

Binding Analysis of Cholesterol and its Derivatives with 13 Chosen Respiratory Allergens: An *in-silico* Study

Radhakrishnan Narayanaswamy*, Biswajit Das, Sachin B S

Department of Biochemistry, Saveetha Medical College and Hospital, Saveetha Institute of Medical and Technical Sciences (Deemed to be University), Saveetha University, Thandalam, Chennai, Tamil Nadu, INDIA.

ABSTRACT

Background and Objectives: Respiratory allergens are generally non-parasite proteins in nature, which induces more amounts of Immunoglobulin E (Ig E) levels in atopic persons. A steady increasing prevalence of asthma and other allergy related disorders, which has been turn a huge public health issue throughout the globe. In the present investigation, we aimed to study four chosen cholesterol and its derivatives as potent modulating agents against 13 selected respiratory allergens using docking methods. **Materials and Methods:** The 13 chosen respiratory allergens proteins were studied on the docking behaviour with four selected ligands namely i) cholesterol, ii) 17:1 cholesteryl ester, iii) cholesterol formate and iv) cholesterol palmitate by using the swissdock method. In addition to docking, physicochemical properties of 13 chosen allergens proteins were determined using ProtParam web server. **Results:** With reference to physicochemical property analysis, three selected respiratory allergen proteins (Mite allergen Bio t5, Major allergen Can f 1 and Allergen Can f 1) have exhibited instability index value greater (?) than 40. The docking results revealed that Mite allergen Der f 21.0101 has exhibited the Highest Binding Energy [HBE] with all four target ligands [i) cholesterol (-8.18 kcal/mol); ii) 17:1 cholesteryl ester (-10.48 kcal/mol); iii) cholesterol formate (-8.41 kcal/mol) and iv) cholesterol palmitate (-9.63 kcal/mol)]. Interestingly, Allergen Can f 1 has exhibited amino acids interaction with three target ligands [cholesterol (Pro55); 17:1 cholesteryl ester (Lys131); and cholesterol palmitate (Tyr97)]. **Conclusion:** Thus, the present finding gives new knowledge about the four selected ligands (cholesterol and its derivatives) as potent modulating agents against 13 chosen respiratory allergens, which will aid in developing allergy mitigation strategies.

Keywords: Allergen Can f 1, Cholesterol, Docking, Good Health and Well-being, Mite allergen Der f 21.0101, Physicochemical Property and Respiratory Allergens.

Correspondence:

Dr. Radhakrishnan Narayanaswamy
Department of Biochemistry, Saveetha Medical College and Hospital, Saveetha Institute of Medical and Technical Sciences (Deemed to be University), Saveetha University, Thandalam, Chennai-602 105, Tamil Nadu, INDIA.
Email: kishnanbio07@gmail.com

Received: 06-02-2026;

Revised: 24-04-2026;

Accepted: 19-06-2026.

INTRODUCTION

Allergens are generally non-parasite proteins in nature, which induces more amounts of Immunoglobulin E (Ig E) levels in atopic persons (Kausar *et al.*, 2022; Lin *et al.*, 2022). The i) outdoor pollen, ii) molds, iii) indoor mites and iv) air-pollution are the major source of allergens (Ichikawa *et al.*, 2009). Apart from these few allergens are reported from “domesticated animals” [like cat, cow, dog, guinea pig, hamster, horse and rabbit] and “pets” [such as American (*Periplaneta americana*) and German (*Blattella germanica*) cockroach]. Moreover, mice and rat are also reported to cause occupational allergens in some laboratory animal handlers (Min *et al.*, 2023).

Majority of allergens are regarded as “respiratory allergens” (Min *et al.*, 2023). According to recent publication, asthma and allergic rhinitis are the two most popular respiratory allergies and are constantly growing globally (Kausar *et al.*, 2022). *Blomia tropicalis* (Blo t), *Dermatophagoides farina* (Der f), *Dermatophagoides microceras* (Der m) and *Dermatophagoides pteronyssinus* (Der p) are the major House Dust Mites (HDM) species that induce allergic immune reactions or responses which lead to asthma and dermatitis (Ichikawa *et al.*, 2005; Tai *et al.*, 2018; Hu *et al.*, 2022). Moreover, *Blattella germanica* (Bla g) and *Periplaneta americana* (Per a) are the two main cockroach species that induce allergic immune reactions (Offermann *et al.*, 2014). Furthermore cat (Fel d 7) and dog (Can f 1) are the two major indoor allergens that induce allergic immune responses (Min *et al.*, 2023).

