

References

- Ahmed, N. E., Al-Akabway, L. M., Ramadan, M. Y., Abd El-Gawad, S. M., & Moustafa, M. (2017). Serological and PCR-sequencing assays for diagnosis of *Toxoplasma gondii* and *Neospora caninum* infecting camels in Egypt. *Benha Veterinary Medical Journal*, 33(2), 200-210.
- Alsoufi, A. S. M., Pączkowski, C., Długosz, M., & Szakiel, A. (2019). Influence of selected abiotic factors on triterpenoid biosynthesis and saponin secretion in marigold (*Calendula officinalis* L.) in vitro hairy root cultures. *Molecules*, 24(16), 2907.
- Bailey, T. L., & Elkan, C. (1994). Fitting a mixture model by expectation maximization to discover motifs in biopolymers. In *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology* (pp. 28-36). AAAI Press.
- Barde, M. P., & Barde, P. J. (2012). What to use to express the variability of data: Standard deviation or standard error of mean?. *Perspectives in clinical research*, 3(3), 113-116.
- Behdad, A., & Ganjeali, A. (2025). Phytohormones and microbial elicitation on glycyrrhizin production and gene expression in the hairy root of *Glycyrrhiza glabra* L. *Plant Cell, Tissue and Organ Culture (PCTOC)*, 160(1), 4.
- Behera, S., & Voshall, A. (2022). Plant transcriptome assembly: Review and benchmarking. *Bioinformatics*.
- Bell, K. L., Fowler, J., Burgess, K. S., Dobbs, E. K., Gruenewald, D., Lawley, B., ... & Brosi, B. J. (2017). Applying pollen DNA metabarcoding to the study of plant–pollinator interactions. *Applications in plant sciences*, 5(6), 1600124.
- Benjamini, Y., & Hochberg, Y. (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal statistical society: Series B (Methodological)*, 57(1), 289-300. <https://doi.org/10.1111/j.2517-6161.1995.tb02031.x>

- Binns, D., Dimmer, E., Huntley, R., Barrell, D., O'Donovan, C., & Apweiler, R. (2009). QuickGO: A web-based tool for Gene Ontology searching. *Bioinformatics*, 25(22), 3045–3046. <https://doi.org/10.1093/bioinformatics/btp536>
- Cao, X. W., Wang, F. J., Liew, O. W., Lu, Y. Z., & Zhao, J. (2020). Analysis of triterpenoid saponins reveals insights into structural features associated with potent protein drug enhancement effects. *Molecular pharmaceutics*, 17(2), 683-694.
- Chen, R. Y., Shi, J. J., Liu, Y. J., Yu, J., Li, C. Y., Tao, F., ... & Chen, J. (2024). The state-of-the-art antibacterial activities of glycyrrhizin: A comprehensive review. *Microorganisms*, 12(6), 1155.
- Cheng, Y., Liu, H., Tong, X., Liu, Z., Zhang, X., Chen, Y., ... & Yu, X. (2021). Effects of shading on triterpene saponin accumulation and related gene expression of *Aralia elata* (Miq.) Seem. *Plant Physiology and Biochemistry*, 160, 166-174.
- Choi, Y.-H., Hussain, R. A., Pezzuto, J. M., Kingborn, A. D., & Morton, J. F. (1989). Abrusosides A-D, Four Novel Sweet-Tasting Triterpene Glycosides from the leaves of *Abrus precatorius*. *Journal of Natural Products*, 52(5), 1118–1127. doi:10.1021/np50065a032
- Chrzanowski, J., Chrzanowska, A., & Graboń, W. (2021). Glycyrrhizin: An old weapon against a novel coronavirus. *Phytotherapy Research*, 35(2), 629-636.
- Corchete, L. A., Rojas, E. A., Alonso-López, D., De Las Rivas, J., Gutiérrez, N. C., & Burguillo, F. J. (2020). Systematic comparison and assessment of RNA-seq procedures for gene expression quantitative analysis. *Scientific reports*, 10(1), 19737. <https://doi.org/10.1038/s41598-020-76881-x>
- CSIRO. (2020). *Abrus precatorius*. Lucidcentral.org; Fact Sheet Fusion v2. https://apps.lucidcentral.org/rainforest/text/entities/abrus_precatorius.htm
- Dong, M., Li, J., Yang, D., Li, M., & Wei, J. (2023). Biosynthesis and pharmacological activities of flavonoids, triterpene saponins and polysaccharides derived from *Astragalus membranaceus*. *Molecules*, 28(13), 5018.

