

Catechin and Quercetin ligand based analysis against peanut allergy using computational studies

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[Received-25/03/2015, Published-17/04/2015]

ABSTRACT

Peanut allergy is common, especially in children. Peanut allergy symptoms can range from a minor irritation to anaphylaxis. For some people with peanut allergy, even tiny amounts of peanuts can cause a serious reaction. Peanut allergy is one of the most common causes of severe allergy attacks. In a Western community about 3 in 500 children had a reaction to peanut by 5 years of age.

The peanut allergen enters the body with uptake of peanut. After digestion it is absorbed by specialized M cells. The allergen is then presented to the antigen processing cells. The allergen protein is then processed into peptide fragments. These fragments are then presented to MHC-II. The T_H cells in the surrounding region recognize this MHC-allergen complex and triggers humoral and cellular immunity. Activation of T_H cells leads to release of cytokines which stimulate B cells which in turn produce IgE. Two types of T_H cells are involved in the mechanism T_{H1} and T_{H2} . Activation of T_{H1} leads to release of IL-2, INF- γ and TNF- α whereas activation of T_{H2} leads to release of IL-4, IL-5, IL-9 and IL-13. IgE binds with the peptide fragment presented by MHC-II and activates the mast cells along with basophils and eosinophils from the surrounding region. IgE binds through the high affinity surface receptor $F_{c\epsilon}RI$ to the activated cells. Binding of mast cells and basophils causes release of Histamines, Heparin, etc whereas binding of eosinophil causes release of eosinophil peroxidase and eosinophil derived neurotoxin.

The work was performed with virtual library of Quercetin and Catechin derivatives which were collected from PubChem and screened them for Ara h1 binding. Further, prediction models for predicting the antiallergic activity of these compounds were developed based on binding interaction with Ara h1 as descriptor.

Keywords: Peanut, Ara h1, IgE, Quercetin, Catechin, antiallergic.

INTRODUCTION:

Drug design, sometimes referred to as rational drug design or more simply rational design, is the inventive process of finding new medications based on the knowledge of a biological target.^[17] The drug is most commonly an organic small molecule that activates or inhibits the function of a biomolecule such as a protein,

which in turn results in a therapeutic benefit to the patient. In the most basic sense, drug design involves the design of small molecules that are complementary in shape and charge to the biomolecular target with which they interact and therefore will bind to it. Drug design frequently but not necessarily relies on computer

modeling techniques.^[18] This type of modeling is often referred to as computer-aided drug design.

Peanut allergy is common, especially in children. Peanut allergy symptoms can range from a minor irritation to a life-threatening reaction (anaphylaxis). For some people with peanut allergy, even tiny amounts of peanuts can cause a serious reaction. Peanut allergy is one of the most common causes of severe allergy attacks.^[2] When someone has a food allergy, his/her body sort of misfires. Instead of treating the peanut like any old food, the body reacts as if the peanut is harmful. In an attempt to protect the body, the immune system produces antibodies against that food.^[4] In a Western community about 3 in 500 children had a reaction to peanut by 5 years of age. Overall about 1-2% of the populations have a clinical reaction to peanuts. About 3% of children have a positive peanut allergy test (such as a skin prick test) but only 1/3 of these will develop reactions on eating peanuts. The occurrence of peanut allergy in childhood differs greatly in different countries. Antibodies called immunoglobulin E (IgE) is designed to fight off the invaders. IgE antibodies trigger the release of chemicals into the body. One of these is histamine. The release of histamine can affect a person's lungs, gastrointestinal tract, skin, and cardiovascular system, causing allergy symptoms like stomachache, vomiting, itchy hives, and swelling. An allergic response to peanuts usually occurs within minutes after exposure, and symptoms range from mild to severe.^{[1][3]}

The peanut allergen enters the body with uptake of peanut. After digestion it is absorbed by specialized epithelial cells (M cells). The allergen is then presented to the antigen processing cells (dendritic cells). The allergen protein is then processed into peptide fragments. These fragments are then presented to MHC-II. The T_H cells in the surrounding region recognize this MHC-allergen complex and triggers humoral and cellular immunity. Activation of T_H cells leads to release of cytokines which stimulate B cells which in turn

produce IgE. Two types of T_H cells are involved in the mechanism T_{H1} and T_{H2}. Activation of T_{H1} leads to release of IL-2, INF- γ and TNF- α whereas activation of T_{H2} leads to release of IL-4, IL-5, IL-9 and IL-13. IgE binds with the peptide fragment presented by MHC-II and activates the mast cells along with basophils and eosinophils from the surrounding region. IgE binds through the high affinity surface receptor Fc ϵ RI to the activated cells. The activated cells cross link with the peanut allergen and release chemical compounds. Binding of mast cells and basophils causes release of Histamines, Heparin, etc whereas binding of eosinophil causes release of eosinophil peroxidase and eosinophil derived neurotoxin. These chemical compounds upon their release show symptoms like vomiting, diarrhea asthma and in severe cases anaphylaxis and even death.^{[5][6][7]} The symptoms shown by the patients suffering from peanut allergies include skin reactions, such as hives, redness or swelling, itching or tingling in or around the mouth and throat, digestive problems, such as diarrhea, stomach cramps, nausea or vomiting, tightening of the throat, shortness of breath or wheezing, runny nose.

The work was performed with virtual library of Quercetin and Catechin derivatives which were collected from PubChem and screened them for Ara h1 binding. Further, prediction models for predicting the antiallergic activity of these compounds were developed based on binding interaction with Ara h1 as descriptor. This prediction model was used for predicting the antiallergic activity of newly developed analogues. Molecular modeling techniques (molecular docking and rescoring using OPLS-2005) were used to find the series of Quercetin and Catechin analogues that should be modified for energetically favorable interaction with Ara h1 and for better antiallergic activity.

Peanut Allergens:

Peanut allergens are class I allergens, are water-soluble glycoprotein and are stable to heat, acid

and enzymatic digestion. Into Allergome database, at this time the most all-inclusive collection of allergen data and on protein family database, allergens were classified in protein families. In the last few years has been an explosion in the identification and sequencing of food allergens and among these of peanut allergens. So if in October 2006 were 10 listed allergenic proteins in peanut (agglutinin, Ara h1, Ara h1, Ara h2, Ara h3, Ara h4, Ara h5, Ara6, Ara h7, Ara h8, oleosin) in October 2009, 11 peanut allergens, named Ara h1 – Ara h11, have been identified, largely characterized and accepted by Allergen Nomenclature Subcommittee of the International Union of Immunological Societies (IUIS).^[8]

ALLERGEN	BIOCHEMICAL NAME	MW(SDS_PAGE), (kDa)
ARA h1	Cupin (Vicillin-type, 7S globulin)	64
ARA h2	Conglutin (2S albumin)	17
ARA h3	Cupin (Legumin-type, 11S globulin, Glycinin)	60
ARA h4	Cupin (Legumin-type, 11S, Glycinin)	37
ARA h5	Profilin	15
ARA h6	Conglutin (2S albumin)	15
ARA h7	Conglutin (2S albumin)	15
ARA h8	Pathogenesis-related protein, PR-10	17
ARA h9	Nonspecific lipid-transfer protein 1	9.8
ARA h10	16 kDa oleosin	16
ARA h11	14 kDa oleosin	14

Table No.1: Peanut Allergens.^[8]

ALLERGENS:^[8]

Ara h1 is a major peanut allergen recognized by over 90% of peanut sensitive population and the most analyzed peanut allergen. Amino acid sequence presents high sequence similarity with other plant vicilins, member of the cupin superfamily. It is a highly stable glycoprotein

homotrimer acidic complex, with mannose and complex N-glycans, consists of four domains: α helical bundle on one end, two sets of opposing antiparallel β sheets and α helical bundle on the opposite end which held together via hydrophobic interactions. Besides it is classified as conarachin because it was purified from the 40% to 85% fraction of ammonium sulphate saturation. Its pI is 4.55. Ara h1 has 23 allergenic epitopes of which 4 are immunodominant being recognized by more than 80% of patients. It is very abundant in peanut representing around of 12- 16% of total protein. Ara h1 has thermal stability and its allergenic properties are unaffected by thermal denaturation. It is resistant to proteolytic hydrolysis too.

