

MOLECULAR DOCKING APPLICATION OF JUSTICIA BEDDOMEI ON ANGIO TENSIN CONVERTING ENZYME IN ANTI-HYPERTENSIVE ACTIVITY

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ABSTRACT:

Justicia beddomei is a siddha herbal drug having many therapeutic value. Plan of the research application is to catch out the functioning ingredient of Justicia beddomei to bind including ACE by molecular Close method. In tHis application is to catch the efficacy of the lead particle in the Plant Justicia beddomei to bind including core bio functioning amino acid residues, which involve in the enzymatic activity of the Angiotensin -converting enzyme (ACE) that has greater level of important in the management of blood pressure. For tHis application arrangement of Ligand of Justicia beddomei arranged and Translucent metamorphose of the spot protein Human ACE including PDB 1O86 is regained from Protein Data Bank. Based on the sequel of the computational application it was introduce that the bio-functioning blend's like Anisotine, Orientin, Adhatodine and Vasicoline being in the Plant *Justicia beddomei* letout remarkable binding opposed to the spot protein Angiotensin converting enzyme by binding including functioning protein molecule being on the functioning location thereby it was decided that these amalgam have assuring anti-hypertensive activity. It was decided that the phyto chemicals being in the plant *Justicia beddomei* possess important anti-hypertensive activity.

KEY WORDS:

Siddha drug, *Justicia beddomei* , Kuruthi azhal, Adatodai,ACE.

INTRODUCTION:

Adatodai (*Justicia beddomei*) is a siddha herbal Drug belongs to the Acanthacea family. It is called as Malabar Nut in English. Adatodai (*Justicia beddomei*) is grown as shrub. Leaf, Flower, Bark and Root used as medicinally in Siddha system of medicine. It has anti spasmodic, Expectorant, Germicide, Anthelmintic and Diuretic activity [2-7]. *Justicia beddomei* leaf especially used to treat the Kuruthi azhal Noi (Hyper tension) in siddha. Adatodai in siddha used in the treatment of hyper tension in the form of Leaf juice 10-20 drops including honey, Leaf decoction including cardamomum extract decoction. A combination *Justicia beddomei* root, Grapes (*Vitis vinifera*), *Terminalia chebula* decoction including honey and sugar [2]. In tHis molecular Close application help to identifying the functioning particle in the *Justicia beddomei* in the treatment of Hypertension including Standard drug Captopril. This molecular close application was done in Noble research solutions in Chennai.

Tab-1 List of Phytochemicals Chosen for close [1]

Name of the Herb[3]	Phytochemicals Name
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<i>Adhathoda vasica(Adatodai)</i>	<ul style="list-style-type: none"> • Adhatodine • Vasicinone • Vasicoline • Orientin • Anisotine • Aniflorine
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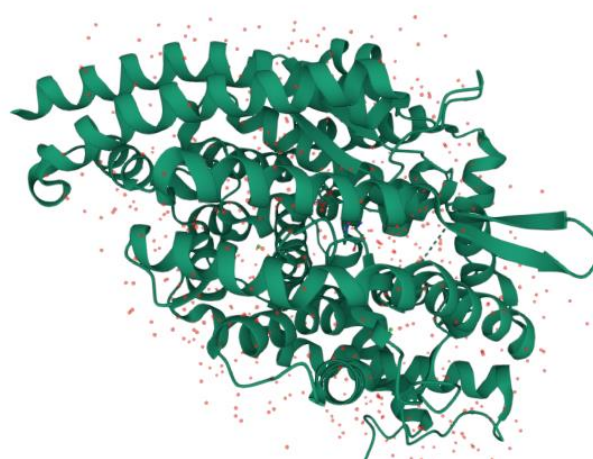
Standard – Captopril

Objective:[6-8]

The major objective of the application is to catch the efficacy of the lead particle in *Adhathoda vasica(Adatodai)* to bind including these core bio functioning amino acid residues, GLU162, GLN 281, HIS 353, ALA 354, HIS 383, GLU 384, HIS 387 , HIS 513, GLU 411, LYS 511, TYR 520, TYR 523 which mediates the enzymatic activity of the Angiotensin-converting enzyme (ACE) that has greater level of significance in the management of blood pressure. ACE involved in the conversion of angiotensin I to Angiotensin ii. Angiotensin ii tend to increase blood pressure (Kuruthi azhal) by narrowing of blood vessels. Hence controlling these amino acid residues hinderthe enzymatic activity of ACE thereby lower the blood pressure (Kuruthiazhal) by exhausting the release of Angiotensin II. Lead particle in the Adhatoda vasica, that hinderthe enzyme ACE will considerably has greatertherapeutic potential in lowering greaterblood pressure (Kuruthi azhal) and in the management of hypertension.

