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OPEN PEER REVIEW

Phenolic Compounds from *Diarthron iranica*: Enzymatic and in Silico Insights Into α-Amylase Inhibitory Activity

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1 Original submission

5 comments · 12 Aug 2025 – 19 Aug 2025

Referee 1 Reviewer

MINOR REVISION 12 Aug 2025

Dear authors
Thank you for your efforts in this study.
My comments:
Please add information about reagents and chemicals, general experimental procedures, and types of 2DNMR and DEPT spectra to the manuscript.
The area where the plant was collected should be described more accurately and precisely.
For compound 3, the inconsistent data on molecular mass (357, 370) and type of spectroscopy (EI, ESI) should be corrected.
In the introduction section, no proper reference is made to figure 1.
For compound 4, the mass fragmentation data (with their intensity values) should be presented in the Results section. The rest of the related content should be moved to the Discussion section.
The agreement of the spectral data with previous reports should be stated clearly and individually in the text.
Previous reports of the identification of each of these 4 compounds in this plant species should be presented clearly, one by one.
Finally, I would like to thank you again for your valuable research.

Referee 2 Reviewer

MAJOR REVISION 16 Aug 2025

1. All abbreviations should be defined before their first use.
2. The steps of extraction, purification, and fractionation could be shown on a chart to make them more comprehensible.
3. It would be better to use the complete forms of words in titles and subtitles.
4. The methods used for the physicochemical characterization of the extracted compound should be described in the methods section.
5. Indicate how many compounds were detected in each extract sample or fraction.
6. Why were only the mass spectra of one compound presented in more detail in the manuscript? No data about the bioactivity or molecular docking of this compound were presented in the manuscript! Additionally, this compound was not discussed in the discussion section.
7. The data on the characterization of all compounds could be presented in supplementary files.
8. What was the logic behind the compound selection for the in vitro and in silico enzyme inhibitory activity assay?
9. Line 207-208: state exactly which chemical structure is related to which compound. Then, in the following discussion, clearly state which of your results are being compared with the literature; in general, the discussion section is not clear.
10. A statistical comparison of the enzyme inhibitory activity of the compounds with that of luteolin as a standard should be presented.

Referee 3 Reviewer

REJECT 17 Aug 2025

Dear Editor, the manuscript entitled “Phenolic compounds from Diathron iranica: Enzymatic and In Silico Insights into α-amylase Inhibitory Activity” is about the isolation of phenolic compounds from Diathron iranica and testing their α-amylase inhibitory activity.
My comments are as follows:
• The abstract is not clear.
• The aim of this study is unclear. What is the rationale for evaluating the α-amylase inhibitory activity?
• Including a flow chart of the extraction and preparation process could help readers better understand and follow the methodology used.
• The specifications of the materials used (enzyme, buffer, etc.) and the instruments (GC-MS, NMR, HPLC, columns, mobile phases, spectrophotometer, etc.) in this study are not provided. In the NMR section for compound 2, “: δ 3.81(3H, s, —, H-6-OMe),” what does H-6-OMe mean?
• What does the line “-” stand for in the interpretation of the NMR analysis?
Compound 2: “δ 3.81(3H, s, —, H-6-OMe),”” s, —, H-5′)”
• For compound 3, the reported number of hydrogens is 17, not accounting for phenolic hydrogens, while the molecular formula of pinoresinol is $C_{20}H_{22}O_6$. Please clarify this discrepancy.
• What do the numbers in figure 2 represent?
• It is recommended that the final reported compounds be presented in a table including their structures, molecular formulas, molecular weights, physical states (oil or crystal), and colors.
• The spectra used (1D and 2D-NMR, GC/MS, ESI, …) should be added as supplementary material.
• Why were only two compounds (1 and 3) chosen for the α-amylase inhibitory test?
• Why was luteolin chosen as the reference compound in the α-amylase inhibitory test?
• What control was used in the α-amylase inhibitory test?
• How many times was the experiment repeated? The n is not mentioned.
• In the α-amylase inhibitory section, the sentence “and 20 µL of varying 97 concentrations (0.30, 0.42, 0.60, 1.30, 1.80, 2.30, and 2.80 mg/mL) were incubated” is unclear. To which compounds do these concentrations correspond?
• The solvent used for the compounds, the pH, and the buffer type used for the α-amylase test have not been specified.
• What does the * in Figure 3 indicate?
• The reported IC50 values are presented without the corresponding RMSE.
• The IC50 curves need to be included.
• How significant are carbon-hydrogen interactions in docking results?
• Have the α-amylase inhibitory activities of the mentioned compounds been previously reported in the literature? If so, please include this information and provide an appropriate reference.