Catechin - Compound Summary

Molecular Formula: C₁₅H₁₄O₆

Molecular Weight: 290.

IUPAC Name: (2R,3S) -2- (3,4-dihydroxyphenyl) -3,4-dihydro-2H-chromene-3,5,7-triol

Two catechin derivatives (C-1 and C-2) with potent antiallergic activity were isolated from Taiwanese oolong tea by HPLC techniques. From NMR and FAB-MS analyses, the structures of C-1 and C-2 were elucidated as (-)-epigallocatechin 3-O-(3-O-methyl)gallate and (-)-epigallocatechin 3-O-(4-O-methyl)gallate, respectively. Oral doses of C-1 and C-2 (5-50 mg/kg) significantly inhibited type I allergic (anaphylactic) reactions in mice sensitized with ovalbumin and Freund's incomplete adjuvant. These inhibitory effects exceeded that of the major tea catechin, (-)-epigallocatechin 3-O-gallate, which has known antiallergic properties.^[12]

The antiallergic effects of green tea, oolong tea, and black tea extracts by hot water were examined. These extracts inhibited the passive cutaneous anaphylaxis (PCA) reaction of rat after oral administration. Three tea catechins, (-)-epigallocatechin (EGC), (-)-epicatechingallate (ECg), and (-)-epigallocatechingallate (EGCg) isolated from green tea showed stronger inhibitory effects than that of a green tea extract on the PCA reaction. The inhibitory effects of EGC and EGCg

on the PCA reaction were greater than that of ECg. Caffeine also showed an inhibitory effect on the PCA reaction. These results indicate that tea could provide a significant protection against the type-I allergic reaction. These findings also suggest that tea catechins and caffeine play an important role in having an inhibitory effect on the type-I allergic reaction.^[13]

Quercetin - Compound Summary

Molecular Formula: C₁₅H₁₀O₆

Molecular Weight: 286.2363

IUPAC Name:2-(3,4-dihydroxyphenyl)-3,7-dihydroxychromen-4-one

Quercetin is a bioflavonoid found in red wine, grapefruit, onions, apples, black tea, and, in lesser amounts, in leafy green vegetables and beans. Quercetin has an antioxidant and anti-inflammatory activity and prevents cancer. Quercetin inhibits the growth of certain malignant cells in vitro, and histamine and most cyclin-dependent kinases and also displays unique anticancer properties. Quercetin is a natural compound that blocks substances involved in allergies and is able to act as an inhibitor of mast cell secretion, causes a decrease in the release of tryptase, MCP-1 and IL-6 and the down-regulation of histidine decarboxylase (HDC) mRNA from few mast cell lines. Quercetin is a safe, natural therapy that may be used as primary therapy or in conjunction with conventional methods.^[14]

Quercetin is one of the more powerful of the body's antioxidants, and it can also be used to reduce the rate of histamine release by the body normally initiated by contact with an allergenic substance (for which your immune system has designed an antigen). Quercetin's anti-histamine properties are now well established, it has been found to stabilize mast cells¹³ in a way that helps lower stress-induced anxiety and allergic reactions.^[15]

Histamine is an amine released as part of the body's immune response to allergens, and Quercetin inhibits its manufacture and release. This amine is an irritant and can itself cause

inflammation and the other symptoms associated with allergies such as runny and itchy eyes, a stuffy nose, sneezing and itchy spots. Quercetin can be used to alleviate these symptoms by blocking the manufacture in the body of the histamine that causes them.^[16]

MATERIALS AND METHOD:

Finding the analogues from PubChem:

Catechin and Quercetin has been reported as antiallergic (anti histamines) were used as Seed drug to obtain similar analogues from PubChem at 99% similarity.

Ligand preparation and Conformer generation:

The LigPrep process consists of a series of steps that perform conversions, apply corrections to the structures, generate variations on the structures, eliminate unwanted structures, and optimize the structures. Many of the steps are optional and are controlled by selecting options in the LigPrep panel or by specifying command-line options. Each step is performed by the script or program. Ligand preparation involves energy minimization and generation of more stable conformers of the ligands prior to docking. The impact Minimization (Schrodinger) tool was used to minimize the potential energies of the imported ligands. No constraints were applied and force field was calculated using OPLS 2005. Minimization algorithm used here was Gradient and Energy. Ligprep is capable of generating multiple output structures by a process called "Expansion", where conformers are generated based on ionization states, tautomers, and stereochemistry and ring confirmations. Here again OPLS 2005 was used to calculate force field. The 'Generate tautomers' option was set to yes in order to generate all possible confirmation.

Receptor preparation:

The target Ara h1 was obtained from the PDB database. The PDB ID for Ara h1 is 3S7I. This structure was experimentally determined by X-ray crystallography was last revised on 14/12/2011.

The Protein Preparation Wizard (shipped by Schrödinger) was used to import the receptor file and prepare it for docking analysis. The X-ray crystallographic structure of Ara h1 is obtained at resolution of 2.35Å (PDB ID 3S7I) was imported. Only polar hydrogens are displayed for the sake of convenience. During preprocessing bond orders are assigned, hydrogens are added where it is required; water molecules beyond the heteroatoms were deleted. After preprocess, analyze only option was selected. Next since 2 chains were identical, the B chain was removed so as to reduce the complexity of analysis along with the metal ion Cl. Next was the hydrogen bond assignment step where the receptor entry was optimized using the technique ‘Sample Water Orientation’. The next step involved ImprefMinimisation (Schrödinger) where again OPLS 2005 algorithm was used to determine the force field and the molecule was minimized to an RMSD of 0.25.^[9]

Active site determination:

Active site determination was done with the use of CASTp. The PDB id of the target protein was given as an input and active site prediction was done and the numbers of pockets present in the target protein were identified along with their volume and amino acid position.

Docking and Rescoring:

The docking tool from Glide molecule of Schrödinger 2008 has been used for virtual screening and docking. The receptor grid file

contains all the physical properties of the area of the interest in the protein molecule. The receptor grid generation tool available under glide molecule of Schrödinger is used to generate the protein grid. The grid was generated for drug molecule active site (Arg171, Asn172, Asn173, Pro174, Tyr176, Pro178, Arg180, Arg181, Gln197, Gln201, Arg202, and Ser203). The grid file generated is in .zip format. No constraints were used here. First the Standard Precision (SP) was done which gave a rough idea about the docking abilities of ligands. Next Extra Precision (XP) docking was done with the SP output which gave more precise XP dock scores. These processes were first done with the above mentioned active site. Glide generates conformations internally and passes through a series of filters. A small number of surviving docking solutions can be subjected to Monte Carlo procedure to try and minimize the energy score. The final energy evolution is done with a Glide score and a single best pose is generated as the output for a particular ligand.