PDB	Name of the Spot of the Application
1O86	Arrangement of Human Angiotensin Converting enzyme (ACE)

Fig-1- Human angiotensin converting enzyme (1O86)



RECEPTOR ARRENGEMENT

Crystalline structure of the target protein Human angiotensin converting enzyme with PDB 1O86 was retrieved from protein data bank and protein clean-up process was done and essential missing hydrogen atom were being added. Different orientation of the lead molecules with respect to the target protein was evaluated by Autodock version 4 program and the best dock pose was selected based on the interaction study analysis.

Methodology

Docking calculations were carried out for retrieved phytochemicals against target enzyme H1 receptor. Essential hydrogen atoms, Kollman united atom type charges, and solvation parameters were added with the aid of AutoDock tools (Morris, Goodsell et al., 1998). Affinity (grid) maps of $\times\times$ Å grid points and 0.375 Å spacing were generated using the Autogrid program (Morris, Goodsell et al., 1998). AutoDock parameter set- and distance-dependent dielectric functions were used in the calculation of the van der Waals and the electrostatic terms, respectively. Docking simulations were performed using the Lamarckian genetic algorithm (LGA) and the Solis & Wets local search method (Solis and Wets, 1981). Initial position, orientation, and torsions of the ligand molecules were set randomly. All rotatable torsions were released during docking. Each docking experiment was derived from 2 different runs that were set to terminate after a maximum of 250000 energy evaluations. The population size was set to 150. During the search, a translational step of 0.2 Å, and quaternion and torsion steps of 5 were applied. This Docking Study was done in Noble research solution, Chennai.

