



Homology Modelling and Structural Analysis of Cu/Zn Superoxide Dismutase in Sweet Potato (*Ipomoea batatas*)

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ABSTRACT

Superoxide dismutase (SOD) is a ubiquitous antioxidant enzyme essential for protecting cells from damage caused by reactive oxygen species. While the role of SOD in plant stress tolerance, particularly in crops like *Ipomoea batatas* (Sweet Potato), is well-established but high-resolution experimental structure for its isoenzymes is still lacking. This study aimed to predict the three-dimensional structure of the Cu/Zn SOD in *I. batatas* using the homology modelling method. Here, we focus on Cu/Zn SOD because it is the dominant isoform in photosynthetically active tissues and provides the fastest catalytic efficiency, making it the primary defence against reactive oxygen species (ROS) in plant. The target sequence was retrieved from the NCBI database, and a suitable template was identified via sequence alignment with 88.16% sequence identity. The model was generated using SWISS-MODEL and subsequently validated using established tools, including Ramachandran analysis, MolProbity, global model evaluation and local model evaluation including GMQE (Global Model Quality Estimate) QMEANDisCo global score and QMEAN Z-score analysis. The structural models provided insights into key functional regions, including the metal-binding active sites. The Cu/Zn active site displayed a distorted tetrahedral geometry, which is essential for superoxide detoxification. Evaluation of the model generated confirmed that it exhibits high reliability, high stereochemical quality, correct folding and strong suitability. These findings provide valuable insights into the action and regulation Cu/Zn SOD of *I. batatas* and a foundation for guiding targeted enzyme engineering, enhancing our molecular understanding of stress resilience in sweet potato, and supporting future agrobiotechnology efforts. Understanding the structural features of Cu/Zn SOD enables identification of stability-enhancing or activity-boosting residues that can be targeted through gene editing or molecular breeding. Such insights support the development of sweet potato varieties with improved oxidative stress tolerance, higher resilience in changing climates, and better overall crop performance.

Keywords: Superoxide dismutase, *Ipomoea batatas*, Stress tolerance, Homology modelling, Structure prediction

INTRODUCTION

Sweet potato (*Ipomoea batatas*) is a vital crop for food security globally, particularly in developing countries. However, it remains susceptible to environmental stresses, which can affect growth and productivity. Previous molecular studies have identified stress-responsive antioxidant genes in sweet potato, including SOD isoforms (Esmacili et al., 2022; Zhang et al., 2022; Zhao et al., 2025). These stresses lead to the overproduction of reactive oxygen species (ROS), which cause cellular damage and compromise plant growth and yield. Uncontrolled ROS accumulation damages lipids, proteins, and nucleic acids, leading to cellular dysfunction and yield loss (Gill & Tuteja, 2010). To combat oxidative stress, plants have evolved a sophisticated antioxidant defence system consisting of enzymes such as superoxide dismutase (SOD), catalase (CAT), and ascorbate peroxidase (APX).

Among these, Cu/Zn superoxide dismutase is one of the most important antioxidant enzymes in plants. It catalyses the dismutation of the superoxide radical (O_2^-) into oxygen (O_2) and hydrogen peroxide (H_2O_2), reducing oxidative damage under stress (Batool et al., 2022). Based on their metal cofactors, plant superoxide dismutase is categorized into three major types: Cu/Zn-SODs, Mn-SODs, and Fe-SODs. The Cu/Zn SOD isoform is typically localized in the cytosol, chloroplasts, and peroxisomes, where ROS are generated during photosynthesis and respiration (Batool et al., 2022). The enzymatic activity of SOD is a critical component of the plant defence system against these stressors. Understanding the molecular architecture of the sweet potato SOD is crucial for elucidating the precise mechanism of its catalytic activity and its role in stress adaptation.

Although Cu/Zn-SOD has been studied in several crop species, structural information for sweet potato is remains unavailable. To date, no experimentally resolved three-dimensional (3D) structure has been reported for *I. batatas* Cu/Zn-SOD, despite increasing recognition of its role in redox homeostasis and stress resilience. Existing genomic and transcriptomic studies provide only sequence-level annotations (Liu et al., 2025), leaving a critical gap in understanding the enzyme's structural organization, catalytic architecture, and residue-level features associated with stress tolerance.