ADME Descriptor calculation:

Qikprep from Schrödinger 2008 was used to calculate the ADME properties. This tool predicts physically significant descriptor and pharmaceutically relevant properties. About 11 properties are calculated. The properties along with their description and range/recommended values are given below.

Sr. No.	Property/Descriptor	Description	Range/Recommended values
1	Mol MW	Molecular weight of molecule	130.0-725.0
2	SASA	Total solvent accessible surface area (SASA) in square angstroms using a probe with a 1.4 Å radius.	300.0-1000.0
3	FOSA	Hydrophobic component of SASA (saturated carbon and attached hydrogen)	0.0-750.0
4	FISA	Hydrophobic component of SASA (SASA on N, O and H on hetero atoms)	7.0-330.0
5	donorHB	Estimated number of hydrogen bonds that would be donated by the solute to water molecules in an aqueous solution. Values are averages taken over a number of configurations, so they can be non-integer.	0.0-6.0
6	AcceptHB	Estimated number of hydrogen bonds that would be accepted by the solute from water molecules in an aqueous solution. Values are averages taken over a number of configurations, so they can be non-integer.	2.0-20.0
7	QPlogPo/w	Predicted octanol/water partition coefficient	-2.0-6.5

8	QPlogHERG	Predicted IC50 value for blockage of HERG K+ channels.	Concern below -5
9	Percent Human Oral Absorption	Predicted Human Oral Absorption on 0 to 100 % scale	>80% is high >25% is poor
10	Rule of 5	Number of violations of the Lipinski's rule of 5	Maximum is 4
11	Rule of 3	Number of violations of the Jorgensen's rule of 3. The three rules are: QplogS> -5.7, QPPCaco>22nm/s, #primary metabolites<7. Compounds with fewer and (preferably on) violations of this rules are more likely to be more available.	Maximum is 3

Table No. 2: ADME screening properties

Comparative Interaction studies for drug analogue:

Interaction studies were done in Schrodinger maestro workspace by highlighting each selected analogues and selecting the view H- bond option from the tools. Measure the hydrogen acceptor lengths and note down the residues involved along with number of H-binds formed by each analogues.^[9]

RESULTS AND DISCUSSION:

Active Site Determination:^[11]

The active site of the target protein Ara h1 was determined using CASTp. A total of 109 pockets were identified of which pocket number 109 was selected as it had an maximum volume of 6796.4

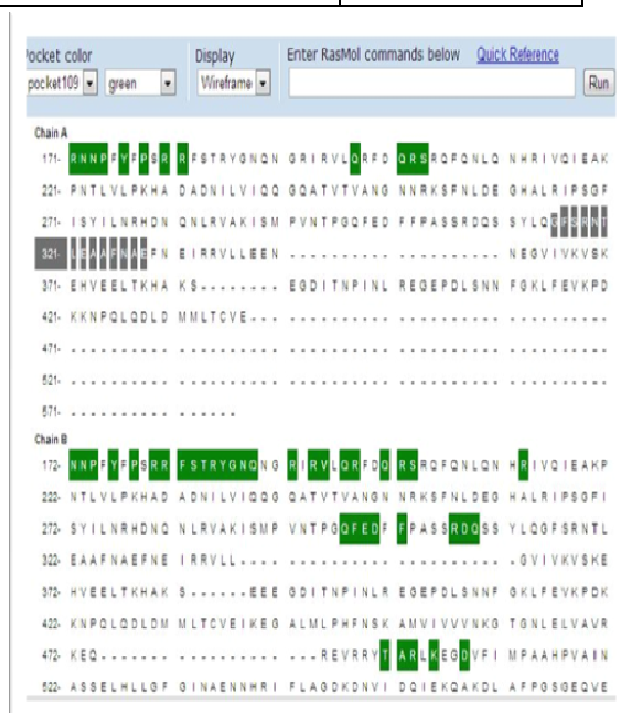
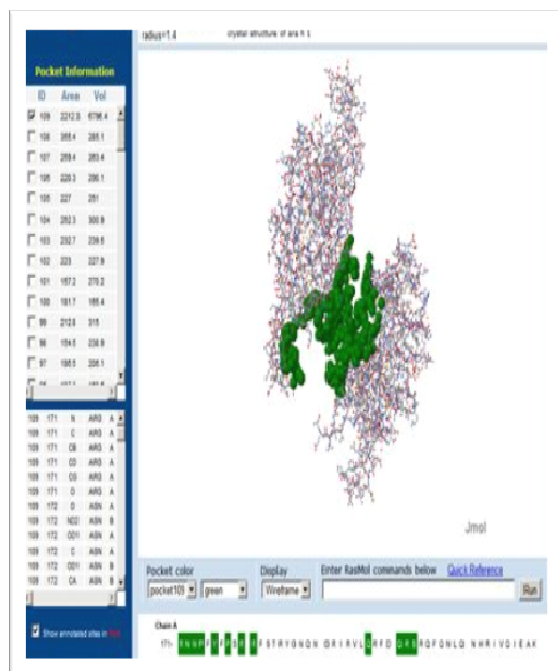


Fig.1: Active site of Ara h1 from CASTp

PubChem:

The two natural chemical compounds named as Quercetin and Catechin showing their activity as antiallergens was examined for their activity against the target protein.^[10]

Quercetin- Drug Molecule (CID 281614)

Molecular Formula: C₁₅H₁₀O₆

Molecular Weight: 28.2363

InChIKey: XHEFDIBZLJXQHF-UHFFFAOYSA-N

IUPAC Name: 2-(3,4-dihydroxyphenyl)-3,7-dihydroxychromen-4-one

Canonical SMILES:

C1=CC(=C(C=C1C2=C(C(=O)C3=C(O2)C=C(C=C3)O)O)O)O

Best analog compounds of Quercetin with respect to glide score:

1. [13C6]-Quercetin -(CID 49849860)

Molecular Formula: C₁₅H₁₀O₇

Molecular Weight: 308.191629

InChIKey: REFJWTPEDVJJIY-ADFQUOOQSA-N

IUPAC Name: 2-(3,4-dihydroxyphenyl)-3,5,7-trihydroxychromen-4-one

Canonical SMILES :
C1=CC(=C(C=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O)O

2. SMR000674606 -(CID 16212154)

Molecular Formula: C₁₅H₁₂O₈

Molecular Weight: 320.25098

InChIKey: OKXFBEYCJRMINR-UHFFFAOYSA-N

IUPAC Name: 2-(3,4-dihydroxyphenyl)-3,5,7-trihydroxychromen-4-one;hydrate

Canonical SMILES :
C1=CC(=C(C=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O)O

3. Quercetin anion - (CID 46906036)

Molecular Formula: C₁₅H₉O₇⁻

Molecular Weight: 301.22776

IUPAC Name: 2-(3,4-dihydroxyphenyl)-5,7-dihydroxy-4-oxochromen-3-olate

InChIKey: REFJWTPEDVJJIY-UHFFFAOYSA-M

Canonical SMILES:
C1=CC(=C(C=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)[O-])O)O

4. NSC-58588 - (CID 24187083)

Molecular Formula: C₁₅H₁₀O₇Zr

Molecular Weight: 393.4597

IUPAC Name: 2-(3,4-dihydroxyphenyl)-3,5,7-trihydroxychromen-4-one;zirconium

InChIKey: XNMWRUABEHVIFB-

UHFFFAOYSA-N

Canonical SMILES
: C1=CC(=C(C=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O)O.[Zr]