Fig-2 -2D and 3D Arrangement of Chosen Ligands

Fig-2 a-Adhatodine

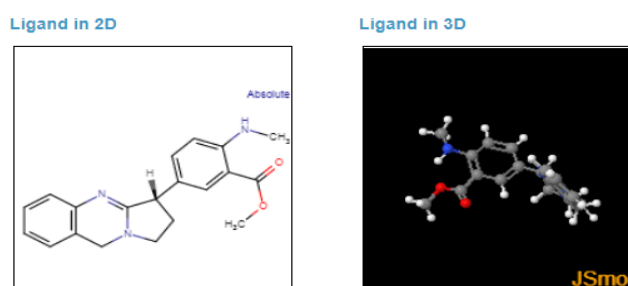


Fig-2 b-Vasicinone

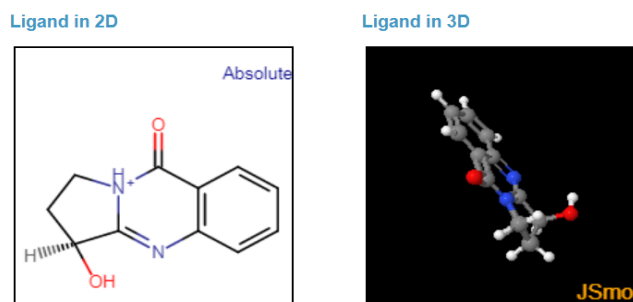


Fig-2 c-Vasicoline

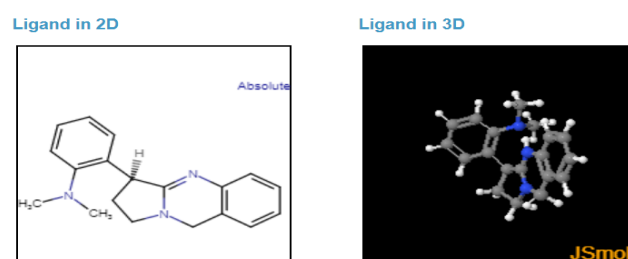


Fig-2 d-Anisotine

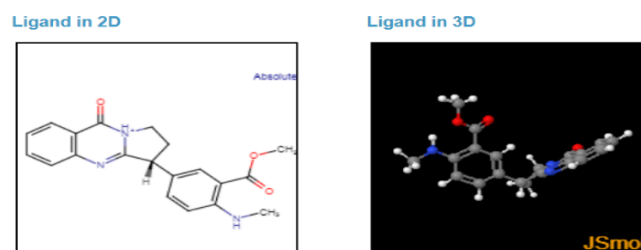


Fig-2 e-Orientin

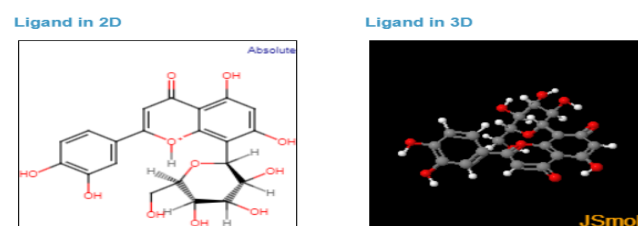


Fig-2 f-Aniflorine

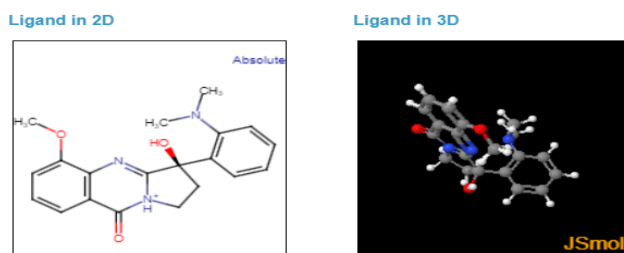
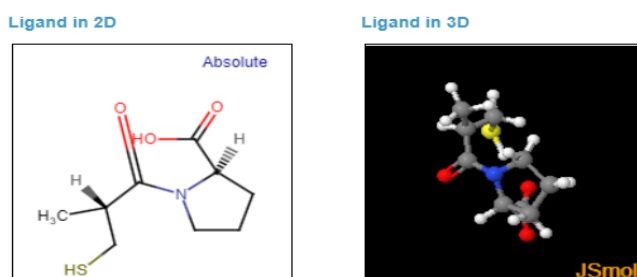


Fig-2 g-Captopril



Tab-2-Ligand Landscape of the Blends chosen for close opposed to Angiotensin converting enzyme (1086)

Blend name	Atomic weight g/mol of Ligands	Atomic Formula of Ligands	Donor H -Bound	Acceptor H -Bound	Rotatable Bounds
Adhatodine	337.416	C ₂₀ H ₂₁ N ₃ O ₂	1	2	4
Vasicinone	202.21	C ₁₁ H ₁₀ N ₂ O ₂	1	3	0
Vasicoline	291.4	C ₁₉ H ₂₁ N ₃	0	2	2
Anisotine	349.4	C ₂₀ H ₁₉ N ₃ O ₃	1	5	4
Orientin	448.14	C ₂₁ H ₂₀ O ₁₁	8	11	3
Aniflorine	351.4	C ₂₀ H ₂₁ N ₃ O ₃	1	5	3
Captopril	217.29	C ₉ H ₁₅ NO ₃ S	2	4	3

Tab-3-Compact of the molecular close studies of blends opposed to Angiotensin converting enzyme (1086)

Blends Name	Bounden Free power Kcal/mol	Hinderion constant Ki μM (*mM)(**nM)	Electrostatic power Kcal/mol	Intersubatomic power Kcal/mol	Total Conjoint Surface
Adhatodine	-7.76	2.04	-1.43	-8.37	772.606
Vasicinone	-4.95	237.11	-0.24	-5.24	506.99

Vasicoline	-7.40	3.76	-1.31	-7.62	671.025
Anisotine	-7.02	7.13	-0.08	-8.19	881.904
Orientin	-8.38	718.10	-0.62	-6.99	974.037
Aniflorine	-6.50	17.12	-0.04	-6.64	710.344
Captopril	-6.75	11.22	-1.47	-7.10	809.837

Tab-4 Amino acid Residue Conjoint of Lead and Standard opposed to Translucent arrangement of Angiotensin converting enzyme

