Original Article



# Evaluation of some plant-derived natural ingredients against SARS-CoV-2: An *in-silico* approach

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#### **Abstract**

**Background:** The novel coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), infected by a new strain of human coronavirus, has engulfed the whole globe with its vicious potential to eradicate humankind. The pandemic has emerged from the Wuhan provinces of China with high transmissibility. Researchers are rushing to discover vaccines and drugs for the disease, which is not known yet. In this study, we have focused on the in-silico screening of phytochemicals occurring naturally in plant extracts that could possibly interact with receptor binding motif (RBM) of spike protein and thereby inhibit virus-cell interaction.

Materials and Methods: In this study, we have taken 100 phytochemicals that have been studied in various viral interactions and have shown antiviral properties. Initially, these compounds were analyzed on the basis of their physicochemical and pharmacokinetic properties, biological activities, possible target interactions, similar compounds in humans, and gene regulations using bioinformatic tools, namely Swiss-ADME, PASS (prediction of activity spectra for substances), SwissTargetPrediction, similar ensemble approach (SEA) search server, DIEGP-pred, respectively and were filtered out on the basis of immunobiological activities and expression of genes involved in cytokine storm regulation and immunostimulation. Further, they were docked with the receptor-binding domain (RBD) of spike protein in the SARS-CoV-2 using SwissDock and analyzed by UCSF Chimera.

**Results:** A hundred phytochemicals were analyzed on the basis of their physicochemical, pharmacokinetics, biological activities, and gene expression. Out of which 20 compounds were found to be fit all the criteria and were docked with the receptor binding domain (RBD) of the spike protein of SARS-CoV-2. Although almost every one of them showed binding with RBD, two phytochemicals, namely, orientin and apigenin, naturally found in Ocimum sanctum and chamomile, were found to bind with RBM and interacted with amino acid sequences that are mainly involved in RBM-ACE2 (angiotensin-converting enzyme 2) interaction.

**Conclusions:** We have got phytochemicals that interact directly in the receptor-binding motif of the spike protein. These phytochemicals were also screened for their pharmacokinetics and physiochemical activities, which make sure that the compound holds efficient drug-like properties. This could be a robust test of an iterative framework of inhibiting virus-receptor interaction with the help of phytochemicals. **Keywords:** Phytochemicals, SARS-CoV-2, Pharmacokinetics, Molecular docking



### Background

The first epidemic of 2019 was burst out in December when novel coronavirus (SARS-CoV-2, severe acute respiratory syndrome coronavirus 2) took place in Wuhan city, China. 1.2 Since the outbreak, it has been rapidly infecting people around the world and turned into a pandemic. The virus conserves significant phylogenetic and structural familiarity (about 80% nucleotide identity and 89.10%

nucleotide similarity) with the SARS-CoV.<sup>3,4</sup> Therefore, it has been named SARS-CoV-2 and has been placed in the same lineage.<sup>5</sup> Vaccines are under development, and to date, there is no permanent solution to eradicate the pandemic from the world. The transmission rate of the virus is massive worldwide, and hence all researchers over the world are keenly looking forward to the effective compounds that could act as anti-CoV therapeutic agents.



The trimeric S protein envelops the surface of coronavirus and plays a crucial role during viral entry.6 During infection, the S protein is cleaved into the N-terminal S1 subunit and C-terminal S2 subunit by host proteases.<sup>7</sup> S1 sequences are relatively well conserved within each coronavirus group but differ markedly between different groups. S1 contains two independent domains, the N-terminal domain and C domain, that can both serve as viral receptor-binding domains (RBDs) C domain binds to aminopeptidase N or angiotensin-converting enzyme 2 (ACE2) in coronaviruses that use them as receptors.8 Compared to the synthetic inhibitors plant baseddrugs have less toxicity and much safer to use. Natural products such as traditional medicines and plant-derived compounds (phytochemicals) are the rich sources of promising antiviral drugs. 9,10 Around 44% of the approved antiviral drugs between 1981 and 2006 were derived from natural products. Phytochemicals have been identified by computational drug development approaches to be effective against SARS-CoV-2.11-15

In this context, in our study, we have taken 100 potential phytochemicals that have been studied extensively in various antiviral interactions with coronavirus and analyzed their interactions with spike protein by using *in silico* approaches.

# Materials and Methods Phytochemicals in the Study

A hundred phytochemicals with reported antiviral properties were selected from the literature. All these phytochemicals were subjected to various physicochemical and pharmacokinetic analyses, and possible targets were predicted.

### Analysis of Physiochemical and Pharmacokinetics Properties Using the SwissADME

The molecules to be estimated for physiochemical and pharmacokinetics studies were input as Canonical SMILES, and the programme was run. Physiochemical properties such as the number of heavy aromatic atoms, fraction Csp3, rotatable bonds, H-bond receptors and donors, molecular refractivity, lipophilicity, and water solubility were determined. Pharmacokinetics properties included GI absorption, blood-brain barrier permeation, permeability glycoprotein (P-GP), and drug metabolism.