The earlier reports engaged us to carry out the current investigation on 13 chosen respiratory allergens proteins which includes i) House dust mite allergen (Der f 2), ii) Mite allergen Der f 2, iii) Mite allergen Der f 21.0101, iv) Der p 2 allergen, v) Group 2 allergen Bio t2 isoform 1, vi) Peptidase 1 (DERF1), vii) Group 2 allergen Bio t2 isoform 9, viii) Mite allergen Bio t5, ix)



DOI: 10.5530/pres.20260217

Copyright Information :

Copyright Author (s) 2026 Distributed under
Creative Commons CC-BY 4.0

Publishing Partner : Manuscript Technomedia. [www.mstechnomedia.com]

Allergen Bla g 4, x) Per a 4 allergen, xi) Major allergen Can f 1, xii) Per a 2 allergen and xiii) Allergen Can f 1

These above said respiratory allergens proteins were aimed to investigate on the docking behaviour with four selected ligands namely i) cholesterol, ii) 17:1 cholesteryl ester, iii) cholesterol formate and iv) cholesterol palmitate by using the swissdock method, which may help in developing allergy mitigation strategies.

MATERIALS AND METHODS

Ligand preparation

The chemical structures of four selected ligands i) cholesterol (CID^o 5997); ii) 17:1 cholesteryl ester (CID^o 24779603); iii) cholesterol formate (CID^o 165217) and iv) cholesteryl palmitate (CID^o 246520) were downloaded from ^oPubChem compound database. The ligands structures were drawn and prepared by utilizing ChemDraw 2D and 3D softwares. Thus, these prepared three-dimensional structures were utilized for further swissdock analysis (Srinivasan *et al.*, 2023; Victor *et al.*, 2023).

Preparation of target proteins

The three-dimensional (3-D) structure of respiratory allergens proteins i) House dust mite allergen -Der f 2 (PDB^o ID: 2FO8 with a resolution of 2.20 Å); ii) Mite allergen-Der f 2 (UniProt^{oo} ID: Q5TIW2 • Q5TIW2_DERFA); iii) Mite allergen- Der f 21.0101 (UniProt^{oo} ID: B2GM84 • ALL21_DERFA); iv) Der p 2 allergen (UniProt^{oo} ID: Q1H8P8 • Q1H8P8_DERPT); v) Group 2 allergen Bio t2 isoform 1 (UniProt^{oo} ID: A6XEN8 • A6XEN8_BLOTA); vi) Peptidase 1-DERF1 (UniProt^{oo} ID: P16311 • PEPT1_DERFA); vii) Group 2 allergen Bio t2 isoform 9 (UniProt^{oo} ID: A6XEP6 • A6XEP6_BLOTA); viii) Mite allergen Bio t5 (UniProt^{oo} ID: O96870 • ALL5_BLOTA); ix) Allergen Bla g 4 (UniProt^{oo} ID: P54962 • BLG4_BLAG); x) Per a 4 allergen (UniProt^{oo} ID: Q1M0Y5 • Q1M0Y5_PERAM); xi) Major allergen Can f 1 (UniProt^{oo} ID: O18873 • ALL1_CANLF); xii) Per a 2 allergen (UniProt^{oo} ID: E7BQV5 • E7BQV5_PERAM); and xiii) Allergen Can f 1 (PDB^o ID: 7DRU with a resolution of 2.50 Å) was downloaded from Protein Data Bank (PDB^o) and UniProt^{oo} databases respectively. 'A' chain of these two proteins (House dust mite allergen -Der f 2 and Allergen Can f 1) were prepared independently by removing other chains, ligands (heteroatoms), and even the crystallographically observed 'water' (H₂O) molecules by utilizing UCSF Chimera software tool (Vishnupriya *et al.*, 2024).

Determination of physicochemical properties

ProtParam web server was utilized to determine the physicochemical properties of 13 respiratory allergen proteins [House dust mite allergen (Der f 2), Mite allergen Der f 2, Mite allergen Der f 21.0101, Der p 2 allergen, Group 2 allergen Bio t2 isoform 1, Peptidase 1 (DERF1), Group 2 allergen Bio t2 isoform

9, Mite allergen Bio t5, Allergen Bla g 4, Per a 4 allergen, Major allergen Can f 1, Per a 2 allergen and Allergen Can f 1] Whole protein sequence of 13 allergens proteins (except House dust mite allergen -Der f 2 and Allergen Can f 1, where "A" chain) was given separately as input data (Vishnupriya *et al.*, 2024; Narayanaswamy *et al.*, 2024).