Associate Editor

MAJOR REVISION 19 Aug 2025

Thanks to the authors,
In its current state, the manuscript does not appear to be acceptable, so please resubmit it for re-review after revising it, making the necessary corrections, and accurately addressing all the reviewers' questions and comments.

Editor-in-Chief MAJOR REVISION 19 Aug 2025

Major Revision

2

Revision 1

AUTHORS' RESPONSE TO REVIEWERS

Authors' reply to reviewers

The next pages contain the authors' point-by-point reply to the comments of this revision round, as submitted with the revised manuscript. It is published as the authors wrote it.

Reviewer 0:

1. All abbreviations should be defined before the first usage

Response: The abbreviations used in the extraction section were corrected.

2. Steps of exaction, purification, and fractionation could be shown on a chart to be more comprehensible

Response: The tree-diagram of extraction and isolation of purified compounds were added to the text.

3. It would be better to use the complete form of words in titles and subtitles

Response: They were corrected.

4. The methods used for the physicochemical characterization of the extracted compound should be described in the methods section

Repose: It was added as follows:

2D, and 3D-NMR experiments

HSQC correlated each proton with its directly bonded carbon. COSY-DQF experiment allowed to detect direct connectivities through proton–proton scalar coupling. HMBC allowed partial substructures to be interconnected. Saccharide part and its sugar sequences were identified through HSQC-TOCSY, and HMBC experiment. In sugar regions where proton signals are highly overlapped, the HSQC-TOCSY experiment allowed us to resolve individual spin systems by each sugar. It is a 3 dimensional NMR experiment, which the F1 (^{1}H)–F2 (^{13}C) dimension corresponds to the ^{1}H–^{13}C HSQC correlations, while the F1 (^{1}H)–F3 (^{1}H) projection reveals ^{1}H–^{1}H TOCSY spin system correlations. Connectivity's between sugars and with aglycone part was determined through HMBC spectra. The spectra are provided in supplementary material file.

5. Indicate how many compounds were detected in each sample of extract or fractions:

Response: It was included in Fig 1: isolating process chart, accordingly.

6. Why were only the mass spectra of one compound presented in more detail in the manuscript?

No data about the bioactivity or molecular docking of this compound was presented in the manuscript! Additionally, this compound was not discussed in the discussion section.

Response: Compound **4** was obtained in insufficient quantity for NMR analysis. Consequently, its structure was elucidated based on mass fragmentation patterns and comparison with the NIST spectral library.

In contrast, compounds **1**–**3** were isolated in adequate amounts, allowing for comprehensive characterization using both NMR and mass spectrometry. Therefore, interpretation of fragmentation patterns was not necessary for their identification.

7. The data of the characterization of all compounds could be presented in supplementary files

Response: It was provided, accordingly.

8. What was the logic behind the compound selection for the in vitro and in silico enzyme inhibitory activity assay?

Response: Considering the points discussed in the introduction regarding the antidiabetic effects of phenolic compounds, particularly their ability to inhibit the α-amylase enzyme, the aim of this study was to investigate the inhibitory effects of these plant-derived compounds. Further, regarding for the valuable comments from the referees, compound **2** was also evaluated for alpha-amylase inhibition and subjected to docking studies. The corresponding data have been incorporated into the manuscript. However, compound 4 was obtained in insufficient quantity for enzymatic assay.

9. Line 207-208: state exactly which chemical structure is related to which compound. Then, in the following discussion, distinctly state that the comparison with other literature is related to which results you obtained; in general, the discussion section is not clear.

Response: We tried to rephrase some sections of the discussion to make them clearer.

10. Statistical comparison of the enzyme inhibitory activity of compounds with luteolin as a standard should be presented

Response: It was added at figure 4 part (e).

Reviewer 1:
Dear Editor, the manuscript entitled" Phenolic compounds from *Diathron iranica*: Enzymatic and In Silico Insights into α-amylase Inhibitory Activity" is about the isolation of phenolic

compounds from *Diathron iranica* and testing their α-amylase inhibitory activity.
My comments are as follows:
• The abstract is not clear.

Response: The abstract has been revised to improve clarity and readability.

• The aim of this study is unclear. What is the rationale for evaluating the α-amylase inhibitory activity?