#### Predicting Biological Activity Using PASS

Evaluation of the general biological potential for druglike compounds based on their structural formula can be performed with a computer program, PASS (prediction of activity spectra for substances). Information of the phytochemicals was input in CANONICAL smiles format. PASS software estimates the predicted activity spectrum of a compound as a probable activity or active (Pa) and probable inactivity or inactive (Pi). The PASS user obtains output information as a list of predicted types of activity with the estimated probability for each type of activity: 'to be active,' Pa and 'to be inactive,' Pi. The probabilities, Pa and Pi values vary from 0.000 to 1.000 and, in general, Pa  $\neq$  Pi =1. In this study, we set to cut off the value of Pa 'to be active' is Pa>0.7 and select the compound for the prediction that occurs above the cut- off.<sup>14</sup>

# Predicting Biological Targets Using Swiss Target Prediction and Similar Ensemble Approach

SwissTargetPrediction is based on the observation that similar biological active molecules are more similar to targets in three different species. Therefore, the targets of a molecule can be predicted by combination with a known compound that is highly similar to the query molecule. A significant prospect is the accuracy similarity between the query molecule and the known compound. Whenever a compound shows a high similarity under the predictions have shown strong bind interactions with similar targets. The target probability value lies between 0 to1, with the largest possible value being reached if the query molecule is a known compound of the target. The name of the target, their classes, and their Uniprot ID are displayed. The probability score indicates the activity of the compound. 15 The similarity ensemble approach (SEA) search server can be used to predict specific molecular targets. The sequence of structural similarity among targets by the similarity of the compound that binds to them is expressed as significant values and maximum Tanimoto similarity. The values exhibited a stronger relationship between compounds.16

### Prediction of Changes in Gene Expression Pattern Based on Protein Using DIGEP-Pred

DIGEP-Pred, which is a web service for *in silico* prediction of drug-induced changes of gene expression profiles. The genes regulated by the phytochemicals -either upor downregulated can be studied on the basis of protein prediction. Parameters set were Pa > Pi and Pa > 0.5.<sup>17</sup>

### Extraction of Compounds on the Basis of Immunobiological Activities Directly Involved During Viral Infection

After analyzing physiochemical and pharmacokinetic properties of 100 phytochemicals, some of them were filtered out as they showed immunobiological activities and expression of genes involved in cytokine storm regulation and immunostimulation. The genes considered mainly were PRDX2, CD14, CD86, CD83, and CCL2. All five of them have a potential role in immunoregulation and antigen presentation during viral entry. CCL2 gene is one of several cytokine genes clustered on the q-arm of chromosome.<sup>17-19</sup>

Protein-Ligand Docking using SwissDock and UCSF

#### Chimera

# Protein Molecular Modeling of Receptor Binding Domain of Spike Protein

The sequence of receptor binding domain (RBD) of the spike protein stretching from 333 to  $527^{20}$  complexed with ACE2 was retrieved from RCSB PDB (ID: 6zlg). Thereafter, both the structures were separated individually, and, in this study, the RBD of spike protein is used as the receptor for protein-ligand docking.

#### Ligand Preparation of the Phytochemicals for Docking

The 3-D structure of filtered phytochemicals was retrieved from PubChem<sup>21</sup> in pdf format. It was then converted in Mol2 using UCSF Chimera.

#### Protein-Ligand Docking Using SwissDock

Both spike protein and ligand were prepared in their respective format (Receptor in PDB and ligand in Mol2) and were subjected for docking. Many binding clusters are generated (blind docking) in the target cavities and their full fitness (Kcal/mol) and delta G (Kcal/mol).

#### Analysis of Docked Models

The interaction of the phytochemicals with the RBD of spike protein was analyzed using UCSF Chimera. Hydrophobic and hydrogen bonding were considered in the region of receptor binding motif (RBM), which extends from 438-506 amino acid sequence.

#### Results

# Physiochemical and Pharmacokinetic Properties of Phytochemicals

The physicochemical and pharmacokinetic properties of the compounds are represented in Table S1. Lipophilicity has correlated to the biological activity of any drug molecule. This is responsible for the stronger binding to the target protein. Lipophilicity affects several other pharmacokinetic parameters of drug molecules such as lower water solubility, higher permeability in the gastrointestinal tract across the blood-brain barrier and other tissue membranes, higher protein binding). As per RO5 (Lipinski's rule of five), a chemical compound to be orally active in human should follow a minimum of three criteria of the following: (a) molecular weight ≤500, (b) XLOGP3 <3.5, (c) hydrogen bond acceptor ≤ 10 and hydrogen bond donor  $\leq$  5. Therefore, compounds following the rules are noted, and others are knocked out. Also, the pharmacokinetics of the compounds are also analyzed (Table S1).

#### Biological Activity of the Compounds

Possible biological activity of all the compounds retrieved was analyzed, and the properties that could involve in the disease regulation are taken into consideration. Properties such as anti-inflammatory, antioxidant, HIV-1 integrase,

antioxidant (Table 1) have been highlighted and taken into further analyses, and other compounds were knocked out. The SEA search server is also used to predicate structural similarity and biological target molecule in different species. We observed many compounds showing structural similarity and active biological target molecules in the human species in the current study. The higher probability compounds in the human species are highlighted in Table 2.

