binding nature of spike proteins Receptor Binding Domain (RBD) of SARS-CoV-2 with the Receptor Binding Domain of human Angiotensin Converting Enzyme (ACE-2) receptor [2], is still a mystery among the real understanding powers. Coronavirus has four structural proteins including Spike (S) protein, envelope (E), nucleocapsid (N) and membrane (M) proteins. Among these, Spike (S) protein is considered to be its vital component in penetration and generation of viruses inside the host cell [3]. Structurally the Spike protein is divided into three major parts; Large ectodomain, Single pass transmembrane (TM) anchor and a short intracellular tail. Large ectodomain consists of Receptor binding subunit S1. During the entrance hour of coronavirus the S1 binds with the receptor of the host cell surface for viral attachment. Single pass Transmembrane anchor also known as Membrane-fusion is consists of subunit S2, which helps to fuse or break the cell membrane of surface host cell through receptor, allowing viral genome to enter into the nucleolus portion of the host cell. The binding capacity of S protein of SARS-CoV-2 with RBD of ACE-2 receptor is found to be higher as compared to SARS CoV [4]. It binds with human ACE-2 receptor domain and impasses the permeability role of ACE-2 receptor. After getting entry into the host cell it controls and manipulate the role of DNA by restricting only to produce its viral copies as a consequence very soon it engulfs and dominates all the regions of lung's alveoli. This leads to massive infection of lungs "Pneumonia" and short breathing complications, even to the deaths. Li et al [5], published an article upon their submitted specific SARS coronavirus (SARS CoV) protein named as 2AJF protein, which binds with the RBD of ACE-2 receptor. It acts as an important mediator for the interaction between Spike protein (S) of coronavirus and Receptor binding domain of ACE-2 receptor. SARS-CoV-2 spike protein is formed by specific protein 7A93 [6]. This Spike protein is also known as Glycoprotein which has a potential to bind with ACE-2 receptor, penetrate the cell membrane and fused viruses into the host cell. The virus spike protein acts as a mediator for both receptor binding and the fusion activities of the membrane into the cell [7].

Computational approaches have been very useful to screen the drugs molecules and identify potential drug agent [8]. Protein-ligand docking has become very important source to authenticate the efficacy of drug designing researches [9]. Computer based docking programme is a popular method for the molecular docking studies [10]. The potential drug molecules can be understood by analyzing its binding capacity with the receptor (protein). Knowing the binding sites of the protein enhances the docking accuracy and efficiencies [11]. However, if binding sites of the polar residues are not known then may attain blind docking method, which is also one of the efficient method to understand the binding characteristics of proteins and ligands. In such situation blind docking is an essential method [12].

Short breathing also known as Dyspnoea [13] is one of the lethal indications exhibited as severe impacts after a median time of 5-8 days of COVID-19 patients [14,15]. One of the main symptom of COVID-19 is shortness of breath [16]. This symptom is analogous or complimentary to Aasthma. Shortness of breath in patient leads to suspects of Asthma [17]. Moreover, Asthma is alluded as potential risk factor among

the COVID-19 patients [18-22]. Newly mutated variant of COVID-19 causes Pneumonia in its earliest stage [23]. Taking these severe symptom of COVID-19, the study is done with an objective to understand the binding affinity of various inhibitors, which are mainly used during Asthma prolongations and Pneumonia complications. Active compounds responsible for contributing binding affinity or binding energy were screened by means of molecular docking analysis. To ensure and authenticate the potential drugs for SARS CoV and SARS CoV-2, the receptors protein of 2AJF and 7A93 were docked with 34 drugs-inhibitors in three major computational sources like AutoDock, AutoDock Vina programming and PyRx. The best docking scores were analyzed from within 34-drug molecules.

2. MATERIALS AND METHODS

2.1. Ligand target preparation

Thirty four (34) major Structure-Data files (SDF) of drug molecules including Aspirin, Bacampicillin, Beclomethasone, Bromhexine, Cefoxitin, Cephalosporin, Ciclesonide, Clopidogrel, Methylprednisolone, Cytarabine, Diclofenac, Fludarabine, Fluticasone propionate, Fluticasone, Formoterol, Ibuprofen, Levalbuterol, Metronidazole, Mometasone, Montelukast, Naproxen, Nelarabine, Penicillin, Prednisone, Pulmicort, Rifamycin, Salbutamol, Streptomycin, Sulfamerazine, Unii-yxv28V1B07 (Ceftobiprole medocaril), Vidarabine, Warfarin, Zafirlukast and Zileuton, were collected from PUBCHEM web sources (www.pubchem.ncbi.nlm.nih.gov). The SDF format files were converted to other necessary formats by means of Babel software.

2.2. Receptor (Protein) target preparation

The three dimensional PDB structures of Spike (S) receptor binding proteins domain 2AJF (PDB ID:2AJF) of SARS CoV and 7A93 (PDB ID:7A93) Spike Glycoprotein of SARS CoV-2 were retrieved from the Protein Databank database sources (www.rcsb.org). The docking study was done as per the blind docking method. Identification and location of binding sites were visualized in PyMOL and BIOVIA Discovery Studio. The docking of protein-ligands were further validated with AutoDOCK, AutoDOCK VINA programming and PyRx softwares with determination of RMSD (Root Mean Square Deviation) score values [24].

2.3. Molecular docking analysis

All together 204 computational analysis were done among thirty four drug molecules individually with two proteins 2AJF and 7A93 respectively by using AutoDock 1.5.6, AutoDock VINA programming and PyRx-Python prescription 0.8. In PyRx the protein molecules (2AJF, 7A93) were loaded and converted into PDBQT (Protein Databank Charge and protein type) through make macromolecules exploration. The SDF inhibitors were inserted turn wise manner and converted into PDB format and

then into Autodock ligand format, which has formulated once again the file into PDBQT format. By means of Vina wizard protein-ligand docking was run in grid box dimensions of; Centre X: 286.048, Y:257.018, Z:278.8807, Dimensions (Angstrom) X: 95.1775, Y:77:6335, Z:182.4349. In AutoDock the blind docking were run in grid box dimensions; Centre X: 31.090 Y:5.481 Z:45.843, similarly in Autodock Vina programming X: -3.118513, Y: -14.726718, Z: 50.608410. The best Binding Energy (ΔG) or Binding Affinity (BA) conformation was chosen from all the docking results. The results were analyzed and saved in BIOVIA Discovery Studio.

