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## Evaluating in Silico Docking, Drug-Likeness, and QSAR Studies of Ayush Kwath as A Potential Immunomodulator



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### ABSTRACT

With the alarming increase in the number of Covid-19 active cases, immunostimulation has become a need for research. A wide range of ayurvedic formulations such as Nilavembu Kudineer, Kabasura Kudineer, and Sudarshan churn is prescribed as a prophylactic measure. **Objective:** This study aims to explore the drug-likeness, docking, and immunomodulatory properties of Ayush Kwath recommended by the Ministry of AYUSH. Ayush Kwath constitutes the herbs found in every Indian kitchen including cinnamon, pepper, ginger, and tulsi. **Method:** The drug-likeness of 22 compounds was evaluated and molecular docking for these compounds was performed against proteins 4QBZ, 4O9H, 2B90, and 2AZ5 by *In silico* techniques. The EC<sub>50</sub> of constituents was collected and selected as the training set. The chemical descriptors were calculated using Padel software. **Results:** All 22 compounds were docked with proteins and the binding energies obtained were in the range of -2.17 to -9.85. The developed QSAR model showed a high activity-descriptor relationship with an accuracy of 95% ( $r^2=0.95$ ) and a prediction accuracy of 90%.



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## INTRODUCTION

It has been almost a year, since the first SARS CoV2(Severe Acute Respiratory Syndrome Corona Virus 2) case was reported in India. Despite the usage of masks, and hand sanitizers and maintaining social distancing the cases continue to increase exponentially. India, from ranking second in the total number of active cases, the present day the active cases began declining after taking necessary precautions and preventive measures. Having hundreds of vaccines in the pre-clinical and clinical stages we are forced to look for alternatives. Ministry of AYUSH (Ayurveda, Yoga & Naturopathy, Unani, Siddha, and Homoeopathy) recommended certain steps to be taken to improve the immunity of an individual such as<sup>[1]</sup>

- Drinking hot water
- Practising yogasanas, meditation and pranayama.
- Consuming chyawanaprash (10 gm), Golden milk (150ml) and Ayush Kadha.

Immunomodulators are medications that help to regulate or normalize the immune system. These include Immuno-adjuvants, Immunostimulants, and Immunosuppressants. Immuno-adjuvants enhance the efficacy of vaccines and therefore could be considered specific immune stimulants. Immunostimulants act by innate as well as adaptive immune responses. Immunosuppressants are often used to treat graft rejections and autoimmune diseases.<sup>[2]</sup> The phytochemical analysis of rasayana plants has revealed that a large number of compounds possess potent immunomodulatory properties<sup>[3]</sup>. Especially ursolic acid showed antimicrobial activity plus an immune-stimulatory effect.<sup>[4]</sup> Moreover, ginger and tulsi were tested for their immunostimulant activities against cancer and the constituents rosmarinic-acid and luteolin was found to be active phytochemicals.<sup>[5]</sup> This study focuses on the immunostimulatory potential of all the major active constituents identified from the constituents of Ayush kwath.

### Phytoconstituents:

Ayush Kwath or Ayush Kudineer or Ayush Joshanda is a combination of four medicinal herbs commonly used in every Indian kitchen - Basil leaves (tulsi), Cinnamon bark (dalchini), *Zingiber officinale* (sunthi), and Krishna marich (*Piper nigrum*).

**Preparation procedure:**

Four parts of Tulsi (*Ocimum sanctum*) leaves, 2 parts of Dalchini (*Cinnamomum zeylanicum*) stem bark, 2 parts of Sunthi (*Zingiber officinale*) rhizome, and 1 part of Krishna marich (*Piper nigrum*) fruit are powdered. Three grams of powder- comprising all ingredients are dissolved in 150ml boiled water. Jaggery, raisin, or lemon juice can be added to the decoction.<sup>[6]</sup>A list of major active constituents is furnished in Table 1.