5. CID 25031947 - (CID 25031947)

Molecular Formula: C₁₅H₁₀O₇Se

Molecular Weight: 381.1957

IUPAC Name: 2-(3,4-dihydroxyphenyl)-3,5,7-trihydroxychromen-4-one;selenium

InChIKey: YPTPWOFQGQGHAFB-UHFFFAOYSA-N

Canonical SMILES
: C1=CC(=C(C=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O)O.[Se]

6. SureCN3786991 - (CID 68786763)

Molecular Formula: C₁₅H₁₀O₈

Molecular Weight: 318.2351

InChIKey: BOVVYLTXCXNLBL-UHFFFAOYSA-N

IUPAC Name: 2-(3,4-dihydroxyphenyl)-3,5,7-trihydroxychromen-4-one;zinc

Canonical SMILES
: C1=CC(=C(C=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O)O

7. M-1214 - (CID 46782412)

Molecular Formula: C₁₅H₁₀O₈

Molecular Weight: 318.2351

InChIKey: BOVVYLTXCXNLBL-UHFFFAOYSA-N

Canonical SMILES:

C1=CC(=C(C=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O)O

8. CID 20670067 - (CID 20670067)

Molecular Formula: C₁₅H₁₀Ac₅O₇

Molecular Weight: 1437.37446

InChIKey: DRSZLDRUKCRBOJ-UHFFFAOYSA-N

IUPAC Name: actinium;2-(3,4-dihydroxyphenyl)-3,5,7-trihydroxychromen-4-one

Canonical SMILES:
C1=CC(=C(C=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O)O

O2)O)O)O)O)O.[Ac].[Ac].[Ac].[Ac].[Ac]

9. 5-Deoxyquercetin - (CID 16213065)

Molecular Formula: C₁₅H₁₂O₇

Molecular Weight: 304.25158

InChIKey: GYHFUROKCOMWNQ-

UHFFFAOYSA-N

IUPAC Name: 2-(3,4-dihydroxyphenyl)-3,7-dihydroxychromen-4-one;hydrate

Canonical SMILES

: C1=CC(=C(C=C1C2=C(C(=O)C3=C(O2)C=C(C=C3)O)O)O)O.O

Catechin - Drug Molecule (CID 9064)

Molecular Formula: C₁₅H₁₄O₆

Molecular Weight: 290.26806

InChIKey: PFTAWBLQPZVEMU-

DZGCQCFKSA-N

IUPAC Name: (2R,3S)-2-(3,4-dihydroxyphenyl)-3,4-dihydro-2H-chromene-3,5,7-triol

Canonical SMILES :

C1C(C(OC2=CC(=CC(=C21)O)O)C3=CC(=C(C=C3)O)O)O

Best analog compounds of Catechin with respect to glide score:

1. CID 56679629

Molecular Formula: C₁₅H₁₄O₇

Molecular Weight: 306.26746

InChIKey: SBZWTSHAFILOTE-

ZNMIVQPWSA-N

IUPAC Name: (2S,3R,4S)-2-(3,4-dihydroxyphenyl)-3,4-dihydro-2H-chromene-

3,4,5,

7-tetrol

Canonical SMILES

: C1=CC(=C(C=C1C2C(C(C3=C(C=C(C=C3O2)O)O)O)O)O)O

2. Catechin - (CID 72276)

Molecular Formula: C₁₅H₁₄O₆

Molecular Weight: 290.26806

InChIKey: PFTAWBLQPZVEMU-

UKRRQHHQSA-N

IUPAC Name: (2R,3R)-2-(3,4-dihydroxyphenyl)-3,4-dihydro-2H-chromene-3,5,7-triol

Canonical

SMILES: C1C(C(OC2=CC(=CC(=C21)O)O)C3=CC(=C(C=C3)O)O)O

3. CID 44224836 - (CID 44224836)

Molecular Formula: C₁₅H₁₄O₆

Molecular Weight: 291.274222

InChIKey: PFTAWBLQPZVEMU-

RNFLDQESSA-N

IUPAC Name: (2R,3R)-4-deuterio-2-(3,4-dihydroxyphenyl)-3,4-dihydro-2H-chromene-3,5,

7-triol

Canonical SMILES

: C1C(C(OC2=CC(=CC(=C21)O)O)C3=CC(=C(C=C3)O)O)O

4. SureCN1330653 - (CID 66995311)

Molecular Formula: C₁₅H₁₄O₆

Molecular Weight: 293.246025

InChIKey: PFTAWBLQPZVEMU-

GERJZVEYSA-N

IUPAC Name: 2-(3,4-dihydroxyphenyl)-3,4-dihydro-2H-chromene-3,5,7-triol

Canonical SMILES

: C1C(C(OC2=CC(=CC(=C21)O)O)C3=CC(=C(C=C3)O)O)O

5. SureCN1433944 - (CID 59024522)

Molecular Formula: C₁₅H₁₄O₆

Molecular Weight: 290.26806

InChIKey: OFZBQQUVMQGHDI-

YMAMQOFZSA-N

IUPAC Name: (2R)-2-(3,4-dihydroxyphenyl)-3,4-dihydro-2H-chromene-3,4,7-triol

Canonical SMILES

: C1=CC(=C(C=C1C2C(C(C3=C(O2)C=C(C=C3)O)O)O)O)O

Descriptor Calculation:

Qikprep result for the traditional ligands along with their conformers was obtained. It was also observed that about 34% of the ligands analyzed, showed properties that were accordance with the main analog and Lipinski's Rule of Five. (The tables showing the Qikprep results are attached below the reference.)

RESULT FOR QUERCETIN:

Quercetin showed interaction with Ara h1 at the position TYR 500 with Glide score -2.47 and Glide energy -24.38. We identified best 9 analogues which showed H bond interaction with

amino acids like ARG, TYR, and ASN with bond length ranging from 1.67-2.47Å. These amino acids were at positions ranging from 176-500. Most analogues showed their interaction with Arginine which is a hydrophilic amino acid.

Ligand/Analog	H Bonds	Type	HB Length (Å)	Residue	Glide Energy	Glide Score
5281614	1	H-OC	2.07	TYR 500	-24.38	-2.47
49849860	1	H-OC	1.69	TYR 176	-34.85	-5.78
	2	O-HN	1.86	ARG 498		
	3	O-HN	2.38	ARG 202		
16212154	1	O-HN	1.855	ARG 498	-36.54	-5.67
	2	O-HN	2.33	ARG 202		
	3	H-OC	1.67	TYR 176		
46906036	1	O-HN	2.29	ARG 498	-28.6	-3.36
	2	O-HN	2.03	ARG 498		
	3	O-HN	2.18	ARG 202		
4187083	1	O-HN	1.81	ARG 498	-31.62	-3.1
	2	O-HN	1.75	ARG202		
	3	O-HN	2.01	ARG 202		
	4	H-OC	1.9	ASN 172		
25031947	1	O-HN	1.8	ARG 498	-31.62	-3.1
	2	O-HN	1.75	ARG 202		
	3	H-OC	1.97	ASN 172		
	4	O-HN	2.01	ARG 202		
68786763	1	O-HN	1.8	ARG 498	-31.62	-3.1
	2	O-HN	1.75	ARG 202		
	3	H-OC	1.97	ASN 172		
	4	O-HN	2.01	ARG 202		
46782412	1	O-HN	1.98	ARG 498	-27.4	-2.94
	2	O-HN	2.47	ARG202		
	3	O-HN	1.96	ARG 202		
20670067	1	O-HN	2.13	ARG 202	-23.75	-2.87
	2	O-HN	2.45	ARG 498		
	3	H-OC	2.09	TYR 500		
16213065	1	H-OC	2.09	TYR 500	-23	-2.77
	2	H-OC	2.13	ARG 202		
	3	O-HN	2.16	ARG 202		

Table No.3: Hydrogen bond interaction of best selected analogs

RESULT FOR CATECHIN:

Catechin showed interaction with Ara h1 at the position TYR176, ARG180, ARG202 and THR 501 with Glide score -5.18 and Glide energy -31.15. We identified best 5 analogues which

showed H bond interaction with amino acids like ARG, TYR, THR and ASN with bond length ranging from 1.76-2.47Å. These amino acids were at positions ranging from 171-501. Most analogues showed their interaction with Arginine which is a hydrophilic amino acid.