In AutoDock vina configuration programme file was created and run docking through the prompt command option. From among the results the best binding affinity (BA) (kcal/mol) conformation was chosen. Similarly, the analysis was validated through AutoDock tools as well. GPF (Grid parameter file) files and DPF (Docking parameter file) files were created using Autogrid executive and Autodock executives respectively. DLG (Docking Log File) were also generated for all the protein-ligand docking activities and analyzed in Autodock. The best run conformation was determined and saved for the further analysis in PYMOL software. The location and distance of interacting polar amino acids and ligand were analyzed and saved.

3. RESULTS

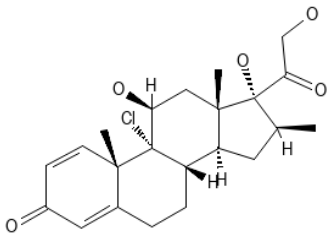
3.1. Computational analysis and result

Table 1. Binding energy attributed from the Protein-Ligand docking between spike (S) protein of 2AJF (SARS CoV), 7A93 (SARS-CoV-2) with 34 different asthmatic drug molecules.

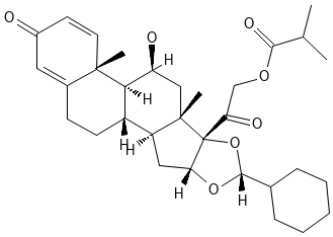
	2AJF (SARS CoV)			7A93 (SARS-CoV-2)		
Ligand molecules	**Autodock VINA (kcal/mol)**	**PyRx**	**AutoDock**	**Autodock VINA (kcal/mol)**	**PyRx**	**AutoDock**
Aspirin	-5.7	-5.4	-6.37 (Run-2)	-5.6	-4.1	-5.08 (Run-7)
Bacampicillin	-7.6	-7.3	-8.35 (Run-5)	-5.7	-5.9	-5.39(Run-7)
Beclomethasone	**-8.0**	**-7.9**	**-9.48 (Run-3)**	**-6.1**	**-6.7**	**-6.68 (Run-5)**
Bromhexine	-6.7	-5.2	-7.86 (Run-1)	-5.2	-4.6	-5.90 (Run-6)
Cefoxitin	-6.6	-6.8	-8.29 (Run-10)	-6.3	-6.5	-5.50 (Run-2)
Cephalosporin	-6.8	-6.2	-6.03 (Run-10)	-5.6	-5.2	-2.75 (Run-5)
Ciclesonide	**-10.0**	**-10.1**	**-11.74 (Run-4)**	**-7.0**	**-8.0**	**-7.47 (Run-7)**
Clopidogrel	-6.7	-6.6	-6.88 (Run-4)	-5.1	-5.7	-5.87 (Run-1)
Methylprednisolone	**-7.4**	**-8.2**	**-8.37 (Run-2)**	**-5.8**	**-6.9**	**-6.74 (Run-2)**
Cytarabine	-6.6	-6.6	-8.71 (Run-4)	-4.8	-6.3	-5.10 (Run-3)

	2AJF (SARS CoV)			7A93 (SARS-CoV-2)		
Ligand molecules	**Autodock VINA (kcal/mol)**	**PyRx**	**AutoDock**	**Autodock VINA (kcal/mol)**	**PyRx**	**AutoDock**
Diclofenac	-6.5	-6.7	-6.21 (Run3)	-5.8	-6.1	-4.99 (Run-3)
Fludarabine	-6.6	-6.7	-7.22 (Run-1)	-5.4	-5.7	-7.12 (Run-9)
Fluticasone propionate	-7.4	-7.4	-9.20 (Run-2)	-5.8	-6.8	-5.82 (Run-5)
Fluticasone	-7.6	-7.6	-9.05 (Run-1)	-6.4	-6.7	-6.75 (Run-6)
Formoterol	-7.6	-7.6	-7.80 (Run-3)	-6.4	-5.6	-5.31 (Run-4)
Ibuprofen	-6.6	-6.3	-7.15 (Run-1)	-5.8	-5.5	-4.73 (Run-7)
Levalbuterol	-6.6	-6.1	-6.75 (Run-6)	-6.3	-5.5	-5.54 (Run-3)
Metronidazole	-4.7	-4.7	-5.87 (Run-5)	-3.9	-5.2	-5.31 (Run-2)
Mometasone	-7.8	-7.7	-9.12 (Run-3)	-6.6	-6.8	-6.85 (Run-4)
Montelukast	**-9.6**	**-9.3**	**-5.18 (Run-6)**	**-6.8**	**-8.3**	**-4.77 (Run-3)**
Naproxen	-6.8	-6.8	-7.45 (Run-1)	-6.4	-6.4	-5.94 (Run-4)
Nelarabine	-6.7	-6.7	-10.01 (Run-6)	-5.0	-6.0	-5.92 (Run-8)
Penicillin	-7.1	-7.1	-10.44 (Run-1)	-6.6	-6.0	-5.92 (Run-8)
Prednisone	-7.8	-7.7	-9.63 (Run-4)	-6.4	-7.8	-6.91 (Run-2)
Pulmicort	**-7.2**	**-8.5**	**-8.25 (Run-3)**	**-6.1**	**-6.3**	**-6.42 (Run-1)**
Rifamycin	-6.6	-9.3	-6.27 (Run-1)	-6.3	-6.8	-7.55 (Run-10)
Salbutamol	-6.4	-6.2	-6.38 (Run-1)	-5.8	-6.0	-4.69 (Run-9)
Streptomycin	-6.8	-7.3	-8.58 (Run-1)	-6.2	-6.6	-4.37 (Run-5)
Sulfamerazine	-6.4	-6.7	-7.77 (Run-7)	-5.2	-6.0	-5.77 (Run-7)
Unii-yxv28V1B07	**-8.8**	**-9.2**	**-13.7 (Run-6)**	**-6.8**	**-8.1**	**-6.86 (Run-3)**
Vidarabine	-6.7	-6.4	-9.44 (Run-9)	-4.9	-5.6	-6.15 (Run-8)
Warfarin	-6.8	-6.9	-7.65 (Run-4)	-5.8	-6.2	-5.21 (Run-9)
Zafirlukast	**-9.4**	**-9.1**	**-7.93 (Run-3)**	**-7.0**	**-8.2**	**-6.08 (Run-10)**
Zileuton	-6.7	-6.7	-8.12 (Run-2)	-6.5	-5.6	-6.27 (Run-3)
Mean	-7.15	-7.20	-8.15	-5.92	-6.28	-5.81
Std. Deviation (SD)	1.06	1.2	1.74	0.70	0.98	0.98
Median	-6.8	-6.85	-8.02	-5.95	-6.15	-5.88
Standard Error (SE)	0.18 ±	0.20 ±	0.29 ±	0.12 ±	0.16 ±	0.16 ±