Response: There is extensive research on the alpha-amylase inhibitory effects of flavones and lignans, and in continue to our previous investigations into digestive enzyme inhibition, we proceeded to evaluate the α-amylase inhibitory activity in this study. The significance of this activity, along with relevant literature on flavones and lignans, was added in the Introduction section.

• Including a flow chart of the extraction and preparation process could help readers better understand and follow the methodology used

Response: We thank the referee for this valuable comment. The tree-diagram of extraction and isolation of purified compounds were added to the text.

• The specifications of the materials used (enzyme, buffer, etc.) and the instruments (GC-MS, NMR, HPLC, columns, mobile phases, spectrophotometer, etc.) in this study are not provided

Response: We thank the referee for this valuable comment. The specifications of the materials and instruments used in this study have been provided. NMR spectra were recorded using a Bruker 400 MHz instrument. HPLC analysis was performed on a Waters system equipped with a Shimpack C-18 column (20 × 250 mm, 5 µm; Shimadzu, Japan). GC-MS analysis was conducted using an Agilent 7890A gas chromatograph coupled with an Agilent 5975C mass selective detector, equipped with an HP-5 capillary column. The revised manuscript includes detailed information on the mobile phase, enzyme source, buffer composition, and spectrophotometric conditions, where applicable

IN nmr section for compound 2, ": δ 3.81 (3H, s, —, H-6-OMe)," H-6-OMe is not clear?

Response: We thank the referee for carefully identifying this point. It was corrected

• What does the line"-" stand for in the interpretation of NMR analysis? Compound 2 : "δ 3.81 (3H, s, —, H-6-OMe),"" s, —, H-5′)"

Response: This dashed line indicated the absence of coupling. It was corrected and removed.

• For compound 3, the reported number of hydrogens is 17, not accounting for phenolic hydrogens, while the molecular formula of pinoresinol is C20H22O6. Please clarify this discrepancy

Response: We appreciate the referee's careful observation. However, upon review, we realized that the original discussion text may have lacked clarity. To resolve this issue, we have revised the relevant section to provide a more accurate and detailed explanation, as follows:

"Compound **3** was inferred to have a molecular formula of $C_{20}H_{22}O_6$, consistent with the DEPT and ^{13}C-NMR spectral data and the calculated hydrogen count. Two methoxy groups were detected at δ_C 42.56 (3′-OMe and 3-OMe) in both the ^{13}C-NMR and DEPT spectra, along with two oxygenated methylene carbons at δ_C 49.72 (C9′ and C9). Six olefinic methine carbons were observed at δC 110.94 (C2′ and C2), 116.11 (C5′ and C5), and 120.01 (C6′ and C6). Additionally, two simple aliphatic carbons appeared at δC 55.15 (C8 and C8′), and two oxygenated aliphatic methine carbons at δ_C 87.13 (C7 and C7′). Six quaternary carbons were identified: two non-oxygenated olefinic carbons at δC 133.74 (C1′ and C1), and four oxygenated olefinic carbons at δC 148.99 (C3′ and C3) and 147.10 (C4′ and C4). Based on the carbon environments, the following proton types were deduced: six protons from two methoxy groups (–OCH_3), four from two oxygenated methylene groups (–CH_2–O), six from olefinic methine (=CH–), two from aliphatic methine (–CH–), and two from oxygenated aliphatic methine carbons- totaling 20 protons. The remaining two protons, not accounted for in the DEPT and ^{13}C-NMR spectra, are attributed to two hydroxyl groups (–OH) from phenolic moieties. These signals support the molecular formula $C_{20}H_{22}O_6$"

• What do the numbers in figure 2 represent?
Response:

These values correspond to the fragment ion analysis in m/z used in structural confirmation of the compound. The figure caption has been revised accordingly to reflect this as follows:

"Fragmentation pattern of the mass spectrum for compound **4**. In the fragmentation analysis of the mass spectrum, the presence of fragment ions at *m/z* 135, 151, 107, 339, 177, and 77, provides structural confirmation of the compound as kusunokinin."

• It is recommended to present the final reported compounds in a table including their structure, molecular formula, molecular weight, physical state (oil or crystal), and color.

Response: It was added.

• The used spectrum (1D and 2D-NMR, GC/MS, ESI,….) should be added as supplementary material.

Response: It was prepared and added as supplementary file.

• Why were only two compounds (1 and 3) chosen for the amylase inhibitory test?