Docking study

The molecular docking analysis was carried out for 13 chosen respiratory allergens proteins with four target ligands (cholesterol, 17:1 cholesteryl ester, cholesterol formate and cholesteryl palmitate) using the Swissdock free web server. Finally, "PyMOL" software was used to determine the binding site of best-docked pose for each ligand (Prakash *et al.*, 2023). Docking protocol was validated using quercetin as standard drug. And the root mean square deviation [RMSD^{oo}] analysis of all the docked complexes (four target ligands) was separately compared with that of quercetin (standard drug) docked complex for each chosen respiratory allergen protein by utilizing the 'align' command in "PyMOL" software (Ramsbottom *et al.*, 2018; Narayanaswamy *et al.*, 2024).

RESULTS

In the current investigation, only one chosen respiratory allergen protein (Der p 2 allergen) has exhibited theoretical Isoelectric Point (PI) value greater (⁞) than 7.0 (as shown in Table 1). Interestingly, three selected allergen proteins (Mite allergen Bio t5, Major allergen Can f 1 and Allergen Can f 1) have shown instability index value greater (⁞) than 40. Similarly, in the present investigation all the chosen respiratory allergen proteins (except four- Group 2 allergen Bio t2 isoform 1, Group 2 allergen Bio t2 isoform 9, Mite allergen Der f 2, Der p 2 allergen) have exhibited lowest grand average of hydropathicity (GRAVY) value.

The current Swissdock investigation showed that Mite allergen Der f 21.0101 has shown the Maximum Binding Energy [MBE] (-8.18 kcal/mol) with the first target ligand cholesterol. On the other hand, Mite allergen Bio t5 has exhibited the minimum binding energy (-6.03 kcal/mol) with cholesterol (as shown in Table 2). Surprisingly, only two respiratory allergen proteins (Allergen Can f 1 and per a 4 allergen) have shown amino acid interactions with the cholesterol (as shown in Table 2).

The present Swissdock analysis showed that Mite allergen Der f 21.0101 has exhibited the Highest Binding Energy [HBE] (-10.48 kcal/mol) with the second target ligand 17:1 cholesteryl ester. On the other hand, Mite allergen Der f 2 has shown the least binding energy (-6.95 kcal/mol) with the 17:1 cholesteryl ester (as shown in Table 3). Interestingly, only four respiratory allergen proteins (Allergen Bla g 4, Allergen Can f 1, Mite allergen Bio t5 and Peptidase 1 (DERF1)) have shown amino acid interactions with the 17:1 cholesteryl ester (as shown in Table 3).

The current Swissdock investigation showed that Mite allergen Der f 21.0101 has shown the Maximum Binding Energy [MBE] (-8.41 kcal/mol) with the third target ligand cholesterol formate. On the other hand, House dust mite allergen (Derf 2) has exhibited the minimum binding energy (-6.44 kcal/mol) with the cholesterol formate (as shown in Table 4a). Surprising, only three respiratory allergen proteins (Allergen Bla g 4, Der p 2 allergen and Group 2 allergen Bio t2 isoform 9) have shown amino acid interactions with the cholesterol formate (as shown in Table 4a).

The present Swissdock analysis showed that Mite allergen Der f 21.0101 has exhibited the Highest Binding Energy [HBE] (-9.63 kcal/mol) with the fourth target ligand cholesteryl palmitate.

On the other hand, Mite allergen Bio t5 has shown the least binding energy (-6.50 kcal/mol) with the cholesterol palmitate. Interestingly, only three respiratory allergen proteins (Allergen Can f 1, Major allergen Can f 1 and Peptidase 1 (DERF1)) have shown amino acid interactions with the cholesterol palmitate (as shown in Table 4b).

DISCUSSION

Respiratory allergens come across two lipid-based barriers namely pulmonary surfactant and luminal plasma membrane of airway (respiratory tract) epithelial cells (Min *et al.*, 2023). Recent year's theory reveals that "epithelial barrier disruptions" leads to both allergy and auto-immune responses (Akdis, 2021).

Table 1: Represents the physicochemical properties of 13 chosen respiratory allergen proteins using ProtParam web server.

Protein name	MW [■]	P1 [°]	NR [■]	PR [°]	Ext.co1 ^{▲▲}	Ext.co2 ^{▼▼}	Instability Index	Aliphatic Index	GRAVY [⚡]
Allergen Bla g 4	20927	6.48	25	23	27640	27390	28.02	72.42	-0.567
Allergen Can f 1	17853	5.66	21	18	13075	12950	45.98	76.01	-0.571
Der p 2 allergen	15890	7.59	16	17	11835	11460	31.56	105.48	0.055
Group 2 allergen Bio t2 isoform 1	15180	6.17	16	14	4845	4470	20.78	93.31	0.128
Group 2 allergen Bio t2 isoform 9	15275	6.17	16	14	4845	4470	24.29	99.51	0.182
House dust mite allergen (Der f 2)	14044	6.45	17	16	8855	8480	21.08	94.42	-0.181
Major allergen Can f 1	19248	5.95	21	19	13075	12950	43.45	87.47	-0.349
Mite allergen Bio t5	15642	5.27	26	19	3105	2980	41	103.43	-0.548
Mite allergen Der f 2	15807	6.93	17	17	10345	9970	26.56	105.48	0.062
Mite allergen Der f 21.0101	15965	4.97	27	20	9970	9970	32.66	92.50	-0.285
Peptidase 1 (DERF1)	36435	5.66	37	30	53665	53290	38.53	79.31	-0.389
Per a 2 allergen	38190	5.46	32	25	33070	32320	29.77	81.88	-0.005
Per a 4 allergen	20517	3.99	26	8	43110	42860	16.40	69.23	-0.262