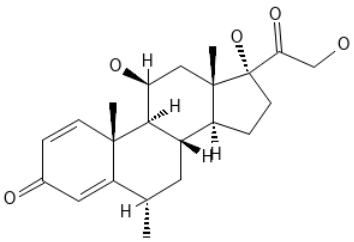
3.2. Molecular structures of top seven binding drug molecules



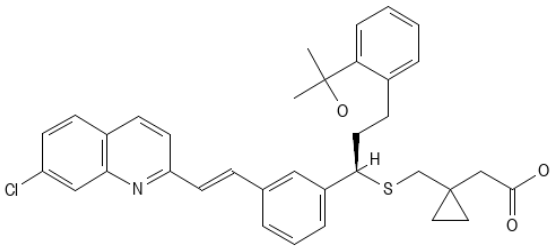
A. Beclomethasone



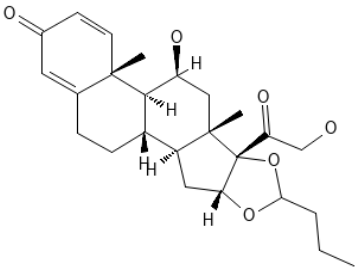
B. Ciclesonide



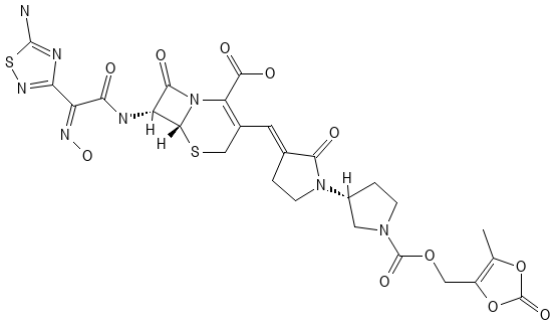
C. Methylprednisolone



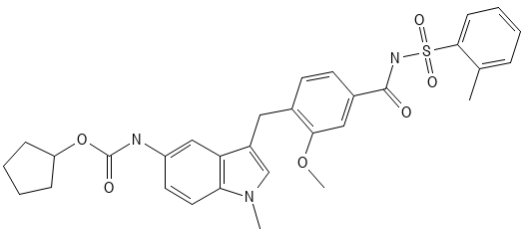
D. Montelukast



E. Pulmicort (Budesonide)



F. Unii-yxv28V1B07



G. Zafirlukast

Fig.1. Binding potential drug molecules: A. Beclomethasone (Formula: $C_{22}H_{29}ClO_5$), B. Ciclesonide (Formula: $C_{32}H_{44}O_7$), C. Methylprednisolone (Formula: $C_{22}H_{30}O_5$), D. Montelukast (Formula: $C_{35}H_{36}ClNO_3S$), E. Pulmicort (Formula: $C_{25}H_{34}O_6$), F. Unii-yxv28V1B07 (Formula: $C_{26}H_{26}N_8O_{11}S_2$), G. Zafirlukast (Formula- $C_{31}H_{33}N_3O_6S$).

3.3. Potential drug molecules

Table 2. Top seven (7) binding potential drug molecules against Spike (S) protein 2AJF (SARS CoV) and Spike (S) protein 7A93 (SARS CoV-2).

	2AJF (SARS CoV)			7A93 (SARS-CoV-2)		
Ligand molecules	**AutoDock VINA (kcal/mol)**	**PyRx**	**AutoDock**	**Autodock VINA (kcal/mol)**	**PyRx**	**AutoDock**
Beclomethasone	-8	-7.9	-9.48	-6.1	-6.7	-6.68
Ciclesonide	**-10**	**-10.1**	**-11.74**	**-7.0**	**-8.0**	**-7.47**
Methylprednisolone	-7.4	-8.2	-8.37	-5.8	-6.9	-6.74
Montelukast	-9.6	-9.3	-5.18	-6.8	-8.3	-4.77
Pulmicort	-7.2	-8.5	-8.25	-6.1	-6.3	-6.42
Unii-yxv28V1B07	**-8.8**	**-9.2**	**-13.7**	**-6.8**	**-8.1**	**-6.86**
Zafirlukast	-9.4	-9.1	-7.93	-7	-8.2	-6.08
Mean	-8.62	-8.9	-9.23	-6.51	-7.5	-6.43
Std. Deviation (SD)	1.11	0.75	2.77	0.49	0.83	0.84
Median	-8.8	-9.1	-8.37	-6.8	-8	-6.68
Standard Error (SE)	0.41 ±	0.28 ±	1.04 ±	0.18 ±	0.31 ±	0.32 ±