**Table No 1. Major phytoconstituents identified**

S.No	Constituents
1	Alpha-Cubebene
2	Apigenin
3	Beta bisabolene
4	Carvacrol
5	Caryophyllene
6	Cinnamaldehyde
7	Cirsilineol
8	Cirsimaritin
9	Dipiperamide D
10	Dipiperamide E
11	Eugenol
12	Gingerol
13	Isothymusin
14	Linalool
15	Piperine
16	Piperitone
17	Rosmarinic acid
18	Shogaol
19	Ursolic acid
20	Wisanine
21	Zerumbone
22	Zingiberene

## MATERIALS AND METHODS

### Drug-likeness:

One of the most traditional methods to evaluate the drug-likeness of a compound is by using Lipinski's rule of five. This was estimated using the online software SwissADME.<sup>[7]</sup> Ghose, Veber, Egan, and Muegge are other filters used to evaluate drug-likeness.

### QSAR:

Quantitative Structure-Activity Relationship (QSAR) models are theoretical models that relate a quantitative measure of chemical structure to a physical property, or a biological activity. A total of 22 major phytoconstituents with immunomodulatory were collected from various databases and literature. 22 phytoconstituents were selected based on their availability in plants. The effective dose EC<sub>50</sub> of constituents was collected from various articles.<sup>[8-18]</sup> Nine compounds were selected as the training set. Four compounds were taken as a test set. The compounds were downloaded and energy was minimized. Molecular descriptors were calculated by using Padel Descriptor. The descriptors include 2D descriptors such as AlogP, autocorrelation, atom count, atom type electron topological state descriptors, Crippen's logP and molar refractivity ring count, molecular linear free energy relation descriptors, etc. The QSAR model development was done by using DTC based on the MLR method. For validation of the developed QSAR model LOO method was used and external validation ( $r^2$ ) is carried out to predict the accuracy of the QSAR model. Correlation coefficient ( $r$ ) quantifies the variation in the data and gives an idea of how closely the observed data tracks the fitted regression line. A perfect relation has  $r = +1$  (positively correlated) or  $-1$  (negatively correlated); no correlation has  $r = 0$ . The more scattered the data points, the lower the value of  $r$ . Leave-one-out (LOO) method was used for internal cross-validation regression coefficient ( $r^2_{cv}$ ), each molecule in the training set was eliminated once and the activity of the eliminated molecule was predicted by using the model developed by the remaining molecules.<sup>[19]</sup> The cross-validation regression coefficient was calculated using the equation which describes the internal stability of a model.

$$r^2 = 1 - \frac{\sum(Y_{pred} - Y)^2}{\sum(Y - \bar{Y})^2}$$

where  $r^2_{cv}$  refers to cross-validation regression coefficient,  $Y$  and  $Y_{pred}$  activity of the molecule in the training set, respectively and  $\bar{Y}$  is the average activity of all molecules in the

training set. The activity of each molecule in the test set was predicted using the model developed by the training set for external validation.

### **Molecular docking:**

The proteins were downloaded from Protein Data Bank (RCSB PDB) and processed with Molegro Molecular Viewer 2.5.0. Crystal structure of human TLR8 (Toll-Like Receptor 8) in complex with DS-802 (4QBZ), Crystal structure of the interleukin-4 (2B90), Structure of Interleukin-6 in complex with a Camelid Fab fragment (4O9H), Crystal Structure of TNF-alpha with a small molecule inhibitor (2AZ5) were obtained. All the proteins were recovered by X-ray diffraction with resolutions 2.00 Å, 2.10 Å, 2.42 Å, and 2.10 Å respectively. Ligands were downloaded from PubChem and energy was minimized in Chem 3D Ultra 8.0. The protein-ligand complexes were analyzed in Molegro Molecular Viewer 2.5.0. and Pymol.

## **RESULTS AND DISCUSSION**

### **Drug-likeness:**

Major active constituents were estimated for their drug-likeness according to Lipinski's rule of five and the violations were tabulated. Seven constituents violate one factor of Lipinski's rule of five. There is a permissible limit of not more than two violations and hence all the active constituents are found to possess drug-likeness<sup>[20]</sup>, the results of which are given in Table 2.

