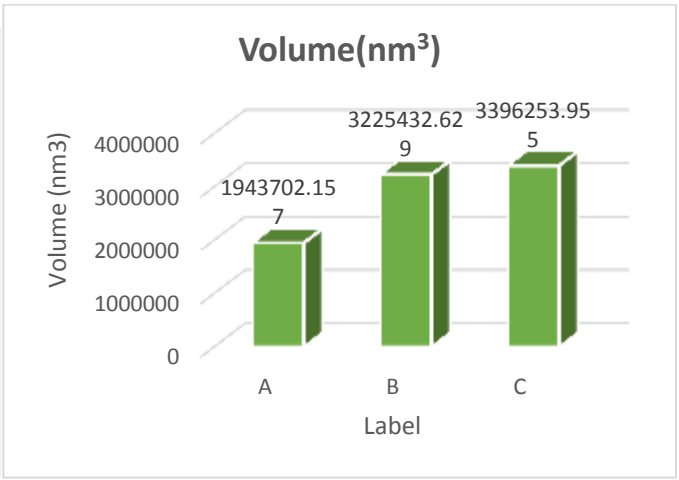

Figure 8. Volume (3D) definitions with COVID-19 protein spikes

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Table 1. COVID-19 Image-J results.

Label	Area(nm^2)	Mean	Std.Deviation	Feret	Volume(nm^3)
1	8902.0230	215.338	53.554	121.933	1147382.5770
2	8418.3800	219.254	49.502	104.514	1960392.7690
3	7632.1490	218.008	54.187	103.869	1970793.4740
A	14795.6400	164.724	79.789	149.674	1943702.1570
B	13730.1300	167.413	80.454	134.191	3225432.6290
C	13082.0800	156.743	89.119	129.675	3396253.9550

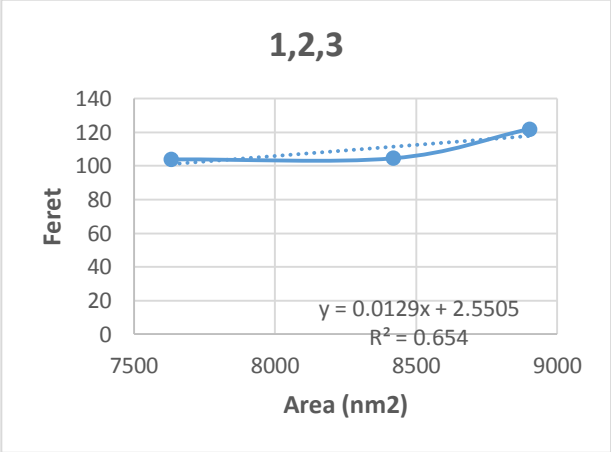

Figure 9. Feret with COVID-19 2D dimension without protein spikes

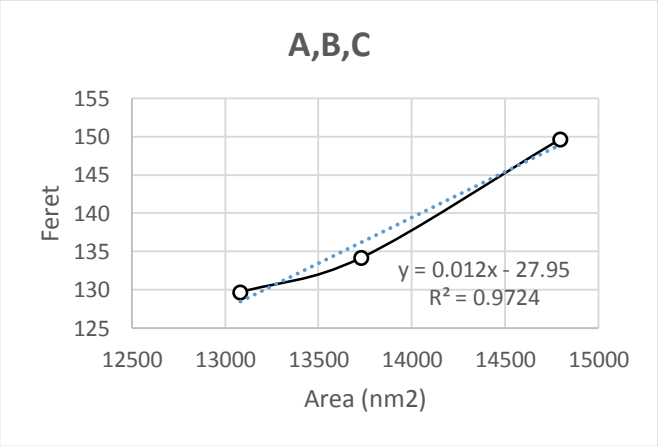

Figure 10. Feret with 2D COVID-19 protein spikes.

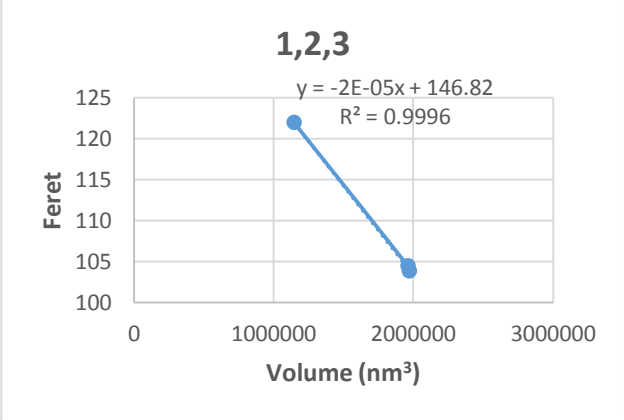

Figure 11. Feret with COVID-19 3D dimension.

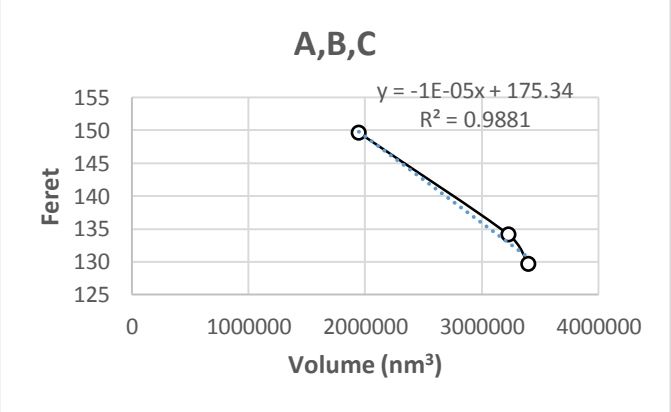

Figure 12. Feret with 3D COVID-19 protein spikes.

Figure 1 is the detailed and labeled structure of COVID-19 which was further elucidated with Scanning electron microscopy (SEM) at a magnification scale of 100nm (Figure 2). The three distinct specimens as captured by SEM were measured as indicated with the red circles (Figure 3) with image analyzer against the whitish central regions without spikes of proteins (1,2,3) and with the spikes of proteins in Figure 4 (A, B, C) which defines the 3D of the structures. Table 1 declares the outcomes with the image J analyzer of COVID-19 at 100nm, 155.2028 pixels and aspect ratio of 1.0. Labels 1, 2, and 3 denote structures without protein spikes and A, B, C with protein spikes. The areas (2D), volumes (3D) and the ferrets; the distance between the two planes that are parallel to each other which prevents any perpendicularity to the same direction were all estimated with the software. Figures 5 and 6 were the area (2D) and volume (3D) histograms of the COVID-19 specimens

acquired with the software. Figures 7 and 8 are the areas and volumes of the structures with the protein spikes around the virus. Figures 9, 10, 11 and 12 were the plots of ferret against the area (Non-protein spiked), area (protein spiked), volume (Non-protein spike) and volume of the protein spiked structures respectively.

3.0 CONCLUSION

COVID-19 has been estimated successfully with java based Nano-image analyzer at the specified condition. By advantage, dimension property like ferret as applied in particle size and distribution determinations typically for cells in tissue section [20] in microscopy on a two-dimensional plane was projected against the areas and volumes of these structures. This affirmed that two and three-dimensional properties do not necessarily alter and affect proportionally. The changes in the surface areas to volume ratio retains a significant implication to the constraints on the structures of the average COVID-19. This further interprets the structures as analyzed to be dynamic in their overall natures.

The partial objective of establishing a fundamental dimension of the virus at a Nanoscale level for the effective inhibitory approach of Nano-synthetic materials or particles against COVID-19 pandemic as it is being experienced presently in the global scene.

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