Note: MW[■]- Molecular weight of respiratory allergen protein, P1[°]- Theoretical Isoelectric point of respiratory allergen protein, NR[■]- Total number of negatively charged residues present in the respiratory allergen protein, PR[°]- Total number of positively charged residues present in the respiratory allergen protein, Ext.co1^{▲▲} Extinction coefficient assuming all pairs of Cys residues form cystines, Ext.co2^{▼▼} - Extinction coefficient assuming all Cys residues are reduced and GRAVY[⚡]- Grand average of hydropathicity of the respiratory allergen protein.

Table 2: The Swissdock binding energy analysis of 13 selected respiratory allergen proteins with the cholesterol ligand using Swissdock method.

Protein name	Swissdock binding energy (-kcal/mol)	Interactions of amino acids residues	Bond distance (Å)	RMSD ⁰⁰ compared with quercetin docked complex (Å) value
Allergen Bla g 4	7.19	NHBI [■]	-	0.00
Allergen Can f 1	7.30	Pro55	2.0	0.00
Der p 2 allergen	6.60	NHBI [■]	-	0.00
Group 2 allergen Bio t2 isoform 1	7.33	NHBI [■]	-	0.00
Group 2 allergen Bio t2 isoform 9	6.58	NHBI [■]	-	0.00
House dust mite allergen (Derf 2)	6.14	NHBI [■]	-	0.00
Major allergen Can f 1	7.06	NHBI [■]	-	0.00
Mite allergen Bio t5	6.03	NHBI [■]	-	0.00
Mite allergen Der f 2	6.73	NHBI [■]	-	0.00
Mite allergen Der f 21.0101	8.18	NHBI [■]	-	0.00
Peptidase 1 (DERF1)	7.08	NHBI [■]	-	0.00
Per a 2 allergen	7.84	NHBI [■]	-	0.00
Per a 4 allergen	7.17	Lys35	3.5	0.00

Note: NHBI[■] – No hydrogen bond interactions, RMSD⁰⁰ -Root Mean Square Deviation.

Table 3: The Swissdock binding energy analysis of 13 selected respiratory allergen proteins with the 17:1 cholesteryl ester ligand using Swissdock method.

Protein name	Swissdock binding energy (-kcal/mol)	Interactions of amino acids residues	Bond distance (Å)	RMSD ⁰⁰ compared with quercetin docked complex (Å) value
Allergen Bla g 4	7.17	Lys145 Gln149	3.3 2.8	2.01
Allergen Can f 1	9.43	Lys131	2.9	4.98
Der p 2 allergen	7.99	NHBI [■]	-	2.42
Group 2 allergen Bio t2 isoform 1	6.92	NHBI [■]	-	2.49
Group 2 allergen Bio t2 isoform 9	7.38	NHBI [■]	-	3.13
House dust mite allergen (Derf 2)	7.05	NHBI [■]	-	4.92
Major allergen Can f 1	7.94	NHBI [■]	-	2.67
Mite allergen Bio t5	7.52	Lys21	3.4	3.30
Mite allergen Der f 2	6.95	NHBI [■]	-	2.07
Mite allergen Der f 21.0101	10.48	NHBI [■]	-	2.38
Peptidase 1 (DERF1)	8.56	Arg103	3.3	1.54
Per a 2 allergen	8.32	NHBI [■]	-	1.51
Per a 4 allergen	7.39	NHBI [■]	-	7.47

Note: NHBI[■] – No hydrogen bond interactions, RMSD⁰⁰ -Root Mean Square Deviation.