**Table no 2. Drug-likeness of the phytoconstituents**

S.No.	Constituent	Molecular formula	Molecular weight (g/mol)	Druglikeness
1	Alpha-Cubebene	C <sub>15</sub> H <sub>24</sub>	204.35	Yes; 1 violation: MLOGP>4.15
2	Apigenin	C <sub>15</sub> H <sub>10</sub> O <sub>5</sub>	270.24	Yes
3	Beta bisabolene	C <sub>15</sub> H <sub>24</sub>	204.35	Yes; 1 violation: MLOGP>4.15
4	Carvacrol	C <sub>10</sub> H <sub>14</sub> O	150.22	Yes
5	Caryophyllene	C <sub>15</sub> H <sub>24</sub>	204.35	Yes; 1 violation: MLOGP>4.15
6	Cinnamaldehyde	C <sub>9</sub> H <sub>8</sub> O	132.16	Yes
7	Cirsilineol	C <sub>18</sub> H <sub>16</sub> O <sub>7</sub>	344.32	Yes
8	Cirsimaritin	C <sub>17</sub> H <sub>14</sub> O <sub>6</sub>	314.29	Yes
9	Dipiperamide D	C <sub>36</sub> H <sub>40</sub> N <sub>2</sub> O <sub>6</sub>	596.71	Yes; 1 violation: MW>500
10	Dipiperamide E	C <sub>34</sub> H <sub>38</sub> N <sub>2</sub> O <sub>6</sub>	570.68	Yes; 1 violation: MW>500
11	Eugenol	C <sub>10</sub> H <sub>12</sub> O <sub>2</sub>	164.2	Yes
12	Gingerol	C <sub>17</sub> H <sub>26</sub> O <sub>4</sub>	294.39	Yes
13	Isothymusin	C <sub>17</sub> H <sub>14</sub> O <sub>7</sub>	330.29	Yes
14	Linalool	C <sub>10</sub> H <sub>18</sub> O	154.25	Yes
15	Piperine	C <sub>17</sub> H <sub>19</sub> NO <sub>3</sub>	285.34	Yes
16	Piperitone	C <sub>10</sub> H <sub>16</sub> O	152.23	Yes
17	Rosmarinic acid	C <sub>18</sub> H <sub>16</sub> O <sub>8</sub>	360.31	Yes
18	Shogaol	C <sub>17</sub> H <sub>24</sub> O <sub>3</sub>	276.37	Yes
19	Ursolic acid	C <sub>30</sub> H <sub>48</sub> O <sub>3</sub>	456.7	Yes; 1 violation: MLOGP>4.15
20	Wisanine	C <sub>18</sub> H <sub>21</sub> NO <sub>4</sub>	315.36	Yes
21	Zerumbone	C <sub>15</sub> H <sub>22</sub> O	218.33	Yes
22	Zingiberene	C <sub>15</sub> H <sub>24</sub>	204.35	Yes; 1 violation: MLOGP>4.15

MW-Molecular weight

MLOGP- Moriguchi logP calculated using SwissADME <sup>[21]</sup>

**QSAR:**

In the present work, the structural activity relationship is represented by developing a QSAR model that relates the 2D chemical descriptors with the biological activity. A set of 13 constituents were used for developing the QSAR model. The descriptor values and pEC50 values are given in Table 3.

**Table 3. Values of molecular descriptors and pEC50 values for training and test set.**

Compound number	Compound name	MR	nC	GATS8s	SpMax_DzZ	CrippenMR	Observed pEC50
1	Apigenin	69.85	15	1.058035	60.75699	74.8344	-1.19
2	Caryophyllene	66.59	15	0	43.58518	66.203	-0.256
3	Cinnamaldehyde	42.82	9	4.708587	19.82403	43.721	1.31
4	Gingerol	82.94	17	0.908696	102.959	85.9956	0.127
5	Piperine	82.14	17	1.336948	86.91907	85.142	0.795
6	Ursolic acid	133.52	30	1.080307	157.4421	135.5846	1.207
7	Rosmarinic acid	91.35	18	0.806936	119.5087	91.978	2.508
8	Shogaol	81.51	17	0.851925	93.50669	84.2418	-0.447
9	Zerumbone	68.4	15	0.879679	46.14586	71.726	0.414
10 <sup>T</sup>	Carvacrol	47.14	10	0	22.91476	48.521	-2.426
11 <sup>T</sup>	Eugenol	48.72	10	2.187413	26.80388	50.709	0.884
12 <sup>T</sup>	Linalool	49.5	10	0.345941	30.074	48.9458	1.602
13 <sup>T</sup>	Piperitone	45.97	10	0	25.46987	49.299	-1.557