Ligand/Analog	H Bonds	Type	HB Length (Å)	Residue	Glide Energy	Glide Score
56679629	1	H-OC	2.1	ASN 173	-32.5	-6.25
	2	O-HN	2.35	ARG 498		
	3	O-HN	2.12	ARG 171		
72276	1	O-HN	1.76	ARG 498	-31.41	-5.57
	2	O-HN	2.16	ARG 202		
	3	H-OC	2.11	TYR 176		
44224836	1	O-HN	1.76	ARG 498	-31.41	-5.57
	2	H-OC	2.11	TYR 176		
	3	O-HN	2.16	ARG 202		
66995311	1	O-HN	2.1	THR 501	-31.08	-5.25
	2	O-HN	2.25	ARG 202		
	3	H-OC	2.18	TYR 176		
59024522	1	H-OC	2.06	TYR 176	-30.79	-5.23
	2	O-HN	1.8	ARG 498		
	3	O-HN	2.17	ARG 202		
9064	1	O-HN	2.263	ARG 202	-31.15	-5.18
	2	H-OC	2.14	TYR 176		
	3	O-HN	2.01	THR 501		
	4	O-HN	2.47	ARG 180		

Table No.4: Hydrogen bond interaction of best selected analogs

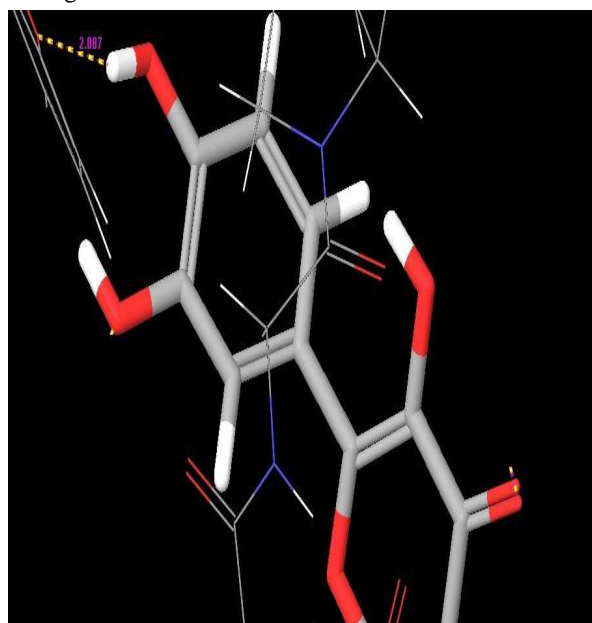


Fig.2: Hydrogen bond interaction of CID 5281614

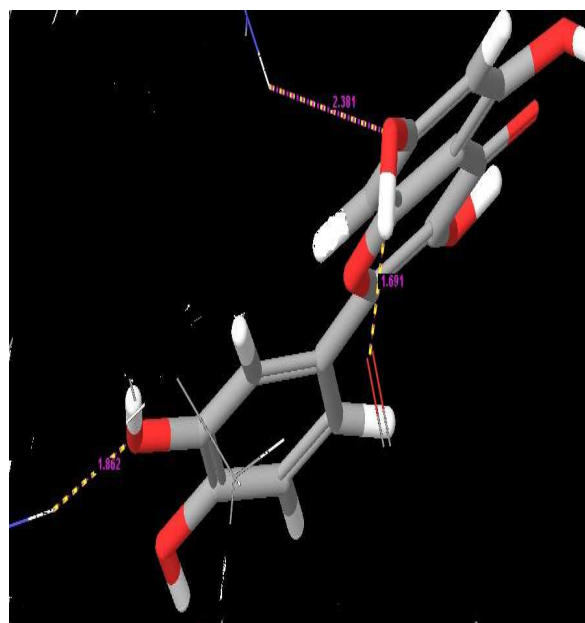


Fig.3: Hydrogen bond interaction of CID 49849860

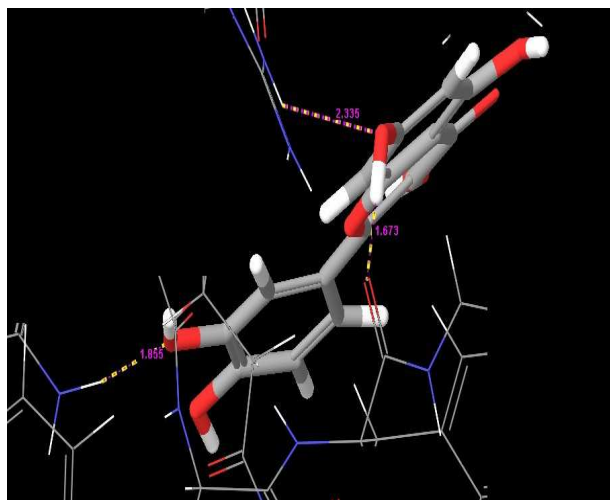


Fig.4: Hydrogen bond interaction of CID 16212154

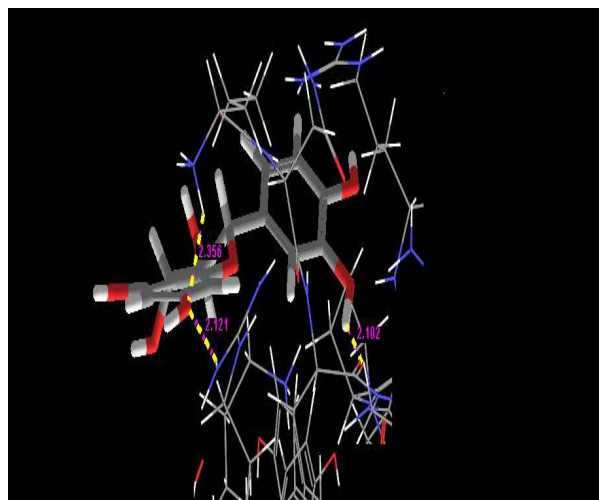


Fig.6: Hydrogen bond interaction of CID 56679629

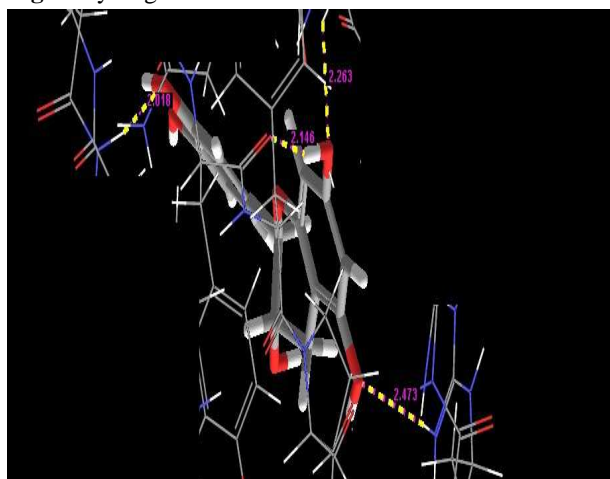


Fig.5: Hydrogen bond interaction of CID 9064

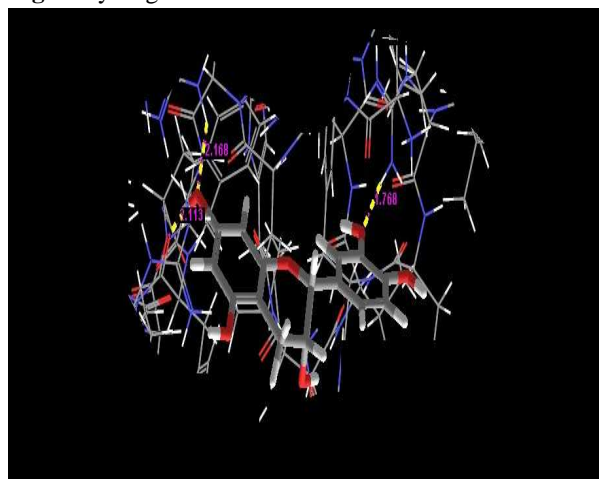


Fig.7: Hydrogen bond interaction of CID 72276

QIKPREP RESULTS:

Sr. No.	CID	G.S.	G.E.	MW	SASA	FOSA	FISA	dHB	aHB	QPlogPo/w	QPlogHERG	HOA	Rule of 5	Rule of 3
1	56679629	-6.25	-32.5	306.271	518.916	43.375	270.029	6	7.15	-0.318	-4.751	2	1	1
2	25000816	-6.02	-31.71	274.273	499.93	69.892	185.277	4	4.7	1.204	-4.812	3	0	0
3	12305025	-5.85	-31.51	290.272	510.56	46.285	229.628	5	6.4	0.292	-4.851	3	0	0
4	15559981	-5.78	-32.74	306.271	515.695	42.813	270.888	6	7.15	-0.31	-4.633	2	1	1
5	169996	-5.69	-33.44	306.271	517.344	46.458	267.892	6	7.15	-0.291	-4.68	2	1	1
6	72276	-5.57	-31.41	290.272	511.539	63.984	238.287	5	5.45	0.46	-4.785	2	0	1