- Duan, Y., Du, W., Song, Z., Chen, R., Xie, K., Liu, J., ... & Dai, J. (2023). Functional characterization of a cycloartenol synthase and four glycosyltransferases in the biosynthesis of cycloastragenol-type astragalosides from *Astragalus membranaceus*. *Acta Pharmaceutica Sinica B*, 13(1), 271-283.
- Dwivedi, R. S. (2022). *Triterpenoids*. In *Alternative Sweet and Supersweet Principles: Natural Sweeteners and Plants* (pp. 323-388). Singapore: Springer Nature Singapore.
- Farag, M. A., Porzel, A., & Wessjohann, L. A. (2015). Unequivocal glycyrrhizin isomer determination and comparative in vitro bioactivities of root extracts in four *Glycyrrhiza* species. *Journal of advanced Research*, 6(1), 99-104.
- Ferre, F. (1992). Quantitative or semi-quantitative PCR: reality versus myth. *Genome Research*, 2(1), 1-9.
- Freitas, F. C., Depintor, T. S., Agostini, L. T., Luna-Lucena, D., Nunes, F. M., Bitondi, M. M., Simões, Z. L. P., & Lourenço, A. P. (2019). Evaluation of reference genes for gene expression analysis by real-time quantitative PCR (qPCR) in three stingless bee species (*Hymenoptera: Apidae: Meliponini*). *Scientific reports*, 9(1), 17692.
- Fry, J. C. (2012). *Natural low-calorie sweeteners*. In *Natural food additives, ingredients and flavourings* (pp. 41-75). Woodhead Publishing.
- Galandarli, L., Mollayeva, C., Javazade, A., Mammadova, A., & Amrahov, N. (2022). Molecular docking of glycyrrhizin with 11 β -HSD1 protein. *Research in: Agricultural & Veterinary Sciences*, 6(3).
- Garaniya, N., & Bapodra, A. (2014). Ethnobotanical and Phytopharmacological potential of *Abrus precatorius* L.: A review. *Asian Pacific Journal of Tropical Biomedicine*, 4, S27-S34.
- Gharabli, H., Della Gala, V., & Welner, D. H. (2023). The function of UDP-glycosyltransferases in plants and their possible use in crop protection. *Biotechnology advances*, 67, 108182.
- Gong, F., Qu, R., Li, Y., Lv, Y., & Dai, J. (2022). *Astragalus Mongholicus*: A review of its anti-fibrosis properties. *Frontiers in Pharmacology*, 13, 976561.

- Gupta, V., Estrada, A. D., Blakley, I., Reid, R., Patel, K., Meyer, M. D., Andersen, S. U., Brown, A. F., & Loraine, A. E. (2015). RNA-Seq analysis and annotation of a draft blueberry genome assembly identifies candidate genes involved in fruit ripening, biosynthesis of bioactive compounds, and stage-specific alternative splicing. *Gigascience*, 4(1), s13742-015.
- Han, X., Zhao, J., Zhou, H., Zhou, X., Deng, Z., Liu, Z., & Yu, Y. (2024). The biosynthesis of asiaticoside and madecassoside reveals tandem duplication-directed evolution of glycoside glycosyltransferases in the Apiales. *Plant Communications*, 5(10).
- Han, Y., Hou, Z., He, Q., Zhang, X., Yan, K., Han, R., & Liang, Z. (2021). Genome-wide characterization and expression analysis of bZIP gene family under abiotic stress in *Glycyrrhiza uralensis*. *Frontiers in Genetics*, 12, 754237.
- Hantemirova, E. V., Belyaev, A. Y., Korchagina, O. S., & Laletina, I. A. (2020). Genetic differentiation and phylogenetic relationships of *Glycyrrhiza glabra* L., *G. uralensis* Fisch., and *G. korshinskyi* Grig. inferred from chloroplast DNA variation. *Russian Journal of Genetics*, 56, 810-821.
- He, C., Huang, W., Xue, X., Liang, Z., Ye, H., Li, K., & Yuan, X. (2022). UPLC-MS fingerprints, phytochemicals and quality evaluation of flavonoids from *Abrus precatorius* leaves. *Journal of Food Composition and Analysis*, 110, 104585.
- Hughes, J., & Hughes, M. A. (1994). Multiple secondary plant product UDP-glucose glucosyltransferase genes expressed in cassava (*Manihot esculenta* Crantz) cotyledons. *DNA sequence*, 5(1), 41-49.
- Hussain, M., Debnath, B., Qasim, M., Bamisile, B. S., Islam, W., Hameed, M. S., Wang, L., & Qiu, D. (2019). Role of saponins in plant defense against specialist herbivores. *Molecules*, 24(11), 2067.
- Isbrucker, R. A., & Burdock, G. A. (2006). Risk and safety assessment on the consumption of Licorice root (*Glycyrrhiza* sp.), its extract and powder as a food ingredient, with emphasis on the pharmacology and toxicology of glycyrrhizin. *Regulatory Toxicology and Pharmacology*, 46(3), 167-192.