Bienboire-Frosini and colleagues (2020) had demonstrated that steroids [i) Androstenedione, ii) Androstenedione, iii) Androstenediol, iv) Corticosterone, v) Dehydroepiandrosterone, vi) Deoxycorticosterone, vii) Dihydrotestosterone, viii) Estradiol, ix) Estrone, x) Hydroxyprogesterone, xi) Pregnenolone,

xii Progesterone and xiii) Testosterone] and fatty acids [i) Capric acid, ii) Dodecanal, iii) Dodecanol, iv) Ethyl laurate, v) Hexadecanamide, vi) Isobutyric acid, vii) Lauric acid, viii) Linoleic acid, ix) Methyl palmitate, x) Myristic acid, xi) Nonanamide,

xii) Octadecanamide, xiii) Oleic acid, xiv) Palmitic acid and xv) Tetradecanol] bind with the major cat allergen Fel d1.

Similarly, Min and co-workers (2023) had reported that 88 fatty acids bind with Can f 1 and Fel d7. Thus, in the present investigation, four target ligands namely i) cholesterol, ii) 17:1 cholesteryl ester, iii) cholesterol formate and iv) cholesterol palmitate was chosen for the docking study.

With regard to physiochemical properties, only one chosen respiratory allergen protein (Der p 2 allergen) has exhibited theoretical isoelectric point (PI) value greater ($>$) than 7.0. This result reveals that Der p 2 allergen protein is basic in nature, which was in good agreement with earlier reports (Kausar *et al.*, 2022; Vishnupriya *et al.*, 2024). Similarly, three selected respiratory allergen proteins (Mite allergen Bio t5, Major allergen Can f 1 and Allergen Can f 1) have shown instability index value greater ($>$) than 40. This finding suggests these are instability protein in nature, which was in good correlation with previous reports (Kausar *et al.*, 2022; Vishnupriya *et al.*, 2024).

With reference to docking, Mite allergen Der f 21.0101 has exhibited the Highest Binding Energy [HBE] with all four target ligands [i) cholesterol (-8.18 kcal/mol); ii) 17:1 cholesteryl ester (-10.48 kcal/mol); iii) cholesterol formate (-8.41 kcal/mol) and iv) cholesterol palmitate (-9.63 kcal/mol). In contrast, Mite allergen Bio t5 has shown the least binding energy with two target ligands [i) cholesterol (-6.03 kcal/mol) and ii) cholesterol palmitate (-6.50 kcal/mol)] respectively. This finding was on par with earlier report, where 13 steroids have docked with major cat allergen Fel

d1 (Bienboire-Frosini *et al.*, 2020). Similarly, cholesterol ligand has shown interaction with Pro55 and Lys35 amino acid residues of Allergen Can f 1 and per a 4 allergen respectively.

Interestingly, 17:1 cholesteryl ester ligand has shown interaction with Lys145 and Gln149; Lys131; Lys21 and Arg103 amino acid residues of Allergen Bla g 4; Allergen Can f 1; Mite allergen Bio t5 and Peptidase 1 (DERF1). This result was in good correlation with previous report, where 88 fatty acids bind with Lys131 amino acid residue of Can f 1 allergen (Min *et al.*, 2023).

Similarly, cholesterol formate ligand has shown interaction with Gln69; Ala13 and Val15; Val11 amino acid residues of Allergen Bla g 4; Der p 2 allergen and Group 2 allergen Bio t2 isoform 9. This result was in close correlation with previous report, where replacement (mutation) of valine (Val) instead of alanine (Ala) at 16th amino acid position in wild-type Der p2 allergen showed significant increase in cholesterol binding capacity (Reginald & Chew, 2019).

Furthermore, cholesterol palmitate ligand has shown interaction with Tyr97; Thr82; Lys35 amino acid residues of Allergen Can f 1; Major allergen Can f 1 and Peptidase 1 (DERF1). This finding was in close agreement with previous report, where Cys35 was reported instead of Lys35 in Der f 1 allergen (Chruszcz *et al.*, 2009; Lin *et al.*, 2023).

The present finding is only based on docking (*in silico*) method which gives new insight into the four chosen ligands and their interactions with 13 selected respiratory allergen proteins. However, further *in vitro* ANS (8-anilino-1-naphthalene

Table 4a: The Swissdock binding energy analysis of 13 selected respiratory allergen proteins with the cholesterol formate ligand using Swissdock method.

Protein name	Swissdock binding energy (-kcal/mol)	Interactions of amino acids residues	Bond distance (Å)	RMSD ⁰⁰ compared with quercetin docked complex (Å) value
Allergen Bla g 4	7.37	Gln69	3.3	0.59
Allergen Can f 1	6.91	NHBI [■]	-	5.59
Der p 2 allergen	7.40	Ala13 Val15	3.3 3.4	0.95
Group 2 allergen Bio t2 isoform 1	6.62	NHBI [■]	-	2.06
Group 2 allergen Bio t2 isoform 9	6.52	Val11	3.4	4.99
House dust mite allergen (Derf 2)	6.44	NHBI [■]	-	1.57
Major allergen Can f 1	6.65	NHBI [■]	-	1.71
Mite allergen Bio t5	6.86	NHBI [■]	-	6.05
Mite allergen Der f 2	6.47	NHBI [■]	-	2.53
Mite allergen Der f 21.0101	8.41	NHBI [■]	-	2.32
Peptidase 1 (DERF1)	7.27	NHBI [■]	-	0.77
Per a 2 allergen	7.87	NHBI [■]	-	2.93
Per a 4 allergen	6.51	NHBI [■]	-	10.50

Note: NHBI[■] – No hydrogen bond interactions, RMSD⁰⁰ – Root Mean Square Deviation.