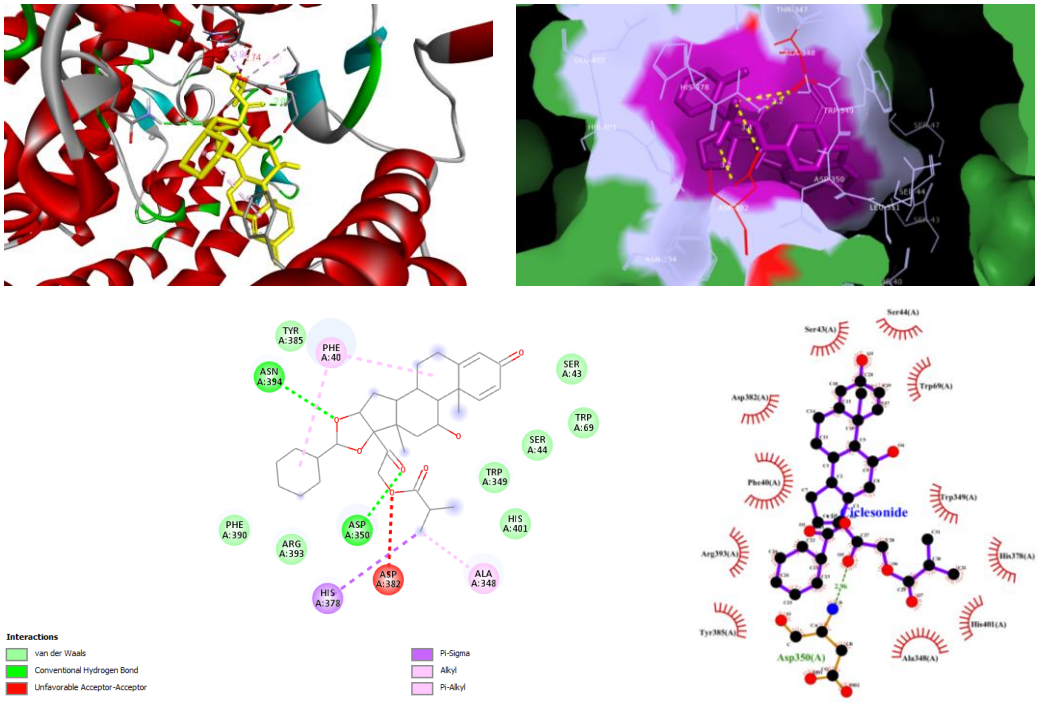
Table 3. Interaction types and Amino Acids involes in 2AJF SARS CoV Spike protein and top seven drug molecules.

Name	Hydrogen Bond (HB) interaction	Bond Length (Å) for HB interaction	Hydrophobic interaction	Pi-sigma and amide interaction	Alkyl Interaction	Pi-sulphur	Carbon-Hydrogen Interaction
Beclomethasone	LEU-100	1.9, 2.1	SER-77, GLN-101, ALA-99, SLN-102, GLN-76,ASN-103,LEU-73,LYS-74,ALA-71, SER-70,SER-106,GLY-104, SER-105,SER-113	-	-	-	-
Ciclesonide	ASP-350, ASP-382	2.0, 2.7	LEU-351, ALA-348,GLU-335,TYR-385, PHE-40,SER-43,SER-44, SER-47,ARG-393,HIS-401, ASN-394	HIS-378	PHE-40,ALA-348	-	
Methylprednisolone	ASN-103, ALA-99, LEU-100	2.2, 2.3, 2.8	GLN-101, GLN-102,GLN-98,LEU-391,PHE-390, PHE-32,TRP-69, LEU-73, SER-70, LYS-74, THR-78, SER-77, GLY-104,SER-105,SER-106, VAL-107	-	LEU-73	-	LYS-74
Montelukast	ASP-382, ASP-350	2.7, 2.0	SER-43, SER-44, TRP-349, ASP-382, HIS-378, HIS-401, TYR-385, ARG-393, ALA-348, PHE-40, TRP-69	-	PHE-40, HIS-401	-	-
Pulmicort	ASN-103, LEU-100, GLN-102, SER-77, ALA-99	2.3, 2.1,3.2, 3.0, 3.2	LYS-74, SER-70, LEU-73, TRP-69, PHE-390, LEU-391,	-	ALA-99, LEU-73	-	-
Unii-yxv28V1B07	ALA-99, LEU-100, SER-77, SER-70, ASP-350, GLN-102	1.7, 3.6, 3.5, 2.5, 2.2, 2.9	LYS-74, THR-347, TRP-349, PHE-40, SER-44, ASP-382, ARG-393, TYR-385, ASN-394, LEU-391	-	LEU-73, PHE-390, TRP-349	-	LEU-100
Zafirlukast	ASP-382, ALA-348	3.2, 3.4, 3.3, 2.2	HIS-401, HIS-378, ASP-382, THR-347, ASP-350, TRP-349, SER-43, SER-44	-	HIS-378, ALA-348	HIS-401	SER-47, SER-44

Table 4. Interaction types and Amino Acids involes in 7A93 SARS CoV-2 Spike protein and top seven drug molecules.