- Kafle, A., Mohapatra, S. S., & Reddy, I. (2018). A brief review on toxicity of *Abrus precatorius* in animals. *Journal of Entomology and Zoology Study*, 6(2), 1102-1104.
- Kernfeld, E., Keener, R., Cahan, P., & Battle, A. (2024). Transcriptome data are insufficient to control false discoveries in regulatory network inference. *Cell systems*, 15(8), 709-724.
<https://doi.org/10.1016/j.cels.2024.07.006>
- Khalid, M. F., Zakir, I., Khan, R. I., Irum, S., Sabir, S., Zafar, N., Ahmad, S., Abbas, M., Ahmed, T., & Hussain, S. (2023). Effect of water stress (drought and waterlogging) on medicinal plants. In Medicinal plants: Their response to abiotic stress (pp. 169-182). *Singapore: Springer Nature Singapore*.
- Kim, T. K. (2017). Understanding one-way ANOVA using conceptual figures. *Korean journal of anesthesiology*, 70(1), 22.
- Kumar, P., & Woolfson, D. N. (2021). Socket2: a program for locating, visualizing and analyzing coiled-coil interfaces in protein structures. *Bioinformatics*, 37(23), 4575-4577.
- Kumar, R., Sangwan, R. S., Mishra, S., Sabir, F., & Sangwan, N. S. (2012). 'In silico motif diversity analysis of the glycon preferentiality of plant secondary metabolic glycosyltransferases. *Plant Omics*, 5(3), 200-210.
- Kudaibergenov, S. E., & Nuraje, N. (2018). Intra-and interpolyelectrolyte complexes of polyampholytes. *Polymers*, 10(10), 1146.
- Li, Y. J., Li, P., Wang, T., Zhang, F. J., Huang, X. X., & Hou, B. K. (2018). The maize secondary metabolism glycosyltransferase UFGT2 modifies flavonols and contributes to plant acclimation to abiotic stresses. *Annals of Botany*, 122(7), 1203-1217.
- Li, Y., Ge, X., Peng, F., Li, W., & Li, J. J. (2022). Exaggerated false positives by popular differential expression methods when analyzing human population samples. *Genome biology*, 23(1), 79.
<https://doi.org/10.1186/s13059-022-02648-4>

- Liang, D. M., Liu, J. H., Wu, H., Wang, B. B., Zhu, H. J., & Qiao, J. J. (2015). Glycosyltransferases: mechanisms and applications in natural product development. *Chemical Society Reviews*, 44(22), 8350-8374.
- Liao, W., Mei, Z., Miao, L., Liu, P., & Gao, R. (2020). Comparative transcriptome analysis of root, stem, and leaf tissues of *Entada phaseoloides* reveals potential genes involved in triterpenoid saponin biosynthesis. *BMC genomics*, 21, 1-12.
- Liu, Q., Dong, G. R., Ma, Y. Q., Zhao, S. M., Liu, X., Li, X. K., Li, Y. J., & Hou, B. K. (2021). Rice glycosyltransferase gene UGT85E1 is involved in drought stress tolerance through enhancing abscisic acid response. *Frontiers in Plant Science*, 12, 790195.
- Lowe, R., Shirley, N., Bleackley, M., Dolan, S., & Shafee, T. (2017). Transcriptomics technologies. *PLoS Computational Biology*, 13(5), e1005457.
- Lu, Y. A. O., Jun, L. U., Juan, W. A. N. G., & Wen-Yuan, G. A. O. (2020). Advances in biosynthesis of triterpenoid saponins in medicinal plants. *Chinese Journal of Natural Medicines*, 18(6), 417-424.
- Ma, L., Rao, X., & Chen, X. (2019). Waterlogging tolerance of 57 plant species grown hydroponically. *HortScience*, 54(4), 749-753.
- Maas, H., & Cock, I. E. (2018). The Interactive Antimicrobial Activity of *Glycyrrhiza glabra* L. Root Extracts and Conventional Antibiotics Against some Bacterial Triggers of Autoimmune Inflammatory Diseases. *Pharmacognosy Communications*, 8(2), 66-74.
- Magedans, Y. V., da S., Phillips, M. A., & Fett-Neto, A. G. (2021). Production of plant bioactive triterpenoid saponins: from metabolites to genes and back. *Phytochemistry Reviews*, 20(2), 461-482.
- Marimuthu, S., Pratap, G. P., Prasad, G. P., Prasad, S. B., Mangal, A. K., & Srikanth, N. (2020). DNA barcoding markers to identify intraspecies genetic variations in three ecotypes of *Abrus precatorius* L. *Pharmacognosy Magazine*, 16(05).