### Gene Expression Studies Induced by the Phytochemical Compounds

The gene expression of the compounds evaluated using DIGEP-Pred, showed a plethora of genes involved in the various kinds of biological activities that have been regulated either positively or negatively by the compounds. In our study, we have taken five genes, namely PRDX2, CD14, CD86, CD83, CCL3, and CCL2 are taken into account from the displayed genes as they could be directly involved in the immunogenicity of the virus and cytokine regulation during disease. PRDX2 plays an antioxidant protective role in cells, and it may contribute to the antiviral activity of CD8(+) T-cells. The protein encoded by the CD14 gene is a surface antigen that is preferentially expressed on monocytes/macrophages. It cooperates with other proteins to mediate the innate immune response. CD86 and CD83 are involved in the antigen presentation, and CCL2 is one of several cytokine genes clustered on the q-arm of chromosome 17. Compounds regulating these were filtered and was subjected to further analysis (Table 3).

### Binding of Phytochemicals With Spike Protein

Out of 100 phytochemicals analyzed, 20 of them were filtered out using various parameters of physical and biological activities. These 20 phytochemicals were subjected to protein docking using SwissDock. The extracted file contained the clusters of docks having various binding affinity and  $\Delta G$  energy. The analysis of the interaction of these 20 phytochemicals with RBD of spike protein was carried out using UCSF Chimera. Although almost every compound showed a binding affinity with RBD in its pocket, it was noted that only two compounds, namely orientin and apigenin, showed hydrogen interactions in the region of RBM, where the spike protein interacts with ACE2.

The phytochemical Orientin binds with RBM of the spike protein with a full fitness of -1482.80 kcal/mol and  $\Delta G$  of -6.61 kcal/mol (Figure 1). Apigenin showed binding with RBM with a full fitness score of -1559.63 kcal/mol and  $\Delta G$  of -6.39 Kcal/mol (Figure 2). We also find that the targeted docking of orientin with RBD interacted with S494, N440, S477, and T478 OF RBD, and apigenin showed interaction with S494 and G502 of RBD.

 Table 1. Biological Activities of Phytochemical compounds.

S NI a	Compound Name	Biological activity (Pa>Pi. Pa>0.7)					
S.No.	Compound Name	Pa Pi		Activity			
		0.912	0.001	Quercetin 2,3-dioxygenase inhibitor			
	Astronia	0.911	0.005	HIF1A expression inhibitor			
		0.826	0.003	APOA1 expression enhancer			
		0.798	0.008	JAK2 expression inhibitor			
	Apigenin	0.791	0.003	Histamine release inhibitor			
		0.732	0.004	Antioxidant			
		0.732	0.002	NOS2 expression inhibitor			
		0.730	0.005	Insulysin inhibitor			
		0.886	0.003	Oxidoreductase inhibitor			
	D	0.849	0.006	Respiratory analeptic			
	Beta-sitosterol	0.796	0.010	Protein-disulfide reductase (glutathione) inhibitor			
		0.762	0.009	Immunosuppressant			
		0.980	0.002	HIF1A expression inhibitor			
		0.962	0.001	JAK2 expression inhibitor			
		0.825	0.003	TNF expression inhibitor			
		0.798	0.001	HIV-1 integrase (Strand Transfer) inhibitor			
	Bisdemethoxycurcumin	0.780	0.002	HIV-1 integrase (3'-Processing) inhibitor			
		0.733	0.003	Choleretic			
		0.723	0.002	HIV-1 integrase inhibitor			
		0.704	0.015	Anti-inflammatory			
		0.858	0.002	MMP9 expression inhibitor			
		0.874	0.018	Membrane integrity agonist			
		0.789	0.004	Neurotransmitter uptake inhibitor			
	Brachyamide B	0.774	0.004	Carminative			
		0.739	0.005	TNF expression inhibitor			
		0.716	0.005	Sigma receptor agonist			
		0.903	0.003	JAK2 expression inhibitor			
;	Caleb in-A	0.812	0.006	Anti-inflammatory			
	cares in 70	0.754	0.004	Insulysin inhibitor			
		0.839	0.006	Respiratory analeptic			
•	Campesterol	0.761	0.010	Immunosuppressant			
		0.934	0.004	HIF1A expression inhibitor			
		0.816	0.027	Ubiquinol-cytochrome-c reductase inhibitor			
,	Cirsilineol	0.769	0.004	Insulysin inhibitor			
		0.760	0.002	NOS2 expression inhibitor			
		0.726	0.004	Histamine release inhibitor			
		0.932	0.004	HIF1A expression inhibitor			
		0.849	0.005	JAK2 expression inhibitor			
}	Cirsimaritin	0.754	0.004	Insulysin inhibitor			
	•	0.730	0.002	NOS2 expression inhibitor			
		0.701	0.002	Histamine release inhibitor			
)	Cordifolioside A	0.852	0.006	Immunostimulant			
	Cordinologide / 1	0.845	0.006	Respiratory analeptic			
0	Cordioside	0.749	0.000	Immunosuppressant			
1	Crategolic acid	0.749	0.011	Insulin promoter			
1	Crategoric acid	0.9/3	0.001	пъчни ргонносет			