Name	Hydrogen Bond (HB) interaction	Bond Length (Å) for HB interaction	Hydrophobic interaction	Pi-sigma and amide interaction	Alkyl Interaction	Pi-sulphur	Carbon-Hydrogen Interaction
Beclomethasone	SER-884, LEU-894, GLN-895, ASP-796	3.3, 2.4, 3.5, 2.7	THR-883, GLN-895, PHE-898, ILE-896, ILE-794, PHE-797, PRO-897, ASP-796	-	ILE-794	-	PHE-797
Ciclesonide	THR-523, ILE-332	2.6, 2.8, 3.0,	CYS-391, CYS-525, THR-523, GLY-526, ALA-522, VAL-362, PRO-330, PHE-329, ASN-331	-	VAL-362, CYS-525	-	-
Methylprednisolone	TYR-741, ARG-1000	2.7, 2.9	LEU-966, CYS-743, GLY-744, ASN-856, ILE-742, MET-740, PHE-855	-	LEU-966, PHE-855	-	-
Montelukast	SER-637, GLU-298	2.9, 3.1, 2.4	TYR-636, VAL-610, VAL-595, PRO-295, PHE-318, ASN-317, THR-315, SER-316	-	VAL-595	-	-
Pulmicort	ASN-978, LEU-977	3.3, 3.0	MET-740, PHE-855, VAL-976, ARG-1000, ASN-856, LEU-966, ASN-978, GLY-744, ASP-745	-	LEU-966, MET-740	-	-
Unii-yxv28V1B07	LEU-110, PHE-135, GLN-239, VAL-83, ASN-81, GLN-134, ASN-137	2.3, 2.8, 3.1,2.6, 3.3, 3.2, 3.4, 2.9	PRO-139, PHE-65, PRO-26, PRO-82, GLN-23, ASN-81	-	PRO-82, PHE-65, PRO-26	-	-
Zafirlukast	ASN-121	3.1	LEU-226, VAL-227, ILE-119, ILE-203, MET-177, ASN-121, PHE-192, ARG-190, ARG-102, TRP-104, ILE-101, PHE-175, SER-172	LEU-226	ILE-119, ILE-203, VAL-227, PHE-175, HIS-207, VAL-126, PHE-192, TRP-104	-	SER-172,

(A). 2AJF-Ciclesonide docking



(B). 2AJF - Unii-xyv28V1B07 docking

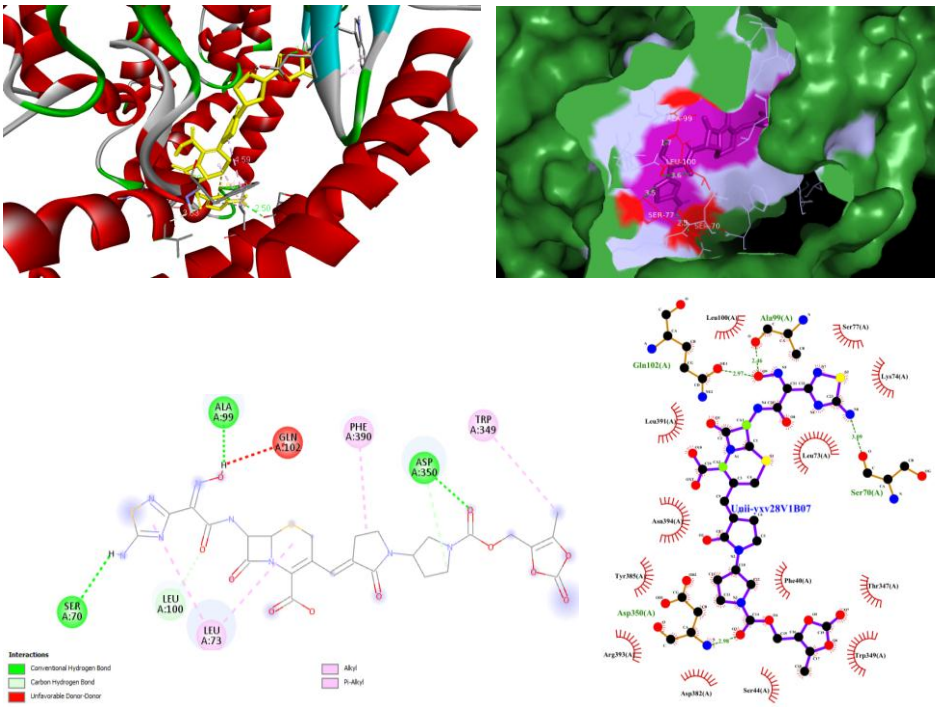
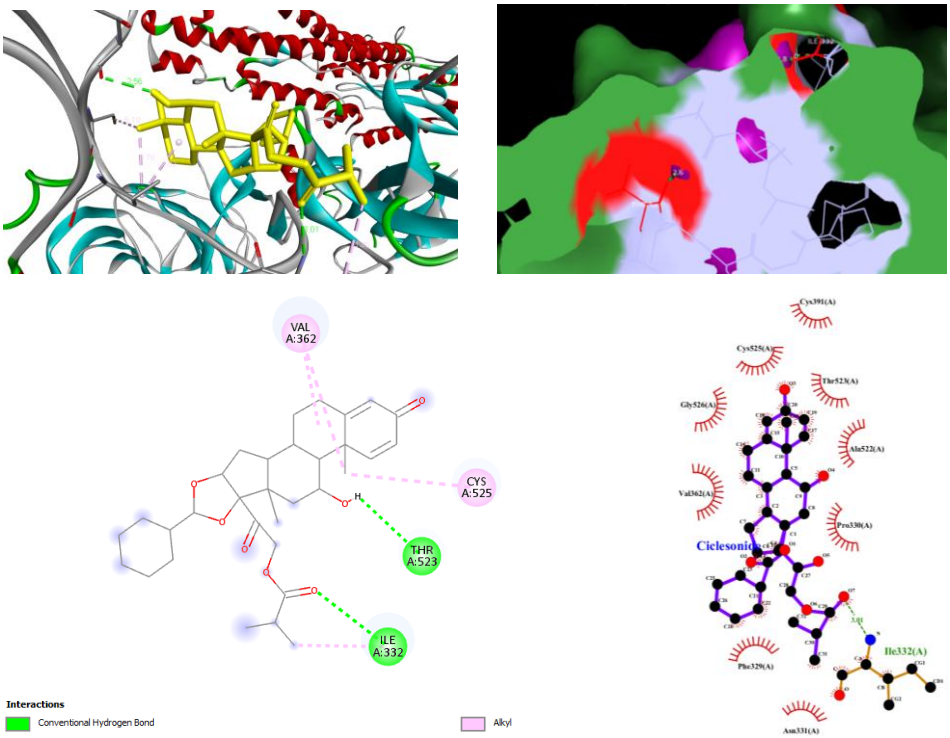


Fig.2. Protein-ligand docking: (A). 2AJF-Ciclesonide docking (B). 2AJF - Unii-xyv28V1B07 docking.