Response: Regarding for the valuable comments from the referees, compound **2** was also evaluated for alpha-amylase inhibition and subjected to docking studies.

• Why was luteolin chosen as the reference compound in the amylase inhibitory test.

Response: Luteolin was selected as the reference compound because it is a well-characterized natural flavonoid with documented α-amylase inhibitory activity. Several studies have reported its consistent and reproducible inhibition of α-amylase, making it a reliable positive control in enzymatic assays [1, 2]. Using luteolin as a reference allows for comparison with previously published data and provides a standard reference for evaluating the inhibitory potential of the tested samples[3].

• What control was used in the alpha amylase inhibitory test?

Response: Luteolin was employed as the positive control inhibitor, whereas samples without any inhibitor served as the negative control.

• How many times was the experiment repeated? The n is not mentioned?

Response: Each experiment was performed in triplicate. The sentence was also added in the method section.

• In the amylase inhibitory section, the sentence“and 20 µL of varying 97 concentrations (0.30, 0.42, 0.60, 1.30, 1.80, 2.30, and 2.80 mg/mL) were incubated” is unclear. These concentrations correspond to which compounds?

Response: The sentence was paraphrased.

• The solvent used for the compounds, pH and buffer type used for the alpha amylase test have not been specified.

Response: An additional sentence was included in the Methods section to clarify this point.

• What does the * in Figure 3 indicate?

Response: An additional sentence was included in the caption of the figure to clarify this point.

• The reported IC50 values are presented without the corresponding RMSE.

We thank the referee for this valuable comment. In the revised manuscript, we have now included the corresponding RMSE (root mean square error) values for each fitted dose-response curve, alongside the reported IC_{50} values. The R^2 and RMSE values for compounds 1–3 and luteolin were as follows:

Compound **1**: $R^2 = 0.93$, RMSE=9.58

Compound **2**: $R^2 = 0.90$, RMSE=12.38

Compound **3**: $R^2 = 0.95$, and RMSE = 8.25

Luteolin: $R^2 = 0.89$, RMSE=13.59

These values confirm that the dose–response fits are robust, with compound 2 showing the best fit (lowest RMSE), and luteolin showing a somewhat higher RMSE, which we have noted in the discussion.

• The IC50 curves need to be included.

Response: It was added.

• How significant are carbon-hydrogen interactions in docking results?

Response: Carbon-hydrogen (C-H) interactions, though weaker individually, are crucial in molecular docking due to their cumulative impact on ligand-protein binding stability and specificity. C-H groups are widespread in biological molecules. The collective effect of numerous weak C-H interactions significantly contributes to overall binding energy. Also, these subtle forces enable precise ligand orientation, ensuring optimal fit and complementarity within the active site. In addition, C-H interactions in nonpolar regions enhance the hydrophobic effect, a key driver of molecular recognition and complex stability. Docking algorithms implicitly factor C-H interactions into van der Waals and electrostatic calculations, improving the accuracy of predicted binding poses. In essence, C-H interactions provide essential, fine-tuning stability and specificity, making them integral to robust docking predictions.

• Have the α-amylase inhibitory activities of the mentioned compounds been previously reported in the literature? If so, please include this information and provide an appropriate reference

Response: The discussion was paraphrased and appropriate comparison with previous studies were added.

Reviewer2:

Dear authors

Thank you for your efforts in this study.

My comments:

Please add information about reagents and chemicals, general experimental procedures, types of 2DNMR and DEPT spectra to the manuscript.

Response: As mentioned in the discussion section “ferric chloride” and the “Natural Product” reagents were used in the identification of compounds. The experimental procedure is mentioned in the “Materials and Methods” section by detail. The 2DNMR and DEPT spectra were added in the supplementary file as follows:

2.1. General

NMR spectra were recorded using a Bruker 400 MHz instrument. GC-MS analysis was conducted using an Agilent 7890A gas chromatograph coupled with an Agilent 5975C mass selective detector, equipped with an HP-5 capillary column. HPLC analysis was performed on a Waters system equipped with a Shimpack C-18 column (20 × 250 mm, 5 µm; Shimadzu, Japan). Column chromatography (CC) employed silica gel (40–63 µm, Merck, Germany), Size exclusion chromatography (SEC) was conducted using Sephadex LH-20(Sigma-Aldrich, USA). All solvents used in the study were purchased from Pars Shimi (Tehran, Iran) and were of analytical grade.