7	44224836	-5.57	-31.41	290.272	511.539	63.984	238.287	5	5.45	0.46	-4.785	2	0	1
8	49787895	-5.57	-33.42	290.272	512.066	63.353	240.2	5	5.45	0.467	-4.761	2	0	1
9	44257148	-5.28	-29.34	306.271	517.407	46.027	265.927	6	7.15	-0.273	-4.691	2	1	1
10	66995311	-5.25	-31.08	290.272	513.277	65.755	236.675	5	5.45	0.488	-4.81	2	0	1
11	59024522	-5.23	-30.79	290.272	510.097	38.749	235.16	5	6.4	0.243	-4.866	2	0	0
12	9064	-5.18	-31.15	290.272	512.198	65.932	236.294	5	5.45	0.487	-4.785	2	0	1
13	12309508	-5.19	-31.15	290.272	512.198	65.932	236.294	5	5.45	0.487	-4.785	2	0	1
14	442686	-5.17	-32.55	740.673	891.69	84.966	503.103	11	14.15	0.332	-5.973	1	3	2
15	146798	-5.15	-33.97	578.528	825.535	70.656	416.96	10	10.9	0.578	-6.532	1	3	2
16	107957	-5.09	-31.28	290.272	512.776	65.947	237.316	5	5.45	0.481	-4.794	2	0	1
17	107957	-5.09	-31.28	290.272	512.776	65.947	237.316	5	5.45	0.481	-4.794	2	0	1
18	147299	-5.05	-34.95	578.528	824.627	78.858	410.752	10	10.9	0.5	-6.604	1	3	2
19	12314983	-5.01	-31.1	290.272	514.756	70.411	238.069	5	5.45	0.474	-4.821	2	0	1
20	11033582	-4.87	-26.83	290.272	507.885	72.769	226.726	5	5.45	0.565	-4.651	2	0	1
21	49787818	-4.85	-29.02	290.272	508.438	69.09	232.032	5	5.45	0.485	-4.729	2	0	1
22	11290930	-4.72	-32.05	290.272	514.134	68.513	237.016	5	5.45	0.481	-4.824	2	0	1
23	21114867	-4.72	-32.05	290.272	514.134	68.513	237.016	5	5.45	0.481	-4.824	2	0	1
24	67326441	-4.72	-32.05	290.272	514.134	68.513	237.016	5	5.45	0.481	-4.824	2	0	1
25	25000817	-4.68	-31.57	274.273	502.441	68.586	185.889	4	4.7	1.179	-4.931	3	0	0
26	474540	-4.55	-33.28	578.528	830.272	87.659	398.107	10	10.9	0.668	-6.667	1	3	2
27	12309509	-4.27	-30.43	290.272	509.799	61.884	240.116	5	5.45	0.481	-4.679	2	0	1

Catechin and Quercetin ligand based analysis against peanut allergy using computational studies