7A93-Ciclesonide docking



7A93- Unii-xyv28V1B07 docking

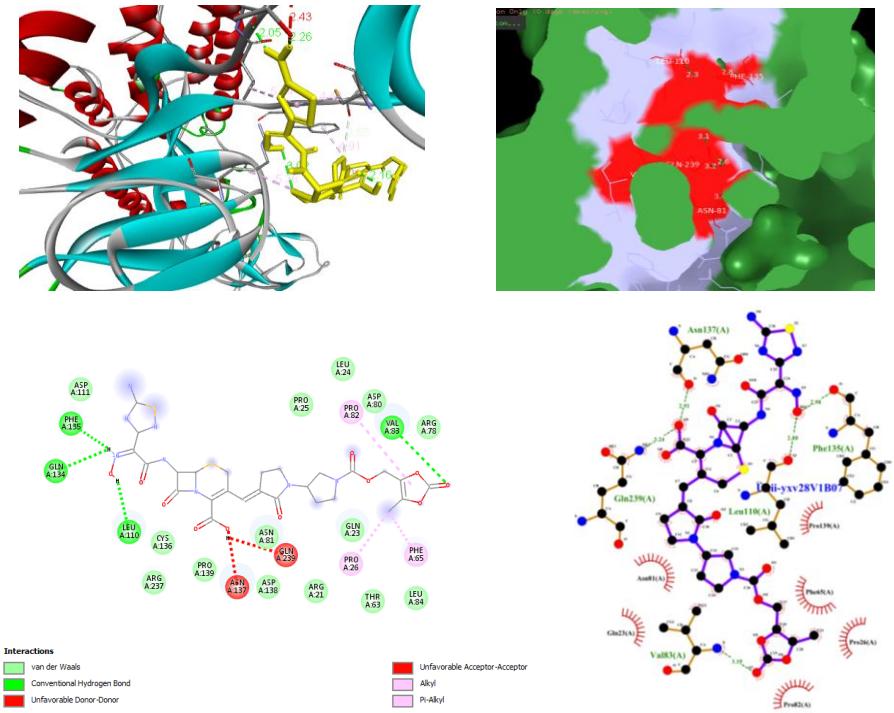
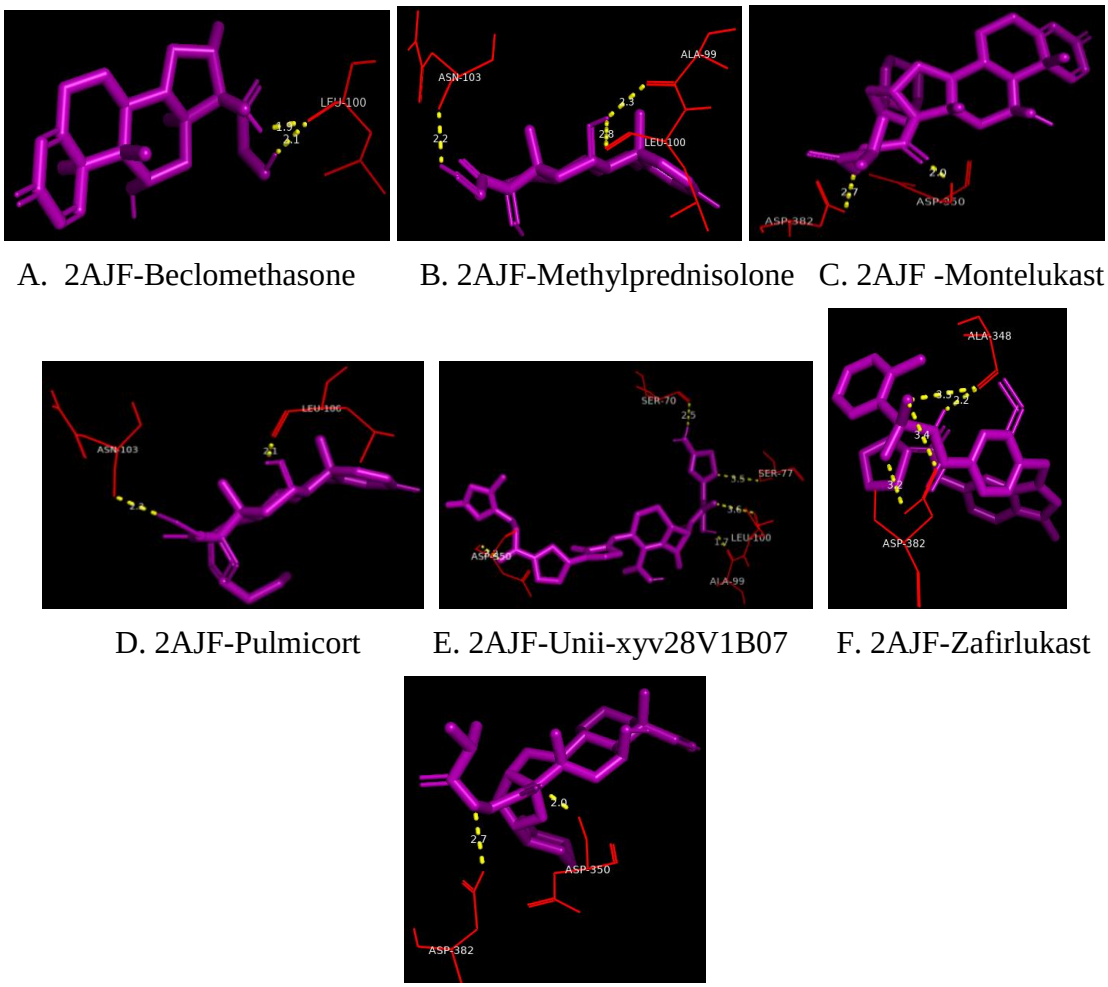


Fig.3. Protein-ligand docking: (A). 7A93-Ciclesonide docking (B). 7A93-Unii-xyv28V1B07 docking.