Despite its biological importance, the 3D structure or detailed structural analysis of Cu/Zn-SOD in sweet potato is currently unavailable, limiting (i) accurate structure–function interpretation, (ii) identification of stress-responsive residues, and (iii) structure-guided enzyme engineering for crop improvement. Homology or comparative modelling is a reliable technique for predicting the 3D structure of a target protein based on its amino acid sequence and the known experimental structure of a related protein (the template), offers a powerful route to address this gap by generating a high-quality structural prediction that can serve as a foundation for functional insights and downstream computational or experimental studies. Therefore, this study aims to predict the 3D structure via homology modelling method to providing the structural framework to better understand the potential role of Cu/Zn SOD in stress tolerance for future engineering aimed at enhancing abiotic stress resilience.

MATERIALS AND METHODS

Target Sequence Retrieval

The primary amino acid sequence for *I. batatas* Cu/Zn-SOD was retrieved from the National Center for Biotechnology Information (NCBI) protein database using the GenBank Accession number (NCBI GeneBank ID: ALP06096.1). The sequence consists of 150 amino acids, extracted from senescent leaves of sweet potato was selected as the target sequence for Cu/Zn SOD protein (Fig. 1).

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>ALP06096.1 superoxide dismutase [Ipomoea batatas]
MVKAVAVLSSSEGVSGTIFFSQEGDGPTTVTGNVSGLKPLHGFHVHALGDTTNGCMSTGPHFNPAGKEH
GAPGDDNRHAGDLGNITVGEDGTASFTITDKQIPLTGANSVIGRAVVVHGDPDDLKGGHELKSTGNAG
GRVACGIIGLQG
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Fig. 1. The sequence of Cu/Zn SOD protein in *I. batatas* retrieved from NCBI used as the target for homology modelling.

Template Search and Selection

Template search with BLAST (Camacho et al., 2009) and HHblits (Steinegger et al., 2019) has been performed against the SWISS-MODEL template library (SMTL, last update: 2025-11-05, last included PDB release: 2025-10-31). The target sequence was searched with BLAST against the primary amino acid sequence contained in the SMTL with a total of 267 templates were found. An initial HHblits profile was built using the procedure outlined in (Steinegger et al., 2019), followed by 1 iteration of HHblits against Uniclust30 (Mirdita et al., 2017) with a total of 279 templates were found. The obtained profile was then searched against all profiles of the SMTL. For each identified template, the template's quality has been predicted from features of the target-template alignment. The templates with the highest quality have then been selected for model building.

The quaternary structure annotation of the template is used to model the target sequence in its oligomeric form. The method (Bertoni et al., 2017) is based on a supervised machine learning algorithm, Support Vector Machines (SVM), which combines interface conservation, structural clustering, and other template features to provide a quaternary structure quality estimate (QSQE). The QSQE score is a number between 0 and 1, reflecting the expected accuracy of the interchain contacts for a model built based on a given alignment and template (Bertoni et al., 2017). Higher numbers indicate higher reliability.

Homology modelling

The 3D structure of Cu/Zn SOD protein in *I. batatas* were modelled using the SWISS-MODEL server (Waterhouse et al., 2018 & Bienert et al., 2017). The selected template (PDB ID: 2Q2L.1) was served as a Homologous protein structure for generation of 3D model. Model were built based on the target-template alignment using ProMod3 (Studer et al., 2021). Coordinates which are conserved between the target and the template are copied from the template to the model. Insertions and deletions are remodelled using a fragment library. Side chains are then rebuilt. Finally, the geometry of the resulting model is regularized by using a force field. The generated models were visualized and analysed using NGL viewer.

Model Validation

The quality and stereochemical properties of the predicted Cu/Zn SOD model were evaluated using a combination of structural validation tools to ensure its reliability for functional analysis. The Ramachandran plot analysis was used to assess backbone dihedral angles (φ and ψ) and verify the stereochemical integrity of the protein model. A high percentage of residues in the favoured and allowed regions suggests proper folding and stable conformational geometry (Laskowski et al., 1993; Burley et al., 2022). MolProbity analysis provided all-atom contact evaluation and stereochemical verification, assessing bond lengths, bond angles, side-chain rotamers, and steric clashes; lower MolProbity and clash scores reflect higher structural quality (Williams et al., 2018). Global model quality was further assessed using the Global Model Quality Estimate (GMQE) and QMEAN Z-score, both implemented in the SWISS-MODEL workspace (Waterhouse et al., 2018; Waterhouse et al., 2024). The GMQE integrates target–template alignment and template resolution to predict overall reliability, while the QMEAN Z-score compares model parameters with those of high-resolution experimental structures in the Protein Data Bank (Waterhouse et al., 2024). A Z-score close to zero indicates a model

consistent with experimentally resolved protein structures (Waterhouse et al., 2024). In addition, local model quality was examined using the QMEANDisCo global score, which evaluates residue-level consistency based on distance constraints derived from homologous structures (Studer et al., 2020; Waterhouse et al., 2024).