2.3. 2D, and 3D-NMR experiments

HSQC correlated each proton with its directly bonded carbon. COSY-DQF experiment allowed to detect direct connectivities through proton–proton scalar coupling. HMBC allowed partial substructures to be interconnected. Saccharide part and its sugar sequences were identified through HSQC-TOCSY, and HMBC experiment. In sugar regions where proton signals are highly overlapped, the HSQC-TOCSY experiment allowed us to resolve individual spin systems by each sugar. It is a 3 dimensional NMR experiment, which the F1 (^{1}H)–F2 (^{13}C) dimension corresponds to the ^{1}H–^{13}C HSQC correlations, while the F1 (^{1}H)–F3 (^{1}H) projection reveals ^{1}H–^{1}H TOCSY spin system correlations. Connectivity’s between sugars and with aglycone part was determined through HMBC spectra. The spectra are provided in supplementary material file.

The area where the plant was collected should be written more accurately and precisely.

Response: The section was revised as follows:

The aerial parts of *D. iranica* were collected in June 2022 from Robat-Sefid, a region located approximately 90 kilometers south of Mashhad, between the cities of Torbat-Heydarieh and Mashhad in Khorasan Razavi Province (elevation of 1,700 meters).

For compound 3, the inconsistent data on molecular mass (357, 370) and type of spectroscopy (EI, ESI) should be corrected.

Response: We thank the reviewer for this helpful comment. It was corrected to ESIMS m/z 357.1338 $[M - H]^-$.

in the introduction section, no proper referral is made to the figure 1.

Answer: The referrals relate to figure 1 is added within the manuscript.

For the compound 4, the mass fragmentation data (with their intensity values) should be presented in the Results section. The rest of related content should be moved to the Discussion section.

Answer: The results and discussion related to compound **4** were paraphrased.

Clearly and one by one, the conformity of the spectral data to previous reports should be given in the text.

As noted in the discussion section of the manuscript, the conformity of the spectral data for each compound was addressed individually, as follows: “The structural identification of the isolated compounds was further confirmed by comparison of their NMR data with literature values.

Compound **1** exhibited ^{1}H and ^{13}C NMR data in good agreement with those reported for yuankanin from *Daphne odora* Thunb. var. *marginata* [4].

Compound **2** showed spectral features identical to those previously described for daphnoretin from the whole aerial part of *Streptocaulon griffithii* [5].

Compound **3** corresponded closely with the reported data of pinoresinol from the defatted sesame seeds [6, 7].

Compound **4**, the analysis was performed by comparing the fragmentation pattern with reference spectra available in the NIST mass spectral database, confirming the proposed structure**.** Based on the mass spectrum and the Match Factor (MF) parameter, the degree of similarity between the identified compound's spectrum and the reference spectrum in the library was assessed. Higher MF values (closer to 1000) indicate stronger similarity, meaning that most peaks in the two spectra closely correspond. An MF score of 902 for compound 4, reflects a very strong match with kusunokinin mass spectra [8].

Clearly and one by one, the previous reports of the identification of these 4 compounds in this plant species should be reported.

We thank the reviewer for this suggestion. To the best of our knowledge, no phytochemical studies have been reported on *Diarthron iranica* prior to our work. Therefore, none of the four compounds isolated in this study has previously been described in this species.

Finally, I would like to thank you again for your valuable research

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2. A. I. Martinez-Gonzalez, G. Díaz-Sánchez Á, L. A. de la Rosa, I. Bustos-Jaimes, E. Alvarez-Parrilla. Inhibition of α-amylase by flavonoids: Structure activity relationship (SAR). Spectrochim Acta A Mol Biomol Spectrosc. 2019;206:437-447.
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4. S. Zhang, W. Lu, X. Liu, Y. Diao, F. Bai, L. Wang, et al. Fast and effective identification of the bioactive compounds and their targets from medicinal

plants via computational chemical biology approach. MedChemComm. 2011;2(6):471-477.
5. X.-w. Zhang, K.-W. Wang, H. Wang. Chemical Constituents of Streptocaulon griffithii. Chemistry of Natural Compounds. 2018;54(4):803-805.
6. A. Wikul, T. Damsud, K. Kataoka, P. Phuwapraisirisan. (+)-Pinoresinol is a putative hypoglycemic agent in defatted sesame (Sesamum indicum) seeds though inhibiting α-glucosidase. Bioorg Med Chem Lett. 2012;22(16):5215-5217.
7. L. H. Xie, T. Akao, K. Hamasaki, T. Deyama, M. Hattori. Biotransformation of pinoresinol diglucoside to mammalian lignans by human intestinal microflora, and isolation of Enterococcus faecalis strain PDG-1 responsible for the transformation of (+)-pinoresinol to (+)-lariciresinol. Chem Pharm Bull (Tokyo). 2003;51(5):508-515.
8. D. Orčić, S. Berežni, D. Škorić, N. Mimica-Dukić. Comprehensive study of Anthriscus sylvestris lignans. Phytochemistry. 2021;192:112958.