Blend Name	Number of Conjoint s	Name of Amino acid Conjoint s in ACE															
Adhatodine	6 conjoint	353 HISTIDINE	383 HIS	384 GLU	391 PHE	407 PRO	411 GLU	512 PHE	513 HIS	518 VAL	523 TYR						
Vasicinone	4 conjoint	355 SER	383 HIS	384 GLU	387 HIS	512 PHE	518 VAL	523 TYR									
Vasicoline	6 conjoint	162 GLU	281 GLN	353 HIS	354 ALA	369 GLN	376 GLU	377 ASP	380 VAL	384 GLU	511 LYS						
Anisotine	9 conjoint	162 GLU	353 HIS	354 ALA	369 GLN	377 ASP	383 HIS	384 GLU	411 GLU	513 HIS	520 TYR	523 TYR					
Orientin	9 conjoint	162 GLU	277 ASN	279 TRP	281 GLN	282 THR	353 HIS	354 ALA	369 GLN	376 GLU	377 ASP	380 VAL	383 HIS	384 GLU	513 HIS	520 TYR	523 TYR
Aniflorine	5 conjoint	162 GLU	281 GLN	282 THR	353 HIS	376 GLU	377 ASP	380 VAL	383 HIS	457 PHE	523 TYR	527 PHE					
Captopril	8 conjoint	281 GLN	353 HIS	380 VAL	383 HIS	384 GLU	457 PHE	511 LYS	513 HIS	520 TYR	523 TYR	2000 GLY					

Close Pose Fig-3-a-Adhatodine including Angiotensin converting enzyme (PDB-1086)

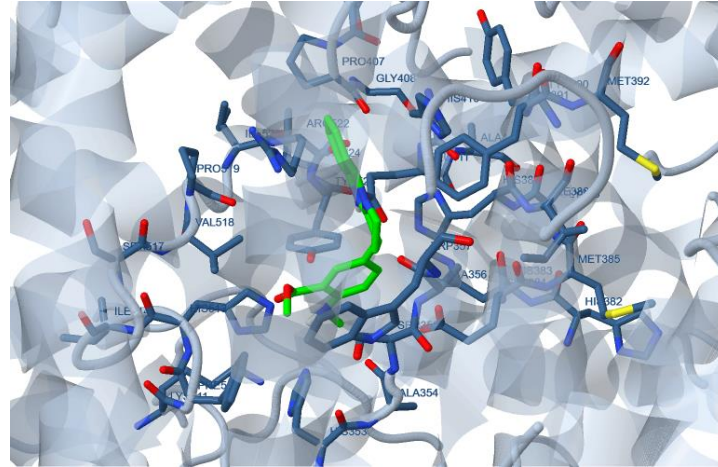


Fig-3-b-2D Conjoint Design Analysis

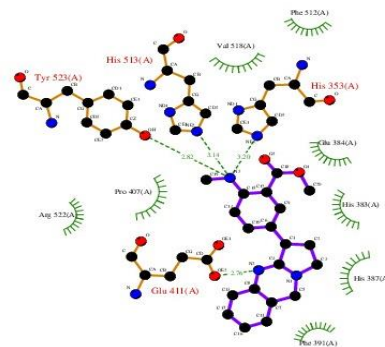


Fig-3-c Hydrogen chain designing along core amino acid Analysis

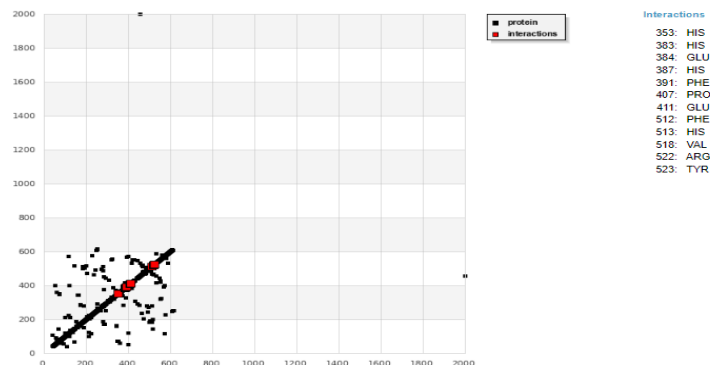


Fig-4-a-Vasicinone along Angiotensin converting enzyme (PDB-1O86)