MR-Molar Refractivity

nC- Number of Carbon atoms

GATS8s and SpMax\_DzZ are autocorrelations and Burden modified eigenvalues respectively

CrippenMR- Crippen Molar Refractivity

pEC50- negative log of Effective concentration 50

The developed QSAR model showed a high activity-descriptor relationship with an accuracy of 95% ( $r^2=0.95$ ) and a prediction accuracy of 90%. The model is developed using five descriptors such as molar refractivity, number of the carbon atom, autocorrelation (GATS8s), Burden modified eigenvalues (SpMax\_DzZ) and Crippen MR correlated with immunostimulatory activity. The QSAR mathematical model equation derived through MLR (developed using DTC laboratory) is given below, representing the relationship between *in vivo* effective concentration (EC<sub>50</sub>) and chemical descriptors:

$$\text{Predicted log EC}_{50}(\text{mg}) = -13.5108(+/-3.65872) + 1.34982(+/-0.28727) * \text{molar refractivity} - 2.83894(+/-0.79643) * \text{nC} + 0.99685(+/-0.33596) * \text{GATS8s} - 0.16204(+/-0.0537) * \text{SpMax\_DzZ} - 0.41123(+/-0.13294) * \text{CrippenMR}$$

$$r^2=0.95, q^2=0.94$$

The values predicted using the developed QSAR model are given in Table 4.

**Table No 4. Comparison of experimental and predicted activity data calculated through the QSAR model based on best correlated chemical descriptors.**

Compound number	Compound name	Predicted activity	Observed pEC50
1	Alpha-Cubebene	-1.86497	
2	Beta-bisabolene	0.047491	
3	Cirsilineol	2.661634	
4	Cirsimaritin	1.176674	
5	Dipiperamide D	5.239269	
6	Dipiperamide E	1.841495	
7	Isothymusin	2.485849	
8	Wisanine	2.710736	
9	Zingiberene	0.377995	
10	Apigenin	-1.37408	-1.19
11	Caryophyllene	-0.49723	-0.256
12	Cinnamaldehyde	2.31004	1.31
13	Gingerol	-0.69377	0.127
14	Piperine	0.136707	0.795
15	Ursolic acid	-1.93585	1.207
16	Rosmarinic acid	0.847432	2.508
17	Shogaol	1.337369	-0.447
18	Zerumbone	1.358373	0.414
19	Carvacrol	1.565397	-2.426
20	Eugenol	-0.95978	0.884
21	Linalool	0.259828	1.602
22	Piperitone	-4.2491	-1.557

The validation is carried out by Leaving one out validation and external validation. Here, the external validation is 0.90, which indicates a prediction accuracy of 90% and  $q^2$  value of 0.94. A prediction accuracy value of 70% and above is favorable.  $r^2$  indicates the correlation between the activity (dependent variable) and descriptors (independent variable) for the training set compounds. From the model, descriptors such as molar refractivity, and GATS8s showed a positive correlation with the activity, where an increase in the value of the descriptor increases the activity. Descriptors such as a number of carbon atoms, SpMax\_DzZ and CrippenMR showed negative correlation, where activity increases with the decreased



value of descriptors. Thus, the developed QSAR model holds good for the prediction of immunostimulatory activity. Figure 1 indicates the scatter plot of observed and predicted activity.