Top seven (7) docking results from the interaction between SARS CoV Spike (S) protein 2AJF with drug molecules.



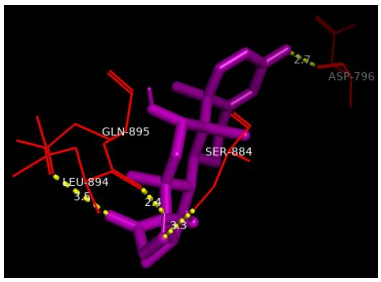
A. 2AJF-Beclomethasone B. 2AJF-Methylprednisolone C. 2AJF -Montelukast

D. 2AJF-Pulmicort E. 2AJF-Unii-xyv28V1B07 F. 2AJF-Zafirlukast

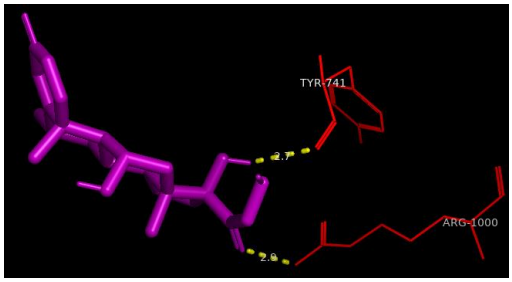
G. 2AJF-Ciclesonide

Fig.4 The binding mode of Protein-ligand docking: (A). 2AJF-Beclomethasone 2-Hydrogen bond interaction in the catalytic pocket; with LEU-100 at distance 1.9 Å and 2.1 Å respectively. (B). 2AJF-Methylprednisolone Hydrogen bond interaction in the catalytic pockets; with ASN-103 at distance 2.2 Å, with LEU-100 at distance 2.8 Å, ALA-99 at distance 2.3 Å. (C). 2AJF-Montelukast Hydrogen bond interaction in the catalytic pockets; with ASP-382 at distance 2.7 Å and ASP-250 at distance 2.0 Å. (D). 2AJF-Pulmicort Hydrogen bond interaction in the catalytic pockets; with ASN-103 at distance 2.2 Å and LEU-106 at distance 2.1 Å. (E). 2AJF-unii-xyv28V1B07 Hydrogen bond interaction in the catalytic pockets: with SER-77 at distance 3.5 Å, ALA-99 at distance 1.7 Å, ASP-350 at distance 2.2 Å and SER-70 at distance 2.5 Å. (F). 2AJF-zafirlukast Hydrogen bond interaction in the catalytic pockets; with ASP-382 at distances 3.2 Å and 3.4, ALA-348 at distance 2.0 Å (G). 2AJF-ciclesonide Hydrogen bond interaction in the catalytic pockets; with ASP-382 at distance 2.7 Å, with ASP-350 at distance 2.0 Å.

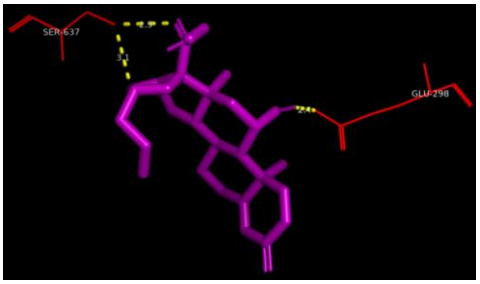
Top seven (7) docking results from the interaction between SARS CoV-2 Spike (S) protein 7A93 with drug molecules.