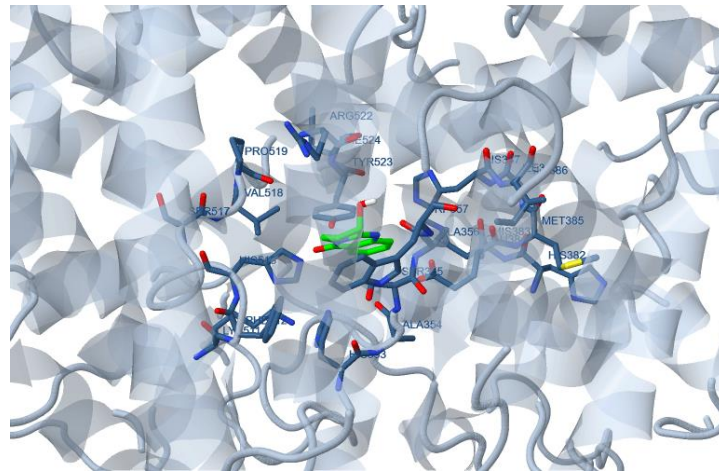


Fig-4-b-2D Conjoint Design Analysis

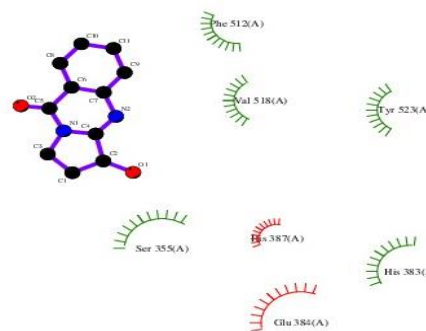


Fig-b-c-Hydrogen chain designing along core amino acid Analysis

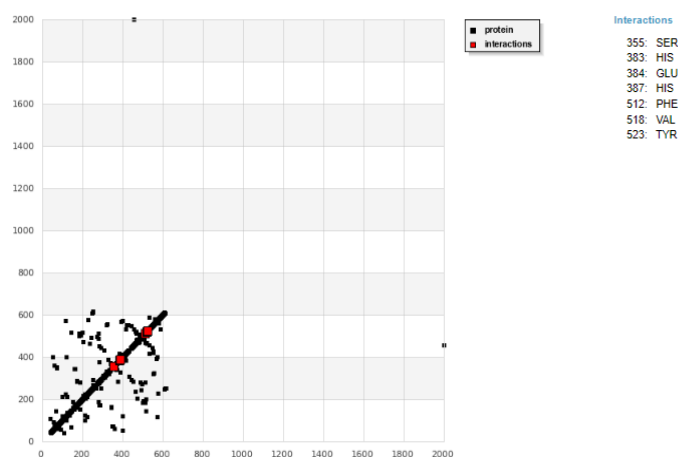


Fig-5-a-Vasicoline along Angiotensin converting enzyme (PDB-1O86)