Table 1. Continued

C NIA	Compound Name	Biological activity (Pa>Pi. Pa>0.7)					
S.No.	Compound Name	Pa	Pi	Activity			
		0.880	0.005	Anti-inflammatory			
		0.744	0.004	Antiviral (Influenza)			
12	Curcumin	0.706	0.002	HIV-1 integrase (Strand Transfer) inhibitor			
		0.837	0.005	JAK2 expression inhibitor			
13	Cyclocurcumin	0.774	0.014	HIF1A expression inhibitor			
		0.723	0.002	NOS2 expression inhibitor			
14	Demethoxycurcumin	0.978	0.001	JAK2 expression inhibitor			
14	Demethoxycurcumin	0.974	0.002	HIF1A expression inhibitor			
		0.806	0.011	HIF1A expression inhibitor			
15	Eugenitin	0.754	0.002	NOS2 expression inhibitor			
		0.735	0.004	Histamine release inhibitor			
		0.877	0.002	Histamine release stimulant			
16	Flavonol glucosida	0.766	0.014	HIF1A expression inhibitor			
10	Flavonol glucoside	0.705	0.006	Antidiabetic			
		0.713	0.014	Anti-inflammatory			
		0.909	0.001	NOS2 expression inhibitor			
17	Hesperetin	0.911	0.005	HIF1A expression inhibitor			
		0.778	0.010	JAK2 expression inhibitor			
		0.959	0.003	HIF1A expression inhibitor			
18	Isothymonin	0.833	0.005         HIF1A expression           0.010         JAK2 expression           0.003         HIF1A expression           0.002         NOS2 expression           0.006         JAK2 expression           0.003         HIF1A expression           0.002         NOS2 expression           0.009         JAK2 expression           0.002         Quercetin 2.3-	NOS2 expression inhibitor			
		0.824	0.006	JAK2 expression inhibitor			
		0.960	0.003	HIF1A expression inhibitor			
19	Isothymusin	0.783	0.002	NOS2 expression inhibitor			
19	isothymusin	0.788	0.009	JAK2 expression inhibitor			
		0.759	0.002	Quercetin 2.3-dioxygenase inhibitor			
		0.969	0.002	HIF1A expression inhibitor			
		0.951	0.001	Quercetin 2.3-dioxygenase inhibitor			
20	Kaempferol	0.797	0.002	NOS2 expression inhibitor			
		0.836	0.002	Antiviral (influenza)			
		0.819	0.005	Anti-inflammatory			
		0.940	0.004	HIF1A expression inhibitor			
		0.774	0.005	Antidiabetic			
21	Orientin	0.759	0.004	Histamine release inhibitor			
	Orientan	0.750	0.002	Antiviral (herpes)			
		0.745	0.004	Antiviral (influenza)			
		0.708	0.004	Histamine release stimulant			
22	Pentadienoylpiperdine (1-Pentadienoylpiperdine)	0.740	0.005	Insulin promoter			
	dine)	0.721	0.004	Histamine release stimulant			
		0.969	0.002	HIF1A expression inhibitor			
		0.934	0.001	Quercetin 2.3-dioxygenase inhibitor			
<b>1</b> 2	Quaranti-	0.850	0.002	NOS2 expression inhibitor			
23	Quercetin	0.787	0.009	JAK2 expression inhibitor			
		0.751	0.003	Histamine release stimulant			
		0.720	0.004	Histamine release inhibitor			

Table 1. Continued

S No	Compound Name	Biological activity (Pa>Pi. Pa>0.7)					
S.No.	Compound Name	Pa	Pi	Activity			
		0.960	0.003	HIF1A expression inhibitor			
		0.873	0.001	NOS2 expression inhibitor			
24	Rhamnetin	0.836	0.002	Quercetin 2.3-dioxygenase inhibitor			
		0.783	0.010	JAK2 expression inhibitor			
		0.736	0.004	Histamine release stimulant			
25	Rosmarinic acid	0.799	0.005	Antidiabetic			
26	Somniferine A (Somniferine)	0.832	0.002	Histamine release stimulant			
27	Stigmasterol	0.782	0.007	Immunosuppressant			
28	Tinocordifolioside	0.738	0.012	Immunosuppressant			
		0.735	0.004	Antiviral (Influenza)			
29	Tinocordioside	0.737	0.013	Immunosuppressant			
		0.713	0.014	Anti-inflammatory			
30	Tinosporide	0.891	0.004	O04 Anti-inflammatory O01 Insulin promoter O01 Transcription factor NF kappa B stimulant O05 Anti-inflammatory O04 Antiviral (Influenza) O05 HIF1A expression inhibitor O02 Antiviral (herpes) O02 Immunosuppressant			
	•	0.970	0.001	•			
		0.927	0.001				
31	0.970	0.005					
		0.761	Pi         Acti           0.003         HIF1           0.001         NOS           0.002         Que           0.010         JAK2           0.004         Hist           0.005         Anti           0.002         Hist           0.007         Imm           0.0012         Imm           0.004         Anti           0.013         Imm           0.004         Anti           0.001         Insu           0.001         Insu           0.001         Tran           0.005         Anti           0.006         HIF1           0.007         Imm           0.008         Imm           0.009         Imm           0.001         Anti           0.002         Anti           0.003         HIF1           0.004         JAK2           0.001         Anti           0.002         Anti           0.003         Anti           0.004         JAK2           0.007         JaK2           0.007         JaK2           0.007         JaK2 <t< td=""><td>,</td></t<>	,			
		0.915	0.005	HIF1A expression inhibitor			
32	Vicenin (Vicenin-2)						
33	Withaferin A	0.850					
34				Immunosuppressant			
35				Immunosuppressant			
36				Immunosuppressant			
37				HIF1A expression inhibitor			
	,	0.873		JAK2 expression inhibitor			
38	Eugenol	0.715		Respiratory analeptic			
39	Glycyrrhizin	0.924		Antiviral (influenza)			
		0.902		Transcription factor NF kappa B stimulant			
40		0.849		Anti-inflammatory			
		0.837		Immunostimulant			
		0.816		JAK2 expression inhibitor			
		0.774		IgA-specific metalloendopeptidase inhibitor			
41	Anthraquinone	0.759		Macrophage colony-stimulating factor agonist			
		0.747		Quinoprotein glucose dehydrogenase inhibitor			
		0.812		Platelet adhesion inhibitor			
		0.813		Histamine release inhibitor			
		0.810		Anti-infective			
42	Baicalin	0.736		Histamine release stimulant			
	Salcaini	0.745		HIF1A expression inhibitor			
		0.741		Anti-inflammatory			
		0.727		Antiviral (influenza)			
		0.969		HIF1A expression inhibitor			
		0.969					
43	Myricetin			Quercetin 2.3-dioxygenase inhibitor			
		0.808		NOS2 expression inhibitor			
		0.733	0.014	JAK2 expression inhibitor			