RESULTS AND DISCUSSION

Template Search and Selection

The target sequence was subjected to target-template alignment utilized by SWISS-MODEL template library (SMTL version 2025-11-05, PDB release 2025-10-31) with BLAST (Camacho et al., 2009) and HHblits (Steinegger et al., 2019) to identify evolutionary related structures matching the target sequence (Fig. 1). A total of 538 templates were identified match to the target sequence. Among these, a crystal structure of Superoxide Dismutase from *P. atrosanguinea* (PDB ID: 2Q2L.1) with 2.37Å resolution was selected as the template due to its high sequence identity 88.16% and 100% coverage (Table 1 and Fig. 2). This template was preferred over other potential templates because it offered the best combination of high sequence similarity, complete structural coverage, and high-resolution crystallographic data, ensuring accurate backbone alignment and reliable modelling of functional residues.

Table 1. The target–template sequence alignment results for the selected template 2Q2L.1

Template	Sequence Identity (%)	QSQE	Method	Resolution (Å)	Sequence Similarity	Range	Coverage
2Q2L.1	88.16	0.63	X-ray	2.37	0.59	1 - 152	1.00

Target	MVKA	VAVL	SSSE	EGV	SGT	IFFS	QEGD	GP	TTVT	GNV	SGL	KPGL	HGF	VHAL	GDT	TNGC	MSTG	PHFN	PAGKE	HGAP	GGDNR	HAGDL	GN	85	
2q2l.1.A	MAK	VAVL	SSSE	EGV	AGTI	LF	QEGD	GP	TTVT	GN	SGL	KPGL	HGF	VHAL	GDT	TNGC	MSTG	PHFN	PAGKE	HGSP	EDTR	HAGDL	GN	85	
Target	ITV	GEDG	TAS	FTI	TDK	QIPL	TGANS	SVI	GRAV	VVHG	DPDDL	GKGG	HEL	SKST	GNAG	GRVAC	GII	GLQ							152
2q2l.1.A	ITV	GGDG	TAC	FTI	VDK	QIPL	TGPH	STI	GRAV	VVH	ADPDDL	GKGG	HEL	SKST	GNAG	GRVAC	GII	GLQ							152

Fig. 2. The sequence alignment of target–template for Cu/Zn SOD protein in *I. batatas* in coloured in clustal scheme

Homology Modelling

The homology model of the sweet potato Cu/Zn SOD protein was successfully generated using the (PDB ID 2Q2L.1) as template by homology modelling approach (Fig. 3). Fig. 3b shows the 3D structure of SOD protein. The model exhibited a typical β -barrel fold, which is characteristic of the Cu/Zn SOD family. Fig. 4 shows the active site of SOD protein in *I. batatas*. Here, Zn^{2+} interacted with three histidine residues (HIS 62, HIS 70, HIS 79) and one aspartic acid (ASP 82) forming four hydrogen bonds resulting in distorted tetrahedral geometry (Fig. 4b) (Furukawa, 2025). Four metal complexes interaction with the Zn^{2+} ligand was entirely conserved with the target Cu/Zn SOD protein. The active site position of this model and geometry crucial for enzyme catalytic activity which stabilize the active site conformation that allows the enzyme to perform efficiently. The active site occurrence at the bottom of a channel where the Cu^{2+} was exposed due to allowing superoxide bound to

it, while Zn^{2+} was enfolded inside the protein (Furukawa, 2025). This flexibility distorted tetrahedral helps to convert superoxide radical into the oxygen and hydrogen peroxide.