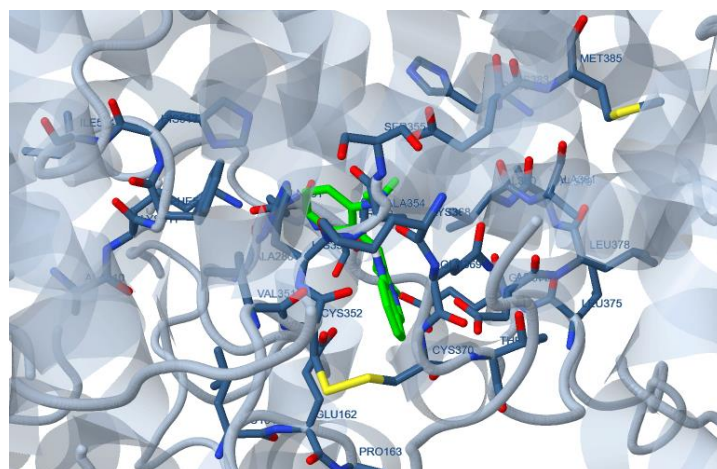


Fig-5-b-2D Conjoint Design Analysis

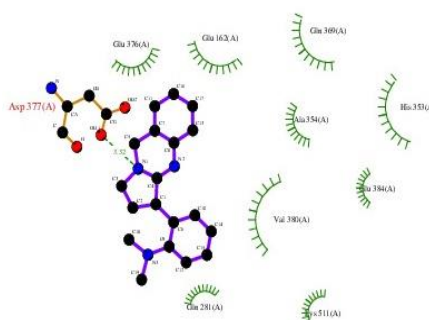
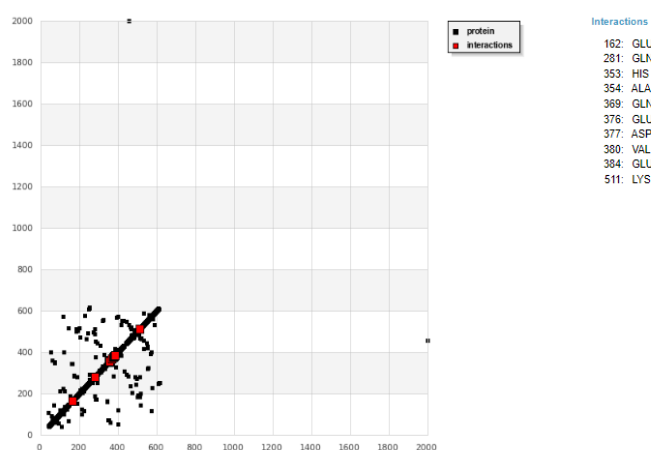


Fig-5-c-Hydrogen chain designing along core amino acid Analysis



References, please cite:

Fig-6-a-Anisotine along Angiotensin converting enzyme (PDB-1086)

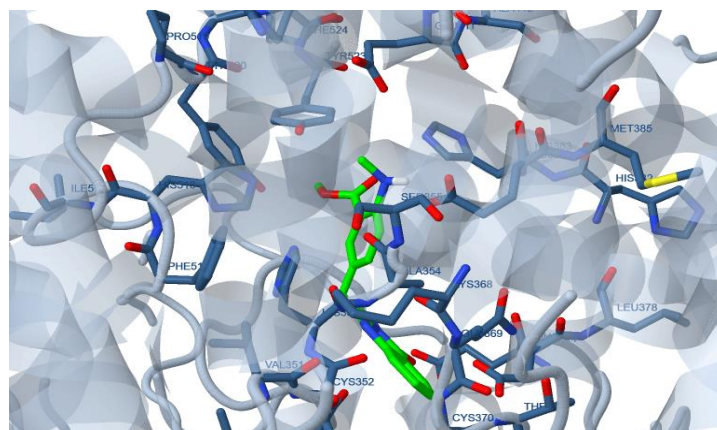


Fig-6-b-2D Conjoint Design Analysis

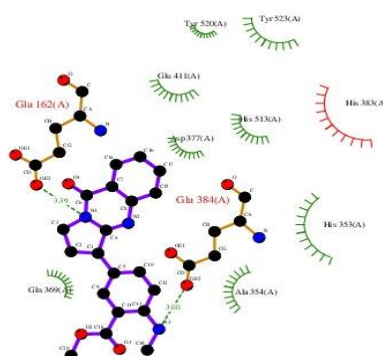


Fig-6-c-Hydrogen chain designing along core amino acid Analysis

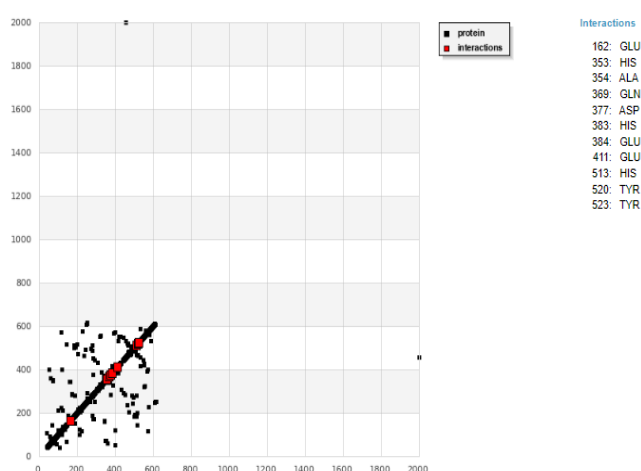


Fig-7-a- Orientin along Angiotensin converting enzyme (PDB-1086)