Table 1. Continued

S.No.	Compound Name	Biological activity (Pa>Pi. Pa>0.7)					
3.1 <b>1U.</b>	Compound Name	Pa	Pi	Activity			
		0.713	0.004	Histamine release stimulant			
		0.710	0.003	Interleukin 4 antagonist			
		0.720	0.013	Anti-inflammatory			
		0.868	0.004	Antileukemic			
44	Andrographolide	0.845	0.005	Anti-inflammatory			
		0.751	0.011	Immunosuppressant			
45	Naringenin	0.911	0.005	HIF1A expression inhibitor			
13		0.846	0.002	NOS2 expression inhibitor			
46	Bavachinin	0.895	0.001	NOS2 expression inhibitor			
	buvaciiiiii	0.728	0.013	Respiratory analeptic			
47	Neobavaisoflavone	0.923	0.002	Histidine kinase inhibitor			
.,	- Treosavaisonavone	0.765	0.014	HIF1A expression inhibitor			
48	Isobavachalcone	0.881	0.001	NOS2 expression inhibitor			
		0.778	0.008	Anti-inflammatory			
49	4'-O-methylbavachalcone	0.854	0.002	NOS2 expression inhibitor			
50	Psoralidin	0.853	0.009	HIF1A expression inhibitor			
		0.964	0.003	HIF1A expression inhibitor			
		0.878	0.001	Quercetin 2.3-dioxygenase inhibitor			
		0.830	0.003	Histamine release inhibitor			
51	Luteolin	0.833	0.006	JAK2 expression inhibitor			
		0.798	0.002	NOS2 expression inhibitor			
		0.754	0.003	Leukotriene-B4 20-monooxygenase inhibitor			
		0.745	0.005	Insulysin inhibitor			
52	Hypericin	0.839	0.009	HIF1A expression inhibitor			
53	Glabridin	0.948	0.003	Anti-infective			
		0.911	0.005	HIF1A expression inhibitor			
54	Psoralidin	0.853	0.009	HIF1A expression inhibitor			
55	Emodin	0.862	0.008	HIF1A expression inhibitor			
		0.741	0.013	JAK2 expression inhibitor			
		0.855	0.008	HIF1A expression inhibitor			
56	Liquiritigenin	0.778	0.002	NOS2 expression inhibitor			
		0.724	0.015	JAK2 expression inhibitor			
		0.709	0.014	Respiratory analeptic			
57	Hydroxytyrosol	0.778	0.010	JAK2 expression inhibitor			
		0.864	0.008	HIF1A expression inhibitor			
58	Carvacrol	0.784	0.005	Anti-infective			
		0.737	0.014	JAK2 expression inhibitor			
		0.810	0.007	JAK2 expression inhibitor			
		0.800	0.002	GABA C receptor agonist			
59	Cinnamic	0.776	0.003	GABA aminotransferase inhibitor			
		0.741	0.003	Inulinase inhibitor			
		0.720	0.018	HIF1A expression inhibitor			
		0.706	0.005	Platelet aggregation stimulant			
		0.822	0.007	JAK2 expression inhibitor			
60	Methyl Cinnamate	0.742	0.005	Insulysin inhibitor			
		0.730	0.004	GABA aminotransferase inhibitor			

Table 1. Continued

C NI-	C IN	Biological activity (Pa>Pi. Pa>0.7)				
S.No.	Compound Name	Pa	Pi	Activity		
		0.840	0.004	Anti-infective Anti-infective		
6.1	The control of the co	0.814	0.011	HIF1A expression inhibitor		
61	Thymohydroquinone	0.754	0.011	Respiratory analeptic		
		0.741	0.013	JAK2 expression inhibitor		
62	Tl I	0.829	0.005	Anti-infective Anti-infective		
62	Thymol	0.808	0.011	HIF1A expression inhibitor		
62	C'arran Halanda	0.819	0.007	JAK2 expression inhibitor		
63	Cinnamaldehyde	0.758	0.011	Complement factor D inhibitor		
		0.911	0.001	Histamine release stimulant		
		0.879	0.007	HIF1A expression inhibitor		
64	Myricitrin	0.762	0.009	Anti-inflammatory		
		0.733	0.006	Anti-infective Anti-infective		
		0.704	0.005	Antiviral (Influenza)		
<b>( F</b>	Complian	0.793	0.003	Histamine release stimulant		
65	Corydine	0.719	0.013	Respiratory analeptic		
66	Aloin	0.717	0.005	Antiviral (influenza)		
		0.883	0.007	HIF1A expression inhibitor		
67	Catechin	0.791	0.003	Histamine release inhibitor		
		0.785	0.009	JAK2 expression inhibitor		