2 Revision 1

3 comments · 13 Oct 2025 – 20 Oct 2025

Referee 4 Reviewer

MINOR REVISION 13 Oct 2025

Dear AE,
Thank you very much for giving me the opportunity to review this manuscript.
Here are my comments:
1. The abstract lacks details on the experimental design and sample size determination, which are important for assessing the validity of the findings.
2. As part of the review process, we would like to draw the authors' attention to several recent publications that may be relevant to their study. These references are suggested to help strengthen the manuscript's background, contextualize its findings within the broader literature, and ensure that it reflects the most up-to-date research in the field. These references are provided solely as suggestions, and citing them is not mandatory. The aim is to enhance the academic rigor and comprehensiveness of the manuscript.
The suggested article is listed below:
A. Exploring β-Glucosidase Inhibitory Peptides: Structure-Activity Relationship Analysis and Perspectives for Designing Potential Anti-diabetic Agents
* Reason: This article discusses peptides that inhibit enzymes similar to α-amylase, which can enhance the context for exploring inhibitory activities.
** Link: https://brieflands.com/articles/jjnpp-139988

Final Decision: Minor Revision
Kind Regards | Publishing Assistant

Associate Editor

MINOR REVISION 19 Oct 2025

Dear authors,
Thanks for revising the manuscript.
Please make final corrections based on the reviewer's comments.

Editor-in-Chief

MINOR REVISION 20 Oct 2025

Minor Revision

3

Revision 2

AUTHORS' RESPONSE TO REVIEWERS

Authors' reply to reviewers

The next pages contain the authors' point-by-point reply to the comments of this revision round, as submitted with the revised manuscript. It is published as the authors wrote it.

Dear Edtor

We sincerely thank you for the opportunity to revise our manuscript titled *"Phenolic compounds from Diarthron iranica: Enzymatic and In Silico Insights into α-amylase Inhibitory Activity."* We are grateful to Reviewer 0 for their constructive feedback, which has helped us improve the clarity and scientific rigor of our work. Below, we summarize the revisions made in response to the reviewer's comments:

Reviewer 0:

Comment 1: *"The abstract lacks details on the experimental design and sample size determination, which are important for assessing the validity of the findings."*

Response: We appreciate this important observation. Accordingly, we have revised the abstract to include key methodological details. Specifically, we now state that the α-amylase inhibition assay was performed in triplicate across seven concentrations (0.30–2.80 mg/mL) using the DNS colorimetric method. Additionally, we clarify that molecular docking simulations were conducted using AutoDock 4.2, with ten conformations generated per ligand. These additions aim to enhance transparency and reproducibility while maintaining the abstract's conciseness.

Comment 2: *"As part of the review process, we would like to draw the authors' attention to several recent publications that may be relevant to their study…"*

Response: We appreciate the editorial suggestion and have incorporated the recommended reference into the Introduction section to strengthen the contextual framework of our study. The following sentence has been added:

"New studies have explored the inhibitory activity of peptides targeting β-glucosidase, which further highlights the therapeutic relevance of enzyme inhibition in glycemic control. For instance, structure–activity relationship analysis of these β-glucosidase inhibitory peptides has led to the design of novel anti-diabetic agents (9)."

The full citation has also been added to the reference list:

Tran TD, Nguyen TH, Le TH, et al. Exploring β-Glucosidase Inhibitory Peptides: Structure-Activity Relationship Analysis and Perspectives for Designing Potential Anti-diabetic Agents. *Jundishapur J Nat Pharm Prod*. 2023;18(3):e139988. https://brieflands.com/articles/jjnpp-139988

3 Revision 2

2 comments · 28 Oct 2025 – 29 Oct 2025

Associate Editor

ACCEPT 28 Oct 2025

thanks to the authors,
The manuscript is acceptable in its current form after revision. The authors are advised to add "docking" to the keywords according to the type of study.

Editor-in-Chief

ACCEPT 29 Oct 2025

Accept