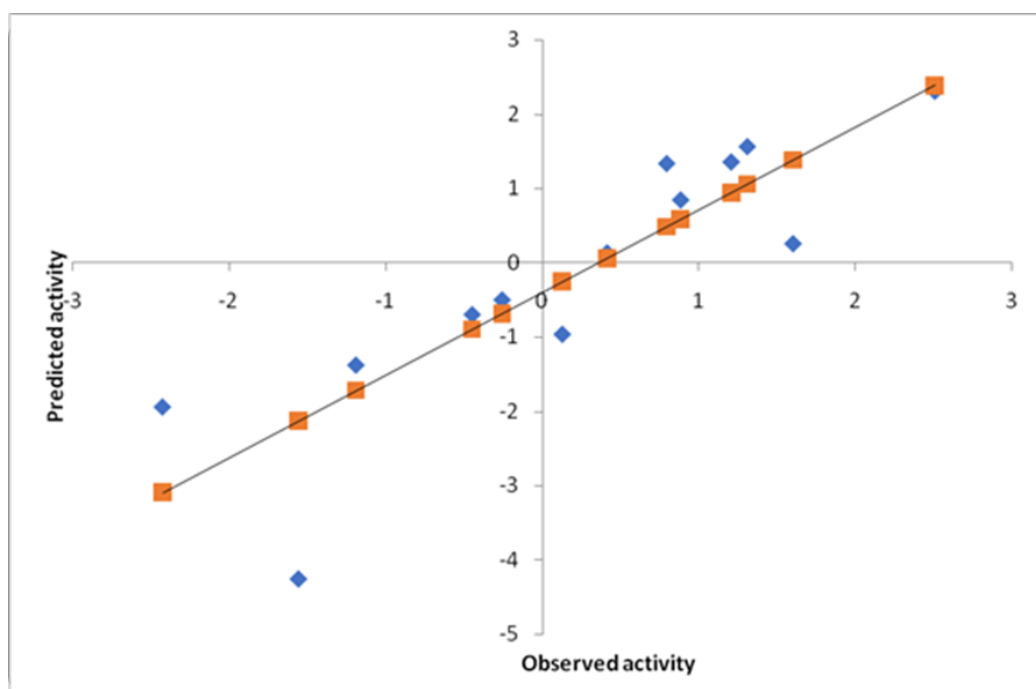


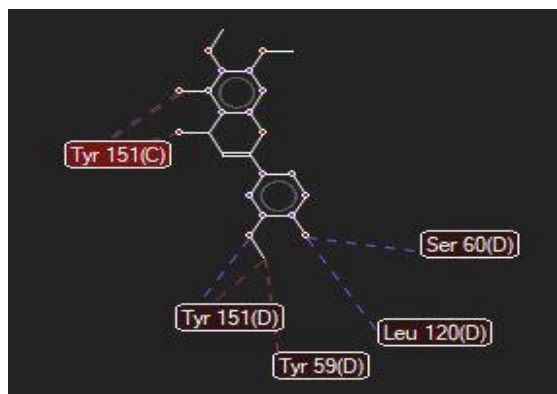
Figure no 1. Scatter plot depicting the predicted and observed activity

### Molecular docking:

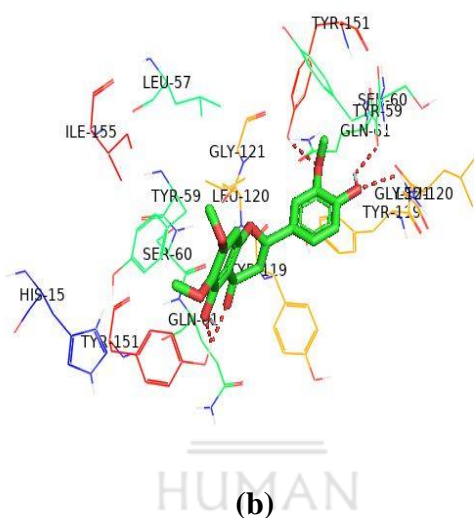
The docking results obtained for TLR8 (4QBZ) ranged from -2.17 to -8.43. The best binding energy was observed with Dipiperamide E and Piperine. The docking results obtained for interleukin-4 (2B90) ranged from -2.55 from -6.84 and IL6 (4O9H) binding energies ranged from -0.9 to -6.21. Crystal Structure of TNF- $\alpha$  (2AZ5) possessed a good binding energy with curvilineal (-8.13), Dipiperamide D (-9.79), Dipiperamide E (-9.85), Wisanine (-8.02), and ursolic acid (-8.89). The binding energy of all the ligands against four receptors is given in Table 5. Figure 2 depicts the binding of cirsilineol with TNF-alpha.