Buried Zn^{2+} ions provide a structural scaffold and contribute to maintaining a positively charged active site, which attracts the superoxide anion (O_2^-). In contrast, Cu^{2+} functions as the electron transfer centre, enabling redox interactions necessary for superoxide dismutation (Miessler & Tarr, 2011). The channel leading to the active site of this model exhibits a funnel-shaped architecture, which is essential for the proper function of Cu/Zn superoxide dismutase (SOD) (Furukawa, 2025). This channel, composed of Cu and Zn cations along with specific amino acid residues, is highly selective toward small negatively charged molecules, particularly superoxide. The strong positive electrostatic potential generated by these metal ions and amino acid residues guides the superoxide anion efficiently toward the active site, thereby facilitating its detoxification and preventing cellular oxidative damage (Pasinelli & Brown, 2006; Furukawa, 2025). Under abiotic stress conditions, when reactive oxygen species levels rise, these structural and electrostatic properties allow Cu/Zn SOD to maintain catalytic activity and structural integrity. Consequently, the enzyme plays a central role in oxidative stress tolerance by preventing cellular damage and maintaining redox homeostasis.

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Model_01:A:MKAVAVLSSSEGVSGTIFFSDEGDGPDTV
Model_01:BMKAVAVLSSSEGVSGTIFFSDEGDGPDTV
2q2l.1.A:MKAVAVLSSSEGVGTIIFDEGDGPDTV

Model_01:A:TGNVSGLKPGLHGFHVALGDTTNGCMSTG
Model_01:BTGNVSGLKPGLHGFHVALGDTTNGCMSTG
2q2l.1.A:TGNVSGLKPGLHGFHVALGDTTNGCMSTG

Model_01:AP:FNPAKGHEGAPGDDNRHAGDLGNITVGE
Model_01:BP:FNPAKGHEGAPGDDNRHAGDLGNITVGE
2q2l.1.AP:FNPAKGHEGAPGDDNRHAGDLGNITVGE

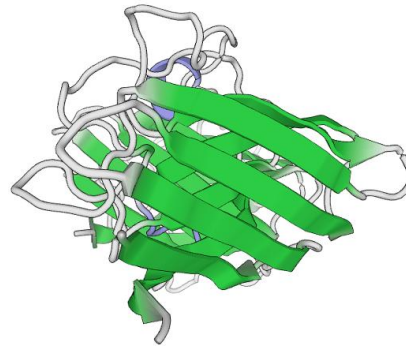
Model_01:ADGTASFTLIDKQIPLTGANSVIGRAVVVHG
Model_01:BDGTASFTLIDKQIPLTGANSVIGRAVVVHG
2q2l.1.ADGTASFTLIDKQIPLTGPHSIIIGRAVVVHA

Model_01:ADPDDLGGKGHELKSTGNAGGRVACGIIGL
Model_01:BDPDDLGGKGHELKSTGNAGGRVACGIIGL
2q2l.1.ADPDDLGGKGHELKSTGNAGGRVACGIIGL

Model_01:AQG
Model_01:BQG
2q2l.1.AQG

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a) Sequence alignment



b) 3D Model

Fig. 3 a) The sequence alignment of 3D structure of generated Cu/Zn SOD protein in *I. batatas* (Model_01) and 3D structure of template (2Q2L.1) b) 3D Model of Cu/Zn SOD protein in *I. batatas*. Both were displayed in secondary structure representation, coloured in green for the β -sheets and the purple for the α -helices.