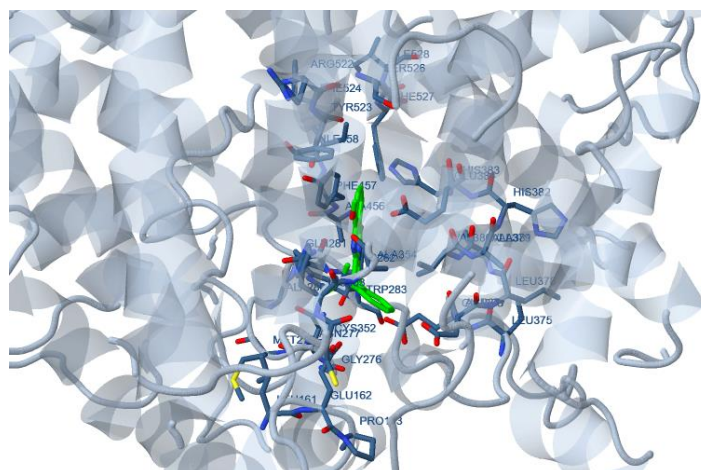


Fig-8-b- 2D Conjoint Design Analysis

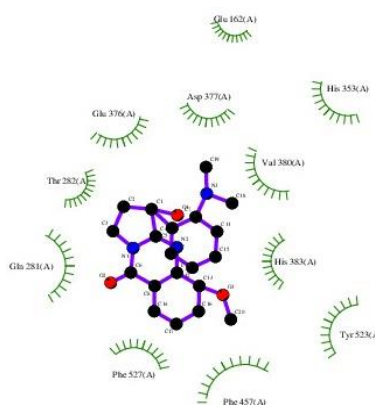


Fig-8c- Hydrogen chain designing along core amino acid Analysis

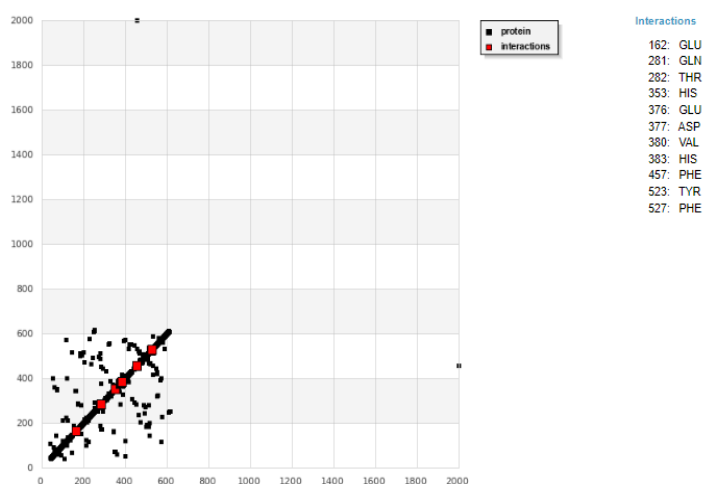


Fig-9-a-Captopril along Angiotensin converting enzyme (PDB-1O86)