28	51371467	-2.98	-31.9	306.271	518.074	47.458	268.299	6	7.15	-0.324	-4.741	2	1	1
29	69378103	-2.96	-26.48	306.271	518.366	38.144	273.933	6	7.15	-0.331	-4.722	2	1	1
30	156680	-2.75	-25.64	562.529	745.63	62.969	372.524	9	10.15	0.882	-5.584	1	3	2
31	440834	-2.72	-26.08	290.272	511.103	61.414	236.463	5	5.45	0.505	-4.749	3	0	0
32	124025	-2.65	-32.88	576.512	802.383	83.175	381.066	9	10.9	0.651	-6.536	1	3	2
33	44257144	-2.6	-25.82	306.271	526.072	37.831	281.225	6	7.15	-0.392	-4.913	2	1	2
34	44187798	-2.59	-27.36	290.272	506.68	48.404	220.838	5	6.4	0.341	-4.796	3	0	0
35	12309896	-2.55	-23.97	274.273	501.395	72.57	190.11	4	4.7	1.132	-4.872	3	0	0
36	51377540	-2.43	-20.5	306.271	512.542	38.544	272.289	6	7.15	-0.337	-4.587	2	1	1
37	5317352	-2.42	-24.35	290.272	502.495	40.96	226	5	6.4	0.347	-4.615	3	0	0
38	44257072	-2.41	-33.57	422.388	670.307	169.172	317.937	7	12.25	-0.796	-5.419	2	1	2
39	59024524	-2.36	-26.82	306.271	515.191	38.84	275.083	6	7.15	-0.355	-4.643	2	1	1
40	44257142	-2.29	-21.35	290.272	506.285	47.097	228.74	5	6.4	0.279	-4.753	3	0	0
41	44257145	-2.05	-27.8	290.272	507.881	47.592	219.368	5	6.4	0.361	-4.832	3	0	0
42	5276454	-2.04	-31.76	442.378	696.186	41.164	369.897	7	8	0.491	-6.122	2	1	2
43	14622420	-2	-20.44	290.272	507.836	58.052	221.761	5	5.45	0.592	-4.795	2	0	1
44	73160	-1.98	-24.52	290.272	507.728	64.194	238.797	5	5.45	0.485	-4.617	2	0	1
45	1203	-1.98	-24.52	290.272	507.728	64.194	238.797	5	5.45	0.485	-4.617	2	0	1
46	59086267	-1.97	-22.61	306.271	518.49	63.879	286.15	6	6.2	-0.189	-4.533	2	1	2
47	65064	-1.97	-25.72	458.378	699.674	48.927	419.989	8	8.75	-0.213	-5.767	1	2	2
48	494064	-1.95	-22.85	306.271	514.413	39.066	272.205	6	7.15	-0.284	-4.556	2	1	1
49	72277	-1.9	-24.91	306.271	521.807	64.609	285.055	6	6.2	-0.198	-4.66	2	1	2
50	10425234	-1.9	-22.88	306.271	522.892	65.516	285.888	6	6.2	-0.181	-4.643	2	1	2
51	471393	-1.83	-24.05	442.378	714.396	61.133	367.399	7	9.45	0.125	-6.332	2	1	2
52	12309507	-1.76	-22.54	290.272	506.662	65.502	237.401	5	5.45	0.486	-4.599	2	0	1
53	114505	-1.64	-25.48	290.272	507.869	61.402	237.297	5	5.45	0.469	-4.694	3	0	0
54	70490063	-1.64	-25.48	290.272	507.869	61.402	237.297	5	5.45	0.469	-4.694	3	0	0
55	24721113	-1.63	-22.95	290.272	512.066	65.707	236.832	5	5.45	0.503	-4.746	2	0	1
56	24871278	-1.63	-22.95	290.272	512.066	65.707	236.832	5	5.45	0.503	-4.746	2	0	1

57	1249	-1.58	-25.48	306.271	523.802	65.215	282.487	6	6.2	-0.168	-4.711	2	1	2
58	65084	-1.58	-25.48	306.271	523.802	65.215	282.487	6	6.2	-0.168	-4.711	2	1	2
59	155660	-1.57	-26.55	388.46	733.429	327.936	200.909	4	5.45	3.368	-6.043	3	0	0
60	69379425	-1.57	-22.01	290.272	506.104	64.46	237.391	5	5.45	0.473	-4.61	2	0	1
61	44257052	-1.55	-21.38	290.272	506.628	68.245	239.393	5	5.45	0.458	-4.59	2	0	1
62	59086270	-1.45	-22.69	306.271	517.087	65.469	285.585	6	6.2	-0.193	-4.497	2	1	2
63	12309543	-1.37	-23.89	306.271	525.796	64.277	285.684	6	6.2	-0.16	-4.707	2	1	2
64	9882981	-1.34	-22.52	306.271	521.731	65.358	283.141	6	6.2	-0.164	-4.632	2	1	2
65	289	-1.2	-14.27	110.112	289.742	0	101.979	2	1.5	0.575	-3.346	3	0	0
66	10236414	-1.14	-22.43	290.272	509.604	66.31	233.788	5	5.45	0.541	-4.66	2	0	1
67	6419835	-0.99	-30.81	442.378	747.249	45.845	354.767	7	8	0.956	-6.924	2	1	2
68	367141	-0.99	-30.81	442.378	747.249	45.845	354.767	7	8	0.956	-6.924	2	1	2
69	73533	-0.15	-31.24	422.388	670.115	173.487	312.902	7	12.25	-0.776	-5.436	2	1	2
70	18716207	0.55	-26.33	290.272	510.105	61.096	237.454	5	5.45	0.488	-4.731	2	0	1

Table No. 5 : Qikprep results for Catechin

Sr. No.	CID	G.S.	G.E.	MW	SASA	FOSA	FISA	dHB	aHB	QPlogPo/w	QPlogHERG	HOA	Rule of 5	Rule of 3
1	56679629	-6.25	-32.5	306.271	518.916	43.375	270.029	6	7.15	-0.318	-4.751	2	1	1
2	25000816	-6.02	-31.71	274.273	499.93	69.892	185.277	4	4.7	1.204	-4.812	3	0	0
3	12305025	-5.85	-31.51	290.272	510.56	46.285	229.628	5	6.4	0.292	-4.851	3	0	0
4	15559981	-5.78	-32.74	306.271	515.695	42.813	270.888	6	7.15	-0.31	-4.633	2	1	1
5	169996	-5.69	-33.44	306.271	517.344	46.458	267.892	6	7.15	-0.291	-4.68	2	1	1
6	72276	-5.57	-31.41	290.272	511.539	63.984	238.287	5	5.45	0.46	-4.785	2	0	1
7	44224836	-5.57	-31.41	290.272	511.539	63.984	238.287	5	5.45	0.46	-4.785	2	0	1
8	49787895	-5.57	-33.42	290.272	512.066	63.353	240.2	5	5.45	0.467	-4.761	2	0	1
9	44257148	-5.28	-29.34	306.271	517.407	46.027	265.927	6	7.15	-0.273	-4.691	2	1	1
10	66995311	-5.25	-31.08	290.272	513.277	65.755	236.675	5	5.45	0.488	-4.81	2	0	1
11	59024522	-5.23	-30.79	290.272	510.097	38.749	235.16	5	6.4	0.243	-4.866	2	0	0
12	9064	-5.18	-31.15	290.272	512.198	65.932	236.294	5	5.45	0.487	-4.785	2	0	1

Table No. 6 : Sorted analogs for Catechin based on Qikprep results

SR. NO.	CID	G.S.	G.E.	MW	SASA	FOSA	FISA	dHB	aHB	QPlogPo/w	QPlogHERG	HOA	Rule of 5	Rule of 3
1	56679629	-6.25	-32.5	306.271	518.916	43.375	270.029	6	7.15	-0.318	-4.751	2	1	1
2	72276	-5.57	-31.41	290.272	511.539	63.984	238.287	5	5.45	0.46	-4.785	2	0	1
3	44224836	-5.57	-31.41	290.272	511.539	63.984	238.287	5	5.45	0.46	-4.785	2	0	1
4	66995311	-5.25	-31.08	290.272	513.277	65.755	236.675	5	5.45	0.488	-4.81	2	0	1
5	59024522	-5.23	-30.79	290.272	510.097	38.749	235.16	5	6.4	0.243	-4.866	2	0	0
6	9064	-5.18	-31.15	290.272	512.198	65.932	236.294	5	5.45	0.487	-4.785	2	0	1

Table No. 7 : Selected analogs of Catechin

Catechin and Quercetin ligand based analysis against peanut allergy using computational studies