Table 4b: The Swissdock binding energy analysis of 13 selected respiratory allergen proteins with the cholesterol palmitate ligand using Swissdock method.

Protein name	Swissdock binding energy (-kcal/mol)	Interactions of amino acids residues	Bond distance (Å)	RMSD ⁰⁰ compared with quercetin docked complex (Å) value
Allergen Bla g 4	8.78	NHBI [□]	-	2.50
Allergen Can f 1	8.94	Tyr97	3.5	5.13
Der p 2 allergen	7.74	NHBI [□]	-	3.14
Group 2 allergen Bio t2 isoform 1	7.56	NHBI [□]	-	7.54
Group 2 allergen Bio t2 isoform 9	8.65	NHBI [□]	-	6.07
House dust mite allergen (Derf 2)	7.47	NHBI [□]	-	4.84
Major allergen Can f 1	8.96	Thr82	3.2	2.81
Mite allergen Bio t5	6.50	NHBI [□]	-	6.75
Mite allergen Der f 2	7.76	NHBI [□]	-	2.19
Mite allergen Der f 21.0101	9.63	NHBI [□]	-	2.14
Peptidase 1 (DERF1)	8.52	Lys35	3.5	6.98
Per a 2 allergen	8.68	NHBI [□]	-	2.05
Per a 4 allergen	7.32	NHBI [□]	-	6.80

Note: NHBI[□] – No hydrogen bond interactions, RMSD⁰⁰ – Root Mean Square Deviation.

sulfonate) binding assay experiments are needed to confirm allergen proteins interactions with four chosen ligands.

CONCLUSION

In the current investigation, the four chosen ligands (cholesterol, 17:1 cholesteryl ester, cholesterol formate and cholesterol palmitate) have shown the potential to dock with 13 selected respiratory allergen proteins. Interestingly, Allergen Can f 1 has exhibited amino acids interaction with three target ligands [cholesterol (Pro55); 17:1 cholesteryl ester (Lys131); and cholesterol palmitate (Tyr97)]. Similarly, Allergen Bla g 4 has exhibited amino acids interaction with two target ligands [17:1 cholesteryl ester (Lys145, Gln149); and cholesterol formate (Gln69)]. Furthermore Peptidase 1 (DERF1) has exhibited amino acids interaction with two target ligands [17:1 cholesteryl ester (Arg103); and cholesterol palmitate (Lys35)]. Thus, the current finding gives new understanding about the four chosen ligands as binding agents with 13 selected respiratory allergen proteins, which may help in developing allergy mitigation approaches.

ACKNOWLEDGEMENT

The authors like to thank authorities of Saveetha Medical College and Hospital (SMCH), Saveetha Institute of Medical and Technical Sciences (SIMATS, Chennai) for providing us support to conduct the study

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

ABBREVIATIONS

Blo t: Blomia tropicallis; **Der f:** Dermatophagoides farina; **Der m:** Dermatophagoides microceras; **Der p:** Dermatophagoides pteronyssinus; **HDM:** House dust mites; **GRAVY:** Grand average of hydropathicity; **CID:** Compound Identifier; **2D:** Two dimensional; **3D:** Three dimensional; **UniProt:** Universal Protein Resource; **PDB:** Protein Data Bank; **HBE:** Highest binding energy; **MBE:** Maximum binding energy; **LBE:** Least binding energy; **RMSD:** Root Mean Square Deviation; **Ext.co1:** Extinction coefficient.

SUMMARY

In the present study, 13 chosen respiratory allergens proteins were studied on the docking behaviour with four chosen ligands namely i) cholesterol, ii) 17:1 cholesteryl ester, iii) cholesterol formate and iv) cholesterol palmitate by using the swissdock method. The docking results revealed that Mite allergen Der f 21.0101 has exhibited the highest binding energy [HBE] with all four target ligands [i) cholesterol (-8.18 kcal/mol); ii) 17:1 cholesteryl ester (-10.48 kcal/mol); iii) cholesterol formate (-8.41 kcal/mol) and iv) cholesterol palmitate (-9.63 kcal/mol)].