**Table 2.** Target Molecules for Phytochemical Compounds

S.No.	Compound Name	Target	Common Name	Uniprot ID	<b>Target Class</b>
		Cyclin-dependent kinase 5/CDK5 activator 1	CDK5R1 CDK5	Q15078 Q00535	Kinase
		Cyclin-dependent kinase 1/cyclin B		Q8WWL7 P06493 P14635 O95067	Other cytosolic protein
ı	Apigenin	Cyclooxygenase-2	PTGS2	P35354	Oxidoreductase
		Cyclin-dependent kinase 6	CDK6	Q00534	Kinase
	-	Tyrosine-protein kinase SYK	SYK	P43405	Kinase
2	Curcumin	Toll-like receptor (TLR7/TLR9)	TLR9	Q9NR96	Toll-like and II-1 receptors
		Tyrosine-protein kinase receptor FLT3	orotein kinase receptor FLT3 FLT3 P3 ate 5-lipoxygenase ALOX5 P0 7-beta-dehydrogenase 2 HSD17B2 P3 TNF P0	P36888	Kinase
3	Kaempferol	Arachidonate 5-lipoxygenase	ALOX5	P09917	Oxidoreductase
		Estradiol 17-beta-dehydrogenase 2	CDK5R1 CDK5 Q15078 Q00 Clin B CCNB3 CDK1 Q8WWL7 PC CCNB1 CCNB2 P14635 O959 PTGS2 P35354 CDK6 Q00534 SYK P43405 TLR9 Q9NR96 OF FLT3 FLT3 P36888 ALOX5 P09917 See 2 HSD17B2 P37059 TNF P01375 IL2 P60568 See 1 HSD17B1 P14061 Peptor IGF1R P08069 P2 P00734 PAURKB Q96GD4 DRD4 P21917 PIK3R1 P27986 SRC P12931 PTK2 Q05397 MMP3 P08254	P37059	Enzyme
		TNF-alpha	-beta-dehydrogenase 2 HSD17B2 P TNF P	P01375	Secreted protein
4	Orientin	Interleukin-2	IL2	P60568	Secreted protein
		Estradiol 17-beta-dehydrogenase 1	PTGS2 P14635 O950 PTGS2 P35354  CDK6 Q00534  SYK P43405  TLR9 Q9NR96  LT3 FLT3 P36888  ALOX5 P09917  HSD17B2 P37059  TNF P01375  IL2 P60568  HSD17B1 P14061  or IGF1R P08069  F2 P00734  urora-B AURKB Q96GD4  DRD4 P21917  PIK3R1 P27986  SRC P12931  PTK2 Q05397	P14061	Enzyme
		Insulin-like growth factor I receptor	IGF1R	P08069	Kinase
		Thrombin	F2	P00734	Protease
		Serine/threonine-protein kinase Aurora-B	AURKB	Q96GD4	Kinase
		Dopamine D4 receptor	DRD4	P21917	Family A G protein- coupled receptor
5	Quercetin	PI3-kinase p85-alpha subunit	PIK3R1	P27986	Enzyme
		Tyrosine-protein kinase SRC	SRC	P12931	Kinase
		Focal adhesion kinase 1	PTK2	Q05397	Kinase
		Matrix metalloproteinase 3	MMP3	P08254	Protease
		Arachidonate 15-lipoxygenase	ALOX15	P16050	Enzyme

Table 2. Continued

S.No.	Compound Name	Target	Common Name	Uniprot ID	Target Class
		Serine/threonine-protein kinase PLK1	PLK1	P53350	Kinase
		Cyclin-dependent kinase 1	CDK1	P06493	Kinase
		Matrix metalloproteinase 9	MMP9	P14780	Protease
		Matrix metalloproteinase 2	MMP2	P08253	Protease
		Protein kinase N1	PKN1	Q16512	Kinase
		Arachidonate 12-lipoxygenase	ALOX12	P18054	Enzyme
		Serine/threonine-protein kinase NEK2	NEK2	P51955	Kinase
		Interleukin-8 receptor A	CXCR1	P25024	Family A G protein- coupled receptor
		CaM kinase II beta	CAMK2B	Q13554	Kinase
		ALK tyrosine kinase receptor	ALK	Q9UM73	Kinase
		Serine/threonine-protein kinase AKT	AKT1	P31749	Kinase
		Serine/threonine-protein kinase NEK6	NEK6	Q9HC98	Kinase
6	Thymoquinone	Serine/threonine-protein kinase PLK1	PLK1	P53350	Kinase
7	Myricetin	Insulin receptor	INSR	P06213	Kinase
		Cyclin-dependent kinase 5/CDK5 activator 1	CDK5R1 CDK5	Q15078 Q00535	Kinase
0	Later Pa	Monoamine oxidase A	MAOA	P21397	Oxidoreductase
8	Luteolin	Cyclin-dependent kinase 1/cyclin B	CCNB3 CDK1 CCNB1 CCNB2	Q8WWL7 P06493 P14635 O95067	Other cytosolic protein
		Lymphocyte differentiation antigen CD38	CD38	P28907	Enzyme
	Cinanserin	Serotonin 1b (5-HT1b) receptor (by homology)	HTR1B	P28222	Family A G protein- coupled receptor
9		Serotonin 2a (5-HT2a) receptor	HTR2A	P28223	Family A G protein- coupled receptor
		Serotonin 2c (5-HT2c) receptor	HTR2C	P28335	Family A G protein- coupled receptor
10	Carvacrol	Cyclooxygenase-1	PTGS1	P23219	Oxidoreductase