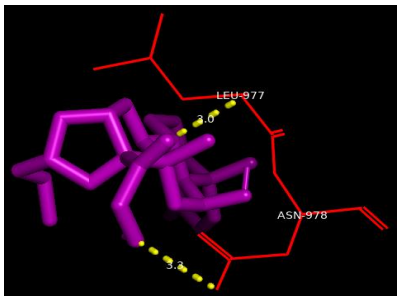
A. 7A93-Beclomethasone



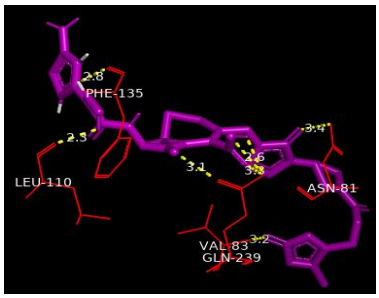
B. 7A93-Methylprednisolone



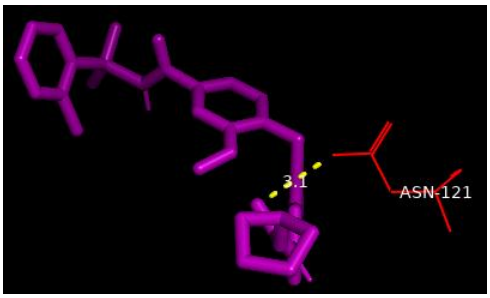
C. 7A93-Montelukast



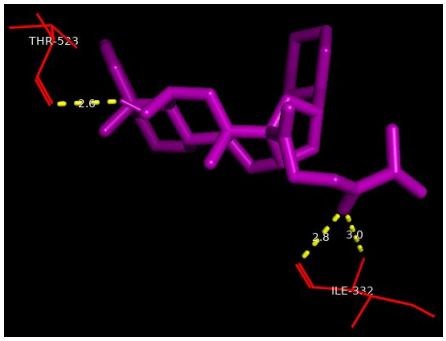
D. 7A93-Pulmicort



E. 7A93-Unii-xyv28V1B07



F. 7A93-Zafirlukast



G. 7A93-Ciclesonide

Fig.5 The binding mode of Protein-ligand docking: (A). 7A93-Beclomethasone 4-Hydrogen bond interactions in the catalytic pocket; with ASP-796 at distance 2.7 Å, SER-884 at distance 3.3 Å, GLN-895 at distance 2.4 Å and LEU-894 at distance 3.5 Å. (B). 7A93-Methylprednisolone 2-Hydrogen bond interaction in the catalytic pockets; with TYR-741 at distance 2.7 Å and ARG-1000 at distance 2.9 Å. (C). 7A93-Montelukast 3-Hydrogen bond interaction in the catalytic pockets; with SER-637 at distance 2.9 Å and 3.1 Å, GLU-298 at distance 2.4 Å. (D). 7A93-Pulmicort 2-Hydrogen bond interactions in the catalytic pockets; with ASN-978 at distance 3.3 Å and LEU-977 at distance 3.0 Å. (E). 7A93-Unii-xyv28V1B07 7-Hydrogen bond interactions in the catalytic pockets: with PHE-135 at distance 2.8 Å, LEU-110 at distance 2.3 Å, 3-bonds with GLN-239 at distance 3.1, 3.3 and 2.6 Å respectively, VAL-83 at distance 3.2 Å and with ASN-81 at distance 3.4 Å. (F). 7A93-Zafirlukast Hydrogen bond interaction in the catalytic pockets; with ASN-121 at distances 3.1 Å. (G). 7A93-Ciclesonide Hydrogen bond interactions in the catalytic pockets; with THR-523 at distance 2.0 Å, 2-bonds with ILE-332 at distance 2.8 and 3.0 Å respectively.

4. DISCUSSION

Docking of macromolecule compound into the binding site of protein followed by the assessment of binding affinity or binding energy of complex is an important process of drug design. It helps in the prediction of active site of the protein. For a successful docking the root mean square deviation (RMSD) value should be less than 2 Å [25]. In this study, 34 drug inhibitors were taken as ligand molecules to conduct docking with spike proteins of SARS CoV and SARS CoV-2. Beclomethasone, Ciclesonide, Methylprednisolone, Montelukast, Pulmicort, Unii-yxv28V1B07 and Zafirlukast, were found to have potential binding affinity from among the selected 34- drug molecules (Table 1,2). Furthermore, the study again analyzed these seven drug molecules and found two major drug molecules, Ciclesonide and Unii-yxv28V1B07 as the most promising drug molecules, which showed efficient binding nature with two spike proteins SARS CoV and SARS CoV-2.

To adhere genuine score values of binding energies, the docking methods were appropriately run and validated in three important computational sources, AutoDock

(1.5.6), AutoDock VINA programming and PyRx-Python prescription 0.8. Ciclesonide molecules when docked with receptor SARS CoV, it has exhibited best binding energy value of -11.74 (RMSD: 0.0). In catalytic pocket, ligand Ciclesonide formed a hydrogen bonds with two polar residues (amino acids) ASP-350 (2.1 Å) and ASP-382 (2.7 Å) of SARS CoV spike protein. It also formed ∏-sigma bond with HIS-378 and alkyl interection with PHE-40, and ALA-348. Similarly, while docking with 7A93, a spike Glycoprotein of SARS CoV-2, Ciclesonide exhibited best binding energy value of -8.0 (RMSD:0.0). It binds with polar residues THR-523 (2.6 Å), ILE-332 (2.8 Å,3.0 Å). It also formed an Alkyl interaction with VAL-362 and CYS-525. However, the binding affinity or binding energy values of compound with target receptor is the significant result of protein-ligand interaction [26]. Based on the values of binding affinity and interaction, it can be stated that Ciclesonide has a potential to dock with the spike proteins of SARS CoV and SARS CoV-2.

The study found that drug Unii-yxv28V1B07 (Ceftobiprole medocaril) exhibited best binding energy of -13.17 (RMSD:0.0) as it formed six (6) hydrogen bonds with spike protein of SARS CoV receptor (Fig.2-B,4-E). In catalytic pocket it binds with polar residues (amino acids) ALA-99 (1.7 Å), LEU-100 (3.6 Å), SER-77 (3.5 Å), SER-70 (2.5 Å), ASP-350 (2.2 Å), GLN-102 (2.9 Å). Among these interacting residues ALA-99, SER-70 and ASP-350 are conventional Hydrogen bonds. While the docking results of Unii-yxv28V1B07 with 7A93 spike protein of SARS CoV-2, exhibited best binding energy of -8.1 (RMSD:0.0). It formed hydrogen bonds with LEU-110 (2.3 Å), PHE-135 (2.8 Å), GLN-239 (2.6 Å,3.1 Å,3.3 Å), VAL-83 (3.2 Å), ASN-81 (3.4 Å), GLN-134 (2.6 Å), ASN-137 (2.9 Å). (Fi.3-B). Among these bonds PHE-135, GLN-134, LEU-110 and VAL-83 are the major conventional hydrogen bonds.

5. CONCLUSION

The asthmatic drug molecule Ciclesonide and Pneumoniac drug molecule Unii-yxv28V1B07 (Ceftobiprole medocaril) exhibited good binding interaction to the catalytic pocket of spike (S) proteins of 2AJF SARS CoV and 7A93 (Glycoprotein) of SARS CoV-2. In a wake of no specific medicine recognized so far for the SARS CoV and SARS CoV-2 viral disease the study has put on a light to ponder upon those available drug molecules.

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