REFERENCES

- Akdis, C. A. (2021). Does the epithelial barrier hypothesis explain the increase in allergy, autoimmunity and other chronic conditions? *Nature Reviews. Immunology*, 21(11), 739–751. <https://doi.org/10.1038/s41577-021-00538-7>, <https://pubmed.ncbi.nlm.nih.gov/33846604/>
- Bienboire-Frosini, C., Durairaj, R., Pelosi, P., & Pageat, P. (2020). The major cat allergen Fel d 1 binds steroid and fatty acid semiochemicals: A combined *in silico* and *in vitro* study. *International Journal of Molecular Sciences*, 21(4), Article 1365. <https://doi.org/10.3390/ijms21041365>, <https://pubmed.ncbi.nlm.nih.gov/32085519/>

- Chruszcz, M., Chapman, M. D., Vailes, L. D., Stura, E. A., Saint-Remy, J.-M., Minor, W., & Pomés, A. (2009). Crystal structures of mite allergens Der f 1 and der p 1 reveal differences in surface-exposed residues that may influence antibody binding. *Journal of Molecular Biology*, 386(2), 520–530. <https://doi.org/10.1016/j.jmb.2008.12.049>, <https://pubmed.ncbi.nlm.nih.gov/19136006/>
- Hu, R.-H., Wu, C.-T., Wu, T.-S., Yu, F.-Y., Ko, J.-L., Lue, K.-H., & Liu, Y.-F. (2022). Systematic characterization of the group 2 house dust mite allergen in *Dermatophagoides microceras*. *Frontiers in Cellular and Infection Microbiology*, 11, Article 793559. <https://doi.org/10.3389/fcimb.2021.793559>, <https://pubmed.ncbi.nlm.nih.gov/35111694/>
- Ichikawa, S., Takai, T., Inoue, T., Yuuki, T., Okumura, Y., Ogura, K., Inagaki, F., & Hatanaka, H. (2005). NMR study on the major mite allergen Der f 2: Its refined tertiary structure, epitopes for monoclonal antibodies and characteristics shared by ML protein group members. *Journal of Biochemistry*, 137(3), 255–263. <https://doi.org/10.1093/jb/mvi039>, <https://pubmed.ncbi.nlm.nih.gov/15809326/>
- Ichikawa, S., Takai, T., Yashiki, T., Takahashi, S., Okumura, K., Ogawa, H., Kohda, D., & Hatanaka, H. (2009). Lipopolysaccharide binding of the mite allergen Der f 2. *Genes to Cells: Devoted to Molecular and Cellular Mechanisms*, 14(9), 1055–1065. <https://doi.org/10.1111/j.1365-2443.2009.01334.x>, <https://pubmed.ncbi.nlm.nih.gov/19678854/>
- Kausar, M. A., Bhardwaj, T., Anwar, S., Alenazi, F., Ali, A., Alshammari, K. F., AboElnaga, S. M. H., Singh, R., & Najm, M. Z. (2022). *In silico* comparative exploration of allergens of *Periplaneta americana*, *Blattella germanica* and *Phoenix dactylifera* for the diagnosis of patients suffering from IgE-mediated allergic respiratory diseases. *Molecules*, 27(24), Article 8740. <https://doi.org/10.3390/molecules27248740>
- Lin, Y., Enyoh, C. E., Wang, Q., Lu, S., Zhang, W., Xiao, K., Zhou, S., Kaneko, T., Seguchi, A., Wang, W., & Guo, Y. (2022). Novel approaches for inhibiting the indoor allergen Der f 2 excreted from house dust mites by todomatsu oil produced from woodland residues. *International Journal of Environmental Research and Public Health*, 19(17), Article 10881. <https://doi.org/10.3390/ijerph191710881>, <https://pubmed.ncbi.nlm.nih.gov/36078598/>
- Lin, Y., Xiao, K., Wang, W., Lu, S., & Wang, Q. (2023). Study on lowering the group 1 protease allergens from house dust mites by exposing to todomatsu oil atmosphere. *Atmosphere*, 14(3), 548. <https://doi.org/10.3390/atmos14030548>
- Min, J., Foo, A. C. Y., Gabel, S. A., Perera, L., DeRose, E. F., Pomés, A., Pedersen, L. C., & Mueller, G. A. (2023). Structural and ligand binding analysis of the pet allergens Can f 1 and Fel d 7. *Frontiers in Allergy*, 4, Article 1133412. <https://doi.org/10.3389/falgy.2023.1133412>, <https://pubmed.ncbi.nlm.nih.gov/36960093/>