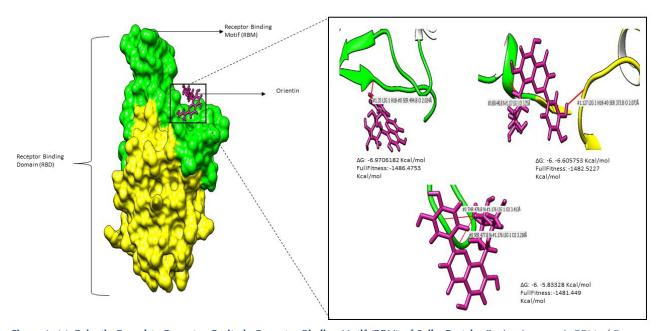


Figure 1. (a) Orientin Bound to Receptor Cavity in Receptor Binding Motif (RBM) of Spike Protein: Region in green is RBM of Receptor Binding Domain, which is represented by both yellow and green. Orientin is colored in violet red. Orientin interacts with RBM, which is the main ligand for the ACE2 enzyme in humans. (b) Amino Acid Residues Involved in the Hydrogen Bonding Between Orientin and RBM: The red line marks the hydrogen bond. Labeling includes ligand cluster, ligand number, atom involved in the interaction at ligand side, an amino acid of RBM involved in the interaction, and the hydrogen bond length. Orientin specifically binds in three positions within RBM.

**Table 3.** Cellular Gene Expressions Induce by Phytochemical Compounds

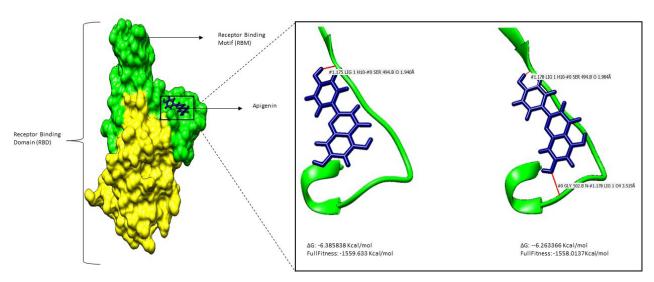
S.No	Compound Names	Pa	Pi	Regulation (Upregulation)
1	Apigenin	0.774	0.005	PRDX2
2	Beta-sitosterol	0.659	0.029	CD14
3	Bisdemethoxycur-	0.639	0.101	CD86
3	cumin	0.585	0.087	CCL2
4	Calab in A	0.551	0.066	CD14
4	Caleb in-A	0.572	0.117	CD86
5	Cirsilineol	0.561	0.025	PRDX2
6	Cirsimaritin	0.54	0.033	PRDX2
7	Cordifolioside A	0.757	0.074	CD86
/	Cordifolioside A	0.555	0.129	CD83
8	Crategolic acid	0.546	0.14	CD83
9	Curcumin	0.62	0.105	CD83
10	Demethoxycurcu- min	0.656	0.097	CD86
11	Eriodictyol	0.55	0.03	PRDX2
12	Flavonol glucoside	0.672	0.056	CD83
14	riavonoi giucosiue	0.54	0.125	CD86
13	Isothymonin	0.615	0.014	PRDX2
14	Isothymusin	0.615	0.014	PRDX2
15	Kaempferol	0.851	0.003	PRDX2
16	Oleanolic acid	0.58	0.107	CD83
17	Pentadienoylpiper- dine (1-Pentadie- noylpiperdine)	0.62	0.078	CD83
18	Quercetin	0.874	0.003	PRDX2
19	Rhamnetin	0.763	0.005	PRDX2
20	D	0.621	0.074	CCL2
20	Rosmarinic acid	0.568	0.055	CD14
21	Somniferine A (Som- niferine)	0.71	0.019	CD14
22	Tinocordifolioside	0.754	0.03	CD83
23	Tinocordioside	0.685	0.052	CD83
24	Ursolic acid	0.549	0.136	CD83
25	Withanolide B	0.513	0.088	CD14
26	Thomas and a con-	0.598	0.043	CD14
26	Thymoquinone	0.556	0.127	CD83
27	Eugenol	0.881	0.024	CD86
28	Glycyrrhizin	0.665	0.058	CD83
		0.546	0.031	PRDX2
29	Anthraquinone	0.546	0.099	CCL2
		0.523	0.159	CD83
30	Honokiol	0.639	0.101	CD86
31	Myricetin	0.85	0.003	PRDX2
32	Andrographolide	0.526	0.082	CD14
33	Naringenin	0.51	0.041	PRDX2
34	4'-O-methylba- vachalcone	0.624	0.104	CD86
35	lambda-Carragee- nan	0.848	0.036	CD86