**Table no 5. Binding energies in Kcal/mol of the selected phytoconstituents against selected immunomodulatory receptors**

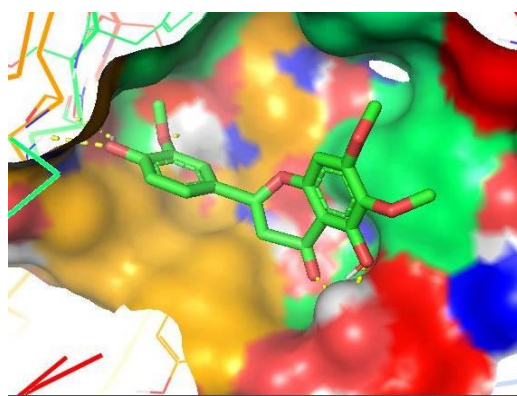
S.No.	Constituent	Binding energy (kcal/mol)			
		4QBZ	2B90	4O9H	2AZ5
1	Alpha-Cubebene	-5.66	-5.08	-4.76	-5.41
2	Apigenin	-7.04	-3.69	-5.56	-5.64
3	Beta bisabolene	-4.38	-3.47	-3.53	-5.93
4	Carvacrol	-5.67	-5.43	-3.46	-4.8
5	Caryophyllene	-6.4	-4.64	-4.84	-6.24
6	Cinnamaldehyde	-5.04	-3.85	-4.31	-4.81
7	Cirsilineol	-5.22	-4.84	-4.91	-8.13
8	Cirsimaritin	-6.63	-5.22	-5.32	-6.67
9	Dipiperamide D	-6.11	-5.32	-6.4	-9.79
10	Dipiperamide E	-7.2	-6.84	-6.07	-9.85
11	Eugenol	-4.77	3.76	-3.69	-3.95
12	Gingerol	-5.08	-2.85	-0.9	-4.57
13	Isothymusin	-6.36	-6.82	-5.23	-6.93
14	Linalool	-4.15	-3.82	-3.42	-4.85
15	Piperine	-8.43	-5.64	-5.81	-7.43
16	Piperitone	-4.7	-5.14	-4.21	-5.08
17	Rosmarinic acid	-5.25	-2.69	-5.73	-5.58
18	Shogaol	-2.17	-2.55	-1.85	-3.26
19	Ursolic acid	-6.6	-6.09	-6.21	-8.89
20	Wisanine	-5.88	-5.1	-5.52	-8.02
21	Zerumbone	-6.54	-4.58	-5.21	-5.15
22	Zingiberene	-4.77	-3.73	-4.16	-5.11



(a)



(b)



(c)

**Figure 2. Cirsilineol binding with TNF-alpha (2AZ5) (a) shows the 3D amino acids interaction with cirsilineol. (b) shows the 2D amino acids' interaction with cirsilineol. (c) the mesh surfaces binding pocket of cirsilineol in TNF-alpha (2AZ5).**

## CONCLUSION

The major phytoconstituents from Ayush Kwath were identified and downloaded from ligand databases. The drug-likeness of the constituents was evaluated using Lipinski's rule of five. The ligands were docked against immunomodulatory receptors like TLR 8, IL-4, IL-6, and TNF-alpha. Compounds like apigenin, cl, cirsimaritin, dipiperamide D, dipiperamide E, isothymusin, piperine, and ursolic acid provided good binding energies. The QSAR analysis established the immunostimulatory activity of the corresponding compounds. The developed QSAR model showed a high activity-descriptor relationship with an accuracy of 95% ( $r^2=0.95$ ) and a prediction accuracy of 90%. A forward feed multiple linear regressions QSAR model was developed using a leave-one out approach for the prediction of immunomodulatory activity and no significant differences were observed in the predicted and observed activities.

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