- Narayanaswamy, R., Harika, V., & Prabhakaran, V.-S. (2024). Human and mouse nephrin and their interactions with 13 proteins: An *in silico* study. *Cureus*, 16(8), Article e66332. <https://doi.org/10.7759/cureus.66332>, <https://pubmed.ncbi.nlm.nih.gov/39246878/>
- Narayanaswamy, R., Rajagopal, D., & Prabhakaran, V.-S. (2024). Molecular docking analysis of four drugs (phenytoin, amoxicillin, aceclofenac and ciprofloxacin) and their association with four human leukocyte antigen (HLA) alleles. *Cureus*, 16(6), Article e62269. <https://doi.org/10.7759/cureus.62269>, <https://pubmed.ncbi.nlm.nih.gov/39006565/>
- Offermann, L. R., Chan, S. L., Osinski, T., Tan, Y. W., Chew, F. T., Sivaraman, J., Mok, Y.-K., Minor, W., & Chruszcz, M. (2014). The major cockroach allergen Bla g 4 binds tyramine and octopamine. *Molecular Immunology*, 60(1), 86–94. <https://doi.org/10.1016/j.molimm.2014.03.016>, <https://pubmed.ncbi.nlm.nih.gov/24769496/>
- Ramsbottom, K. A., Carr, D. F., Jones, A. R., & Rigden, D. J. (2018). Critical assessment of approaches for molecular docking to elucidate associations of HLA alleles with adverse drug reactions. *Molecular Immunology*, 101, 488–499. <https://doi.org/10.1016/j.molimm.2018.08.003>, <https://pubmed.ncbi.nlm.nih.gov/30125869/>
- Reginald, K., & Chew, F. T. (2019). The major allergen Der p 2 is a cholesterol binding protein. *Scientific Reports*, 9(1), Article 1556. <https://doi.org/10.1038/s41598-018-38313-9>, <https://pubmed.ncbi.nlm.nih.gov/30733527/>
- Srinivasan, K., Altemimi, A. B., Narayanaswamy, R., Vasantha Srinivasan, P., Najm, M. A. A., Mahna, N., & GC-MS. (2023). GC-MS, Alpha-amylase, and alpha-glucosidase inhibition and molecular docking analysis of selected phytoconstituents of small wild date palm fruit (*Phoenix pusilla*). *Food Science and Nutrition*, 11(9), 5304–5317. <https://doi.org/10.1002/fsn3.3489>, <https://pubmed.ncbi.nlm.nih.gov/37701203/>
- Surya Prakash, V. S., Radhakrishnan, N., Vasantha-Srinivasan, P., Veeramani, C., El Newehy, A. S., Alsaif, M. A., & Al-Numair, K. S. (2023). *In silico* analysis of selected nutrition rich fruit of Bunch berry (*Lantana camara*) constituents as human acetylcholinesterase (hAChE), carbonic anhydrase II (hCA-II) and carboxylesterase 1 (hCES-1) inhibitory agents. *Saudi Journal of Biological Sciences*, 30(12), Article 103847. <https://doi.org/10.1016/j.sjbs.2023.103847>, <https://pubmed.ncbi.nlm.nih.gov/37961045/>
- Tai, H.-Y., Zhou, J.-K., Yeh, C.-C., Tam, M. F., Sheu, S.-Y., & Shen, H.-D. (2018). The different modes of binding of the dust mite allergens, Der f 7 and der p 7, on a monoclonal antibody WH9 contribute to the differential reactivity. *Journal of Microbiology, Immunology, and Infection*, 51(4), 478–484. <https://doi.org/10.1016/j.jmii.2016.11.011>, <https://pubmed.ncbi.nlm.nih.gov/28693928/>
- Victor, P. P., Narayanaswamy, R., Kadry, S., & Gurunathan, B. (2023). Identification of novel inhibitor against human phosphoethanolamine cytidyltransferase from phytochemicals of *Citrus sinensis* peel extract by *in vitro* and *in silico* approach. *Biotechnology and Applied Biochemistry*, 70(5), 1565–1581. <https://doi.org/10.1002/bab.2453>, <https://pubmed.ncbi.nlm.nih.gov/36824047/>
- Vishnupriya, N., & Narayanaswamy, R. (2024). Human intelectin-1 (hITL-1) as modulator of metabolic syndrome (MetS): An *in silico* study. *Journal of Pharmacy and Bioallied Sciences*, 16(Suppl. 2), S1173–S1180. https://doi.org/10.4103/jpbs.jpbs_518_23, <https://pubmed.ncbi.nlm.nih.gov/38882764/>

Cite this article: Narayanaswamy R, Das B, Sachin BS. Binding Analysis of Cholesterol and its Derivatives with 13 Chosen Respiratory Allergens: An *in silico* Study . *Pharmacog Res*. 2026;18(4):1268-74.