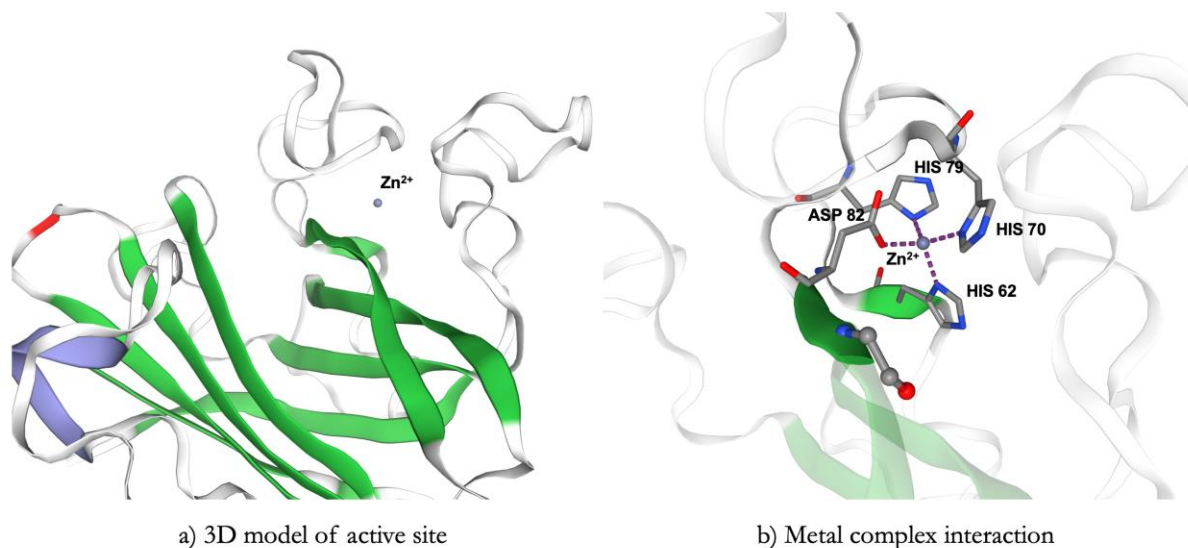


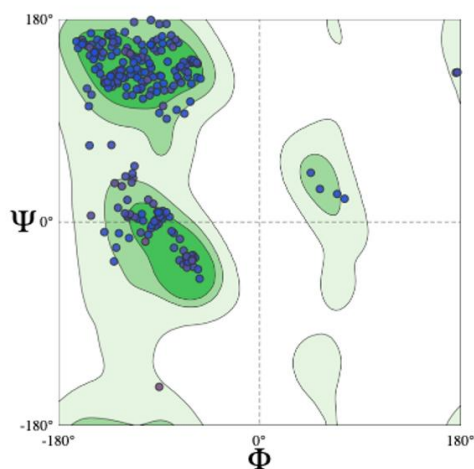
Fig 4. a) 3D model of active site of SOD protein in *I. batatas* b) The metal complex interaction of Zn^{2+} at SOD active site forming hydrogen bonds (dash line)

Model Validation

The structural evaluation of the predicted model demonstrated excellent quality. Superposition of the model with its template resulted in RMSD (Root Mean Square Deviation) of 0.116\AA (Table 2), indicating an almost indistinguishable backbone conformation between the two structures. This low RMSD indicates that the model and template share nearly identical backbone conformations, reflecting high structural conservation. The close agreement is likely due to the high sequence identity between the target and template, resulting in minimal deviation during model building. The structural validation using the Ramachandran plot showed that over 95.33% of the residues were in favoured regions and only 0.33% outliers, reflecting a well-refined geometry (Table 2 and Fig. 5a). The MolProbity score was 1.87 (Table 2 and Fig. 5a) indicating the high-quality and reliable model. The overall quality estimation of the predicted protein model, based on template–target alignment accuracy, conservation of structural features, and statistical reliability of the model geometry, yielded a GMQE score of 0.90 and a QMEANDisCo score of 0.87 ± 0.05 (Table 2). These high scores indicate that the model possesses excellent global and local structural reliability, comparable to experimentally determined protein structures. The GMQE value close to 1.0 reflects strong agreement between the modelled structure and its homologous template (Fig. 5b), while the QMEANDisCo score suggests uniform confidence across most residues, with only minor deviations likely in flexible loop regions (Fig. 5c). In addition, the QMEAN Z-score, 0.49 (Table 2) further supports the model's overall quality, as the value falls within the typical range of high-resolution protein structures. The QMEAN Z-score components further evaluate how closely the predicted Cu/Zn SOD model resembles high-quality experimental structures. Thus, confirm that the modelled structure exhibits high stereochemical quality, correct folding, and strong suitability for further functional or molecular docking analyses.