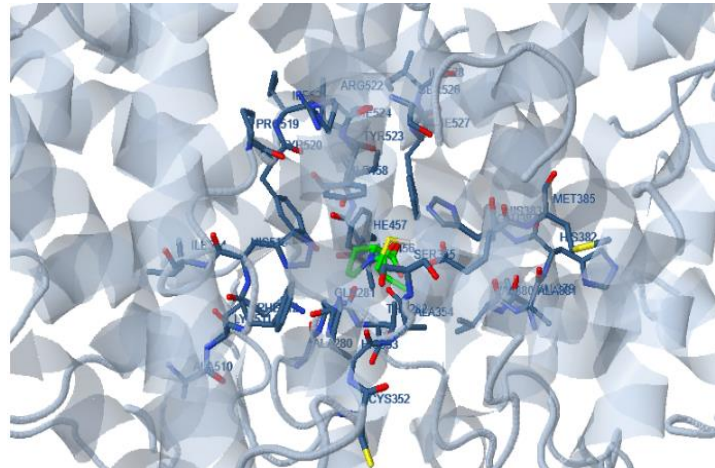


Fig-9-b- 2D Conjoint Design Analysis

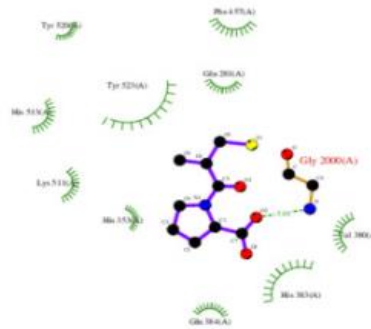
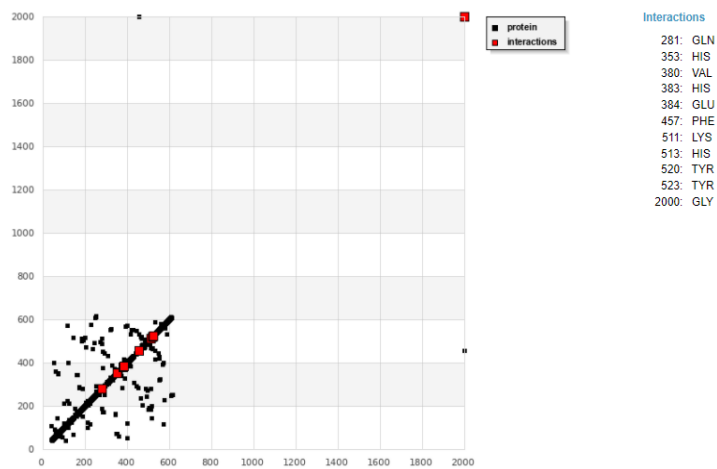


Fig-9-c- Hydrogen chain designing including core amino acid Analysis



Observation and Inference

Total of 6 bio functioning lead blends were regained from the herb *Justicia beddomei*. From reported data of the Plant, The phytochemicals such as Adhatodine, Vasicoline, Anisotine and Orientin reveals maximum of 6 to 9 conjoints including the core functioning amino acid residues being on the spot ACE. Followed by this the blends such as Vasicinone and Aniflorine ranked second including the maximum of 4 to 5 conjoints including the functioning location of the spot enzyme ACE in contrast including standard drug Captopril which reveals 8 conjoints over the spot enzyme.

RESULT AND DISCUSSION

List of Phytocomponents in *Justicia beddomei* Chosen for close shown in Tab-1, Landscape of the Blends chosen for close opposed to Angiotensin converting enzyme (1O86) shown in Tab-2, Summary of the molecular close studies of blends opposed to Angiotensin converting enzyme (1O86) shown in Tab-3, Amino acid Residue Conjoint of Lead and Standard opposed to Translucent arrangement of Angiotensin converting enzyme shown in Tab-4. Standard drug used as Captopril. Fig-1-shows arrangement of Human angiotensin converting enzyme (1O86) from PDB. Fig-2 shows -2D and 3D Arrangement of Chosen Ligands of *Adhathoda vasica*. Fig-3-9- shows Close pose of Ligand (Adhatodine, Vasicinone, Vasicoline, Orientin, Anisotine, Aniflorine) including angiotensin converting Enzyme (PDB -1086). Anisotine has 9 conjoint including amino acids of 162 GLU, 353 HIS, 384 GLU, 513 HIS, 520 TYR, 523 TYR. Orientin has 9 inter activity including amino acids of 162 GLU, 281 GLN, 353 HIS, 354 ALA, 383 HIS, 384 GLU, 513 HIS, 520 TYR, 523 TYR. Adhatodine has 6 conjoint including amino acids of 353 HIS, 383 HIS, 384 GLU, 411 GLU, 513 HIS, 523 TYR. Vasicoline has 6 conjoint including amino acids being in spot ACE of 162 GLU, 281 GLN, 353 HIS, 354 ALA, 384 GLU, 511 LYS. So the herb *Justicia beddomei* possess important anti-hypertensive activity.

CONCLUSION

Based on the results of the computational analysis it was decided that the bio-functioning blend's like Anisotine, Orientin, Adhatodine and Vasicoline being in the herb *Justicia beddomei* reveals important binding opposed to the spot protein Angiotensin converting enzyme by interacting including functioning amino acid being on the functioning location there by it was decided that these blends may exerts assuring anti-hypertensive activity. It was decided that the phytochemicals being in the herb *Justicia beddomei* possess important anti-hypertensive activity.

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