Sr No	CID	PE	GS	GE	MW	SASA	FOSA	FISA	dHB	aHB	QPlogPo/w	Qplog HERG	HOA	Rule Of 5	Rule Of 3
1	5281692	46.67	-5.86	-32.96	302.24	510.85	0	289.8	5	6.25	-0.17	-4.91	2	0	1
2	49849860	60.94	-5.78	-34.85	302.24	509.32	0	281.23	4	5.25	0.37	-4.92	2	0	1
3	16212154	60.94	-5.67	-36.54	302.24	509.48	0	282.26	4	5.25	0.36	-4.92	2	0	1
4	5284452	60.94	-5.51	-35.66	302.24	509.15	0	281.07	4	5.25	0.37	-4.91	2	0	1
5	12305312	60.94	-5.42	-35.04	302.24	508.52	0	280.96	4	5.25	0.37	-4.9	2	0	1
6	49849859	67.13	-5.28	-35.28	302.24	508.57	0	281.29	4	5.25	0.37	-4.89	2	0	1
7	5280343	67.13	-5.04	-31.41	302.24	510.44	0	282.38	4	5.25	0.37	-4.93	2	0	1
8	46906036	66.72	-3.36	-28.6	302.24	509.38	0	281.15	4	5.25	0.38	-4.91	2	0	1
9	24187083	66.72	-3.1	-31.62	302.24	508.1	0	281.9	4	5.25	0.36	-4.89	2	0	1
10	25031947	66.72	-3.1	-31.62	302.24	508.1	0	281.9	4	5.25	0.36	-4.89	2	0	1
11	68786763	66.72	-3.1	-31.62	302.24	508.1	0	281.9	4	5.25	0.36	-4.89	2	0	1
12	46782412	65.89	-2.94	-27.4	318.23	513.35	0	308.76	5	6	-0.16	-4.75	2	1	1
13	20670067	63.93	-2.87	-23.75	302.24	510.9	0	282.02	4	5.25	0.37	-4.95	2	0	1
14	54609735	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
15	57520226	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
16	57520227	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
17	68109312	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
18	69202014	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
19	69887223	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
20	16213065	49.74	-2.77	-23	286.24	501.32	0	241.88	4	5.5	0.5	-5.05	3	0	0
21	5281614	49.74	-2.47	-24.38	286.24	501.35	0	242.88	4	5.5	0.49	-5.04	3	0	0
22	54758660	49.74	-2.14	-25.25	286.24	502.63	0	241.04	4	5.5	0.51	-5.08	3	0	0
23	12309893	49.44	-0.4	-20.74	286.24	502.72	0	241.99	4	5.5	0.5	-5.01	3	0	0
24	21600688	63.93	0.17	-26.23	302.24	513.58	0	282.49	4	5.25	0.4	-5.06	2	0	1

Table No. 8 : Qikprep result for Quercetin.

Sr No	CID	PE	GS	GE	MW	SASA	FOSA	FISA	dHB	aHB	QPlogPo/w	Qplog HERG	HOA	Rule Of 5	Rule Of 3
1	5281692	46.67	-5.86	-32.96	302.24	510.85	0	289.8	5	6.25	-0.17	-4.91	2	0	1
2	49849860	60.94	-5.78	-34.85	302.24	509.32	0	281.23	4	5.25	0.37	-4.92	2	0	1
3	16212154	60.94	-5.67	-36.54	302.24	509.48	0	282.26	4	5.25	0.36	-4.92	2	0	1
4	5284452	60.94	-5.51	-35.66	302.24	509.15	0	281.07	4	5.25	0.37	-4.91	2	0	1
5	12305312	60.94	-5.42	-35.04	302.24	508.52	0	280.96	4	5.25	0.37	-4.9	2	0	1
6	49849859	67.13	-5.28	-35.28	302.24	508.57	0	281.29	4	5.25	0.37	-4.89	2	0	1
7	5280343	67.13	-5.04	-31.41	302.24	510.44	0	282.38	4	5.25	0.37	-4.93	2	0	1
8	46906036	66.72	-3.36	-28.6	302.24	509.38	0	281.15	4	5.25	0.38	-4.91	2	0	1
9	24187083	66.72	-3.1	-31.62	302.24	508.1	0	281.9	4	5.25	0.36	-4.89	2	0	1
10	25031947	66.72	-3.1	-31.62	302.24	508.1	0	281.9	4	5.25	0.36	-4.89	2	0	1
11	68786763	66.72	-3.1	-31.62	302.24	508.1	0	281.9	4	5.25	0.36	-4.89	2	0	1
12	46782412	65.89	-2.94	-27.4	318.23	513.35	0	308.76	5	6	-0.16	-4.75	2	1	1
13	20670067	63.93	-2.87	-23.75	302.24	510.9	0	282.02	4	5.25	0.37	-4.95	2	0	1
14	54609735	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
15	57520226	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
16	57520227	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
17	68109312	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
18	69202014	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
19	69887223	66.72	-2.77	-31.67	302.24	507.06	0	281.94	4	5.25	0.36	-4.86	2	0	1
20	16213065	49.74	-2.77	-23	286.24	501.32	0	241.88	4	5.5	0.5	-5.05	3	0	0
21	5281614	49.74	-2.47	-24.38	286.24	501.35	0	242.88	4	5.5	0.49	-5.04	3	0	0

Table No. 9 : Sorted analogs of Quercetin based on Qikprep results

Sr No	CID	PE	GS	GE	MW	SASA	FOSA	FISA	dHB	aHB	QPlogPo/w	Qplog HERG	HOA	Rule Of 5	Rule Of 3
1	49849860	60.94	-5.78	-34.85	302.24	509.32	0	281.23	4	5.25	0.37	-4.92	2	0	1
2	16212154	60.94	-5.67	-36.54	302.24	509.48	0	282.26	4	5.25	0.36	-4.92	2	0	1
3	46906036	66.72	-3.36	-28.6	302.24	509.38	0	281.15	4	5.25	0.38	-4.91	2	0	1
4	24187083	66.72	-3.1	-31.62	302.24	508.1	0	281.9	4	5.25	0.36	-4.89	2	0	1
5	25031947	66.72	-3.1	-31.62	302.24	508.1	0	281.9	4	5.25	0.36	-4.89	2	0	1
6	68786763	66.72	-3.1	-31.62	302.24	508.1	0	281.9	4	5.25	0.36	-4.89	2	0	1
7	46782412	65.89	-2.94	-27.4	318.23	513.35	0	308.76	5	6	-0.16	-4.75	2	1	1
8	20670067	63.93	-2.87	-23.75	302.24	510.9	0	282.02	4	5.25	0.37	-4.95	2	0	1
9	16213065	49.74	-2.77	-23	286.24	501.32	0	241.88	4	5.5	0.5	-5.05	3	0	0
10	5281614	49.74	-2.47	-24.38	286.24	501.35	0	242.88	4	5.5	0.49	-5.04	3	0	0

Table No.10: Selected analogs of Quercetin

CONCLUSION:

Ara h1 is the abbreviation for “Arachis Hypogea”. Molecular modeling approaches were used to rescore highly potential analogues against Ara h1 which is a protein for its antiallergic activity. Quercetin and Catechin were used to identify selective analogues through PubChem for docking studies. 99 analogues were docked against Ara h1 out of which 16 analogues were identified highly potent after rescoring method (OPLS 2005). These analogues showed quiet high interaction with amino acid like TYR, ASN, ARG and THR with bond length in the range of 1.67-2.47 Å. They were also confirmed with glide score and glide energy which was -2.4 to -6.28 and -23 to -36.54 respectively. ADME properties were identified for the respective analogues and they all satisfied rule of 5, rule of 3, Total solvent accessible surface area (SASA), Hydrophobic component of SASA, Predicted octanol/water partition coefficient, Predicted IC₅₀ value for blockage of HERG K⁺ channels, Predicted Human Oral Absorption on 0 to 100 % scale etc.

This novel approach gives an insight to develop suitable analogues for peanut allergies which can be further cross validated using wet lab approaches like animal studies and small molecule preparations.

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