Table 2. The summary of the structural validation parameters for model evaluation of predicted model Cu/Zn-SOD protein in *I. batatas*

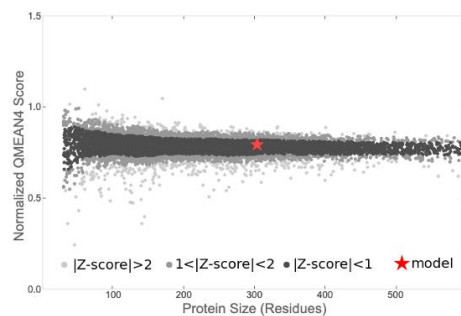
Validation parameter	Value
RMSD (Å)	0.116
Ramachandran Favoured (%)	95.33
Ramachandran Outliers (%)	0.33
MolProbity Score	1.87
GMQE Score	0.90
QMEANDisCo Score	0.87 ± 0.05
QMEAN Z-score	0.49



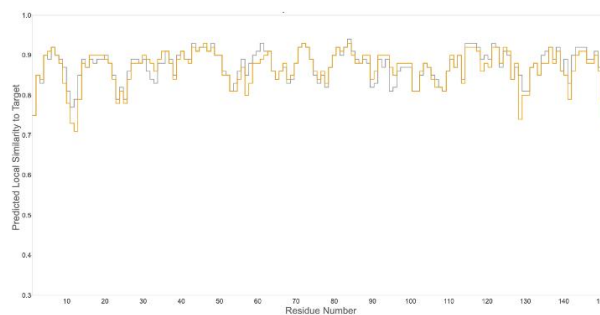
MolProbity Results

MolProbity Score	1.87
Ramachandran Favoured	95.33%
Ramachandran Outliers	0.33%

a) Ramachandran Plot



b) Comparison with Non-redundant Set of PDB



c) Local Quality Estimate – All Chain

Fig. 5. a) Ramachandran Plot of 3D Model of Cu/Zn SOD protein in *I. batatas* b) Comparison of 3D Model of Cu/Zn SOD protein in *I. batatas* with non-redundant set of PDB c) Local Quality Estimate for all chain of 3D Model of Cu/Zn SOD protein in *I. batatas*.

CONCLUSION

This study successfully constructed a high-quality, three-dimensional homology model of the Cu/Zn-SOD enzyme from *I. batatas*. The model exhibited excellent stereochemical quality and conserved the characteristic structural motifs and active site residues essential for catalytic function. The modelled Cu/Zn SOD structure

of *I. batatas* reflects its strong adaptation to oxidative environments stress tolerance. The conserved metal-binding residues, β -barrel fold, and stable electrostatic network support enzyme functionality under abiotic stress. The buried Zn^{2+} ion in Cu/Zn SOD stabilizes the protein structure, while the Cu^{2+} ion mediates redox reactions essential for superoxide dismutation. The positively charged channel surrounding the active site guides negatively charged superoxide radicals toward the catalytic centre, enhancing reaction efficiency. This predicted structure is a valuable resource for guiding targeted enzyme engineering, enhancing our molecular understanding of stress resilience in sweet potato, and supporting future agrobiotechnology efforts aimed at improving global food security, with future work focusing on molecular dynamics and experimental validation to identify key residues for improving stress tolerance.

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REFERENCES

- Batool, R., Umer, M. J., Hussain, B., Anees, M., & Wang, Z. (2022). Molecular mechanisms of superoxide dismutase (SODs)-mediated defense in controlling oxidative stress in plants. In *Antioxidant Defense in Plants: Molecular Basis of Regulation* (pp. 157-179). Singapore: Springer Nature Singapore.
- Bertoni, M., Kiefer, F., Biasini, M., Bordoli, L., & Schwede, T. (2017). Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. *Scientific Reports*, 7, 10480.
- Bienert, S., Waterhouse, A., de Beer, T. A. P., Tauriello, G., Studer, G., Bordoli, L., & Schwede, T. (2017). The SWISS-MODEL Repository: New features and functionality. *Nucleic Acids Research*, 45(D1), D313–D319.
- Burley, S. K., Bhikadiya, C., Bi, C., Bittrich, S., Chen, L., Crichlow, G. V., Duarte, J. M., Dutta, S., Fayazi, M., Feng, Z., Flatt, J. W., Ganesan, S. J., Goodsell, D. S., Ghosh, S., Kramer Green, R., Guranovic, V., Henry, J., Hudson, B. P., Lawson, C. L., Liang, Y., ... Zardecki, C. (2022). RCSB Protein Data Bank: Celebrating 50 years of the PDB with new tools for understanding and visualizing biological macromolecules in 3D. *Protein science: a publication of the Protein Society*, 31(1), 187–208.
- Camacho, C., Coulouris, G., Avagyan, V., Ma, N., Papadopoulos, J., Bealer, K., & Madden, T. L. (2009). BLAST+: Architecture and applications. *BMC Bioinformatics*, 10, 421.
- Esmaeili, N., Shen, G., & Zhang, H. (2022). Genetic manipulation for abiotic stress resistance traits in crops. *Frontiers in plant science*, 13, 1011985.
- Furukawa, Y. (2025). Structure and function of Cu/Zn-superoxide dismutase. In *Coordination chemistry perspectives* (Chapter 1). Royal Society of Chemistry.
- Gill, S. S., & Tuteja, N. (2010). Reactive oxygen species and antioxidant machinery in abiotic stress tolerance in crop plants. *Plant Physiology and Biochemistry*, 48(12), 909–930.
- Laskowski, R. A., MacArthur, M. W., Moss, D. S., & Thornton, J. M. (1993). PROCHECK: a program to check the stereochemical quality of protein structures. *Journal of Applied Crystallography*, 26(2), 283–291.