Table 3. Continued

S.No	Compound Names	Pa	Pi	Regulation (Upregulation)		
36	beta-Carrageenan	0.616	0.08	CD83		
37	Nelfinavir	0.979	0.001	CCL2		
37	Neiillavii	0.894	0.005	CCL3		
38	Luteolin	0.805	0.004	PRDX2		
39	Hibiscus acid	0.522	0.16	CD83		
		0.708	0.043	CCL2		
40	Hydroxytyrosol	0.704	0.087	CD86		
		0.608	0.04	CD14		
41	Saikosaponin	0.829	0.013	CD83		
		0.868	0.029	CD86		
42	Cinnamic	0.754	0.025	CCL2		
42		0.724	0.039	CD83		
		0.677	0.025	CD14		
43	Methyl cinnamate	0.653	0.064	CCL2		
		0.605	0.041	CD14		
	Thymohydro- quinone	0.57	0.115	CD83		
44		0.511	0.089	CD14		
41 42 43		0.517	0.111	CCL2		
		0.628	0.104	CD86		
45	Thymol	0.554	0.096	CCL2		
		0.535	0.15	CD83		
4.6	C'arran Halanda	0.927	0.009	CD86		
46	Cinnamaldehyde	0.724	0.036	CCL2		
47	Allicin	0.55	0.097	CCL2		
		0.532	0.104	CCL2		
48	Carvacrol	0.506	0.092	CD14		
		0.535	0.15	CD83		

#### **Discussion and Conclusions**

The novel coronavirus has become a big challenge for the world. It has taken numerous lives within a span of a short time. After it, the whole world is developing a potential vaccine or drug against it but is not devised yet. Studies are being conducted to repurpose the known drugs used in many viral diseases and have shown varying results.<sup>22,23</sup> Various naturally occurring phytochemicals and other compounds in ancient medicines are also being extensively studied to confront the disease.<sup>24,25</sup> The main focus of all these medications is to inhibit the viral attachment with human receptors or to cease the replication of the viral genome inside the cell. In our study, we have more focused on the phytochemicals that could possibly attach to viral spike protein and thereby inhibit its entry inside the cell. The viral protein involved in the attachment of the virus with a cellular receptor, ACE2, is spike protein (S). It is an assembly of trimer on the surface of viral particles and contains two main functional domains, S1 and S2. The S1 domain at the N-terminal is responsible for receptor binding, and the S2 domain at the C-terminal is Figure 2.a) Figure 2.b)



**Figure 2.** (a) Apigenin bound to receptor cavity in Receptor Binding Motif (RBM) of spike protein. Region in green is RBM of receptor binding domain, represented by both yellow and green. Apigenin is colored in navy blue. Apigenin interacts with RBM, which is the main ligand for the ACE2 enzyme in humans. (b) Amino Acid Residues Involved in the Hydrogen Bonding Between Apigenin and RBM. The red line marks the hydrogen bond. Labeling includes ligand cluster, ligand number, atom involved in the interaction at ligand side, amino acid of RBM involved in the interaction, and the hydrogen bond length. Apigenin specifically binds in two positions within RBM.

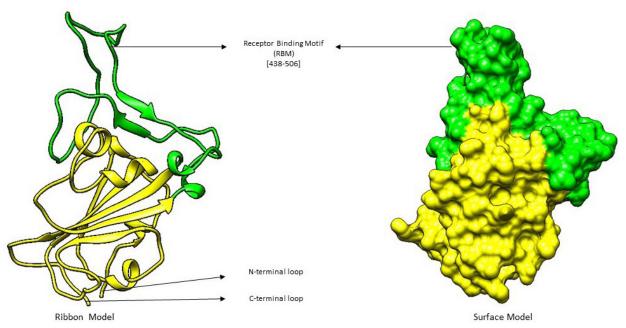


Figure 3. Ribbon and Surface Structure of Receptor Binding Domain (RBD) in the Spike Protein of SARS-CoV-2. Region highlighted in green shows RBM.

responsible for membrane fusion.<sup>26</sup> The recognition of the receptor, ACE2, is achieved by an RBD in the spike protein, which stretches from amino acid 333 to 527.<sup>27</sup> Studies on the crystal structure of the protein showed that the RBD of SARS-CoV-2 contains a core RBM that mediates direct contact with ACE2 receptor.<sup>28</sup> The receptor-binding motif in RBD lies from 438 to 506 within the domain (Figure 3).

The motif has several amino acid sequences, which show a very high binding affinity with the ACE2 protein.<sup>29</sup> The main amino acid sequences involved in the interaction are G446, Y449, L455, F486, N487, Y489, Q493, S494, T500, N501, G502, and Y505. These specific amino acids enhance the efficiency of viral binding with ACE2.<sup>29,30</sup> The binding of the phytochemicals to this specific moiety can

possibly regulate the attachment of the virus to the host cell.

In our study, we have extracted 20 phytochemicals from 100 studied compounds on the basis of their physicochemical and pharmacokinetic properties, biological activities, possible target interactions, similar compounds in humans, and gene regulations using bioinformatic tools and have docked them with the RBD of the spike protein. This makes our effort novel as filtering these compounds through various criteria makes sure that the compound holds efficient drug-like properties inside our body and would possibly inhibit the viral attachment. To our surprise, we got overwhelming results as two of the phytochemicals were found to get bound with the amino acid sequences readily involved in the interaction of RBM in spike protein and ACE2. The bonding could be a robust test of an iterative framework of inhibiting virus-receptor interaction with the help of phytochemicals.

#### **Competing Interests**

None.

#### **Supplementary Materials**

Supplementary file 1 contains Table S1.

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