- Liu, Z., Pan, J., Liu, S., Yang, Z., Zhang, H., Yu, T., & He, S. (2025). Integrated Transcriptome and Metabolome Analysis Provides Insights into the Low-Temperature Response in Sweet Potato (*Ipomoea batatas* L.). *Genes*, 16(8), 899.
- Miessler, G. L., & Tarr, D. A. (2011). *Inorganic Chemistry* (5th ed.). Boston, MA: Pearson.
- Mirdita, M., von den Driesch, L., Galiez, C., Martin, M. J., Söding, J., & Steinegger, M. (2017). Uniclust databases of clustered and deeply annotated protein sequences and alignments. *Nucleic Acids Research*, 45(D1), D170–D176.
- Pasinelli, P., & Brown, R. H. (2006). Molecular biology of amyotrophic lateral sclerosis: Insights from SOD1 mutations. *Nature Reviews Neuroscience*, 7(9), 710–723.
- Steinegger, M., Meier, M., Mirdita, M., Vöhringer, H., Haunsberger, S. J., & Söding, J. (2019). HH-suite3 for fast remote homology detection and deep protein annotation. *BMC Bioinformatics*, 20, 473.
- Studer, G., Rempfer, C., Waterhouse, A. M., Gumienny, R., Haas, J., & Schwede, T. (2020). QMEANDisCo-distance constraints applied on model quality estimation. *Bioinformatics* (Oxford, England), 36(8), 2647.
- Studer, G., Tauriello, G., Bienert, S., Biasini, M., Johner, N., & Schwede, T. (2021). ProMod3—A versatile homology modelling toolbox. *PLOS Computational Biology*, 17(1), e1008667.
- Waterhouse, A., Bertoni, M., Bienert, S., Studer, G., Tauriello, G., Gumienny, R., Heer, F. T., de Beer, T. A. P., Rempfer, C., Bordoli, L., Lepore, R., & Schwede, T. (2018). SWISS-MODEL: Homology modelling of protein structures and complexes. *Nucleic Acids Research*, 46(W1), W296–W303.
- Waterhouse, A. M., Studer, G., Robin, X., Bienert, S., Tauriello, G., & Schwede, T. (2024). The structure assessment web server: for proteins, complexes and more. *Nucleic acids research*, 52(W1), W318–W323
- Williams, C. J., Headd, J. J., Moriarty, N. W., Prisant, M. G., Videau, L. L., Deis, L. N., Verma, V., Keedy, D. A., Hintze, B. J., Chen, V. B., Jain, S., Lewis, S. M., Arendall, W. B., 3rd, Snoeyink, J., Adams, P. D., Lovell, S. C., Richardson, J. S., & Richardson, D. C. (2018). MolProbity: More and better reference data for improved all-atom structure validation. *Protein science: a publication of the Protein Society*, 27(1), 293–315.
- Zhang, H., Wang, Z., Li, X., Gao, X., Dai, Z., Cui, Y., Zhi, Y., Liu, Q., Zhai, H., Gao, S., Zhao, N., & He, S. (2022). The IbBBX24–IbTOE3–IbPRX17 module enhances abiotic stress tolerance by scavenging reactive oxygen species in sweet potato. *New Phytologist*, 233(3), 1133–1152.
- Zhao, L., Zhou, X. H., Qiu, L., & Tao, L. P. (2025). Latest progress on the effects of drought, salinity, and temperature stress on sweet potatoes and their resistance mechanisms. *Bioscience Methods*, 16(1), 1–10.

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