- Marone, M., Mozzetti, S., De Ritis, D., Pierelli, L., & Scambia, G. (2001). Semiquantitative RT-PCR analysis to assess the expression levels of multiple transcripts from the same sample. *Biological Procedures Online*, 3, 19-25.
- McDermaid, A., Monier, B., Zhao, J., Liu, B., & Ma, Q. (2019). Interpretation of differential gene expression results of RNA-seq data: review and integration. *Briefings in Bioinformatics*, 20(6), 2044-2054.
- Mittler, R., Zandalinas, S. I., Fichman, Y., & Van Breusegem, F. (2022). Reactive oxygen species signalling in plant stress responses. *Nature Reviews Molecular Cell Biology*, 23(10), 663-679.
- Na, S. I., Kim, Y. O., Yoon, S. H., Ha, S. M., Baek, I., & Chun, J. (2018). UBCG: up-to-date bacterial core gene set and pipeline for phylogenomic tree reconstruction. *Journal of Microbiology*, 56, 280-285.
- Nair, P. C., Meech, R., Mackenzie, P. I., McKinnon, R. A., & Miners, J. O. (2015). Insights into the UDP-sugar selectivities of human UDP-glycosyltransferases (UGT): a molecular modeling perspective. *Drug metabolism reviews*, 47(3), 335-345.
- Nomura, Y., Seki, H., Suzuki, T., Ohyama, K., Mizutani, M., Kaku, T., Tamura, K., Ono, E., Horikawa, M., Sudo, H., Hayashi, H., Saito, K., & Muranaka, T. (2019). Functional specialization of UDP-glycosyltransferase 73P12 in licorice to produce a sweet triterpenoid saponin, glycyrrhizin. *The Plant Journal*, 99(6), 1127-1143.
- Noor, F., Rehman, A., Ashfaq, U. A., Saleem, M. H., Okla, M. K., Al-Hashimi, A., AbdElgawad, H., & Aslam, S. (2022). Integrating network pharmacology and molecular docking approaches to decipher the multi-target pharmacological mechanism of *Abrus precatorius* L. acting on diabetes. *Pharmaceuticals*, 15(4), 414.
- Oetomo, N. J. (2024). Semi-quantitative analysis of triterpenoid saponin in hydroponics *Abrus precatorius* induced by methyl jasmonate [Undergraduate thesis, Indonesia International Institute for Life Sciences]. I3L Institutional Repository. <http://repository.i3l.ac.id/jspui/handle/123456789/1117>

- Okhale, S. E., & Nwanosike, E.M. (2016). *Abrus precatorius* Linn (Fabaceae): Phytochemistry, ethnomedicinal uses, ethnopharmacology and pharmacological activities. *International Journal of Pharmaceutical Science Research*, 1, 37-43.
- Omar, H. R., Komarova, I., El-Ghonemi, M., Fathy, A., Rashad, R., Abdelmalak, H. D., ... & Camporesi, E. M. (2012). Licorice abuse: time to send a warning message. *Therapeutic Advances in Endocrinology and Metabolism*, 3(4), 125-138.
- Pauwels, L., & Goossens, A. (2011). The JAZ proteins: a crucial interface in the jasmonate signaling cascade. *The Plant Cell*, 23(9), 3089-3100.
- Perkasa, A. Y. (2024). Utilization of The Saga Plant *Abrus Precatorius* L. in Indonesian Folk Medicine. *Muş Alparslan Üniversitesi Tarım ve Doğa Dergisi*, 4(1), 1-8.
- Pfaffl, M. W. (2001). A new mathematical model for relative quantification in real-time RT–PCR. *Nucleic acids research*, 29(9), e45-e45.
- Pfaffl, M. W. (2007). Relative quantification. In *Real-time PCR* (pp. 89-108). Taylor & Francis.
- Pfaffl, M. W., Horgan, G. W., & Dempfle, L. (2002). Relative expression software tool (REST©) for group-wise comparison and statistical analysis of relative expression results in real-time PCR. *Nucleic acids research*, 30(9), e36-e36.
- Piñol, J., Mir, G., Gomez-Polo, P. R. I. S. C. I. L. A., & Agustí, N. (2015). Universal and blocking primer mismatches limit the use of high-throughput DNA sequencing for the quantitative metabarcoding of arthropods. *Molecular Ecology Resources*, 15(4), 819-830.
- Qian, H., Wang, L., Li, Y., Wang, B., Li, C., Fang, L., & Tang, L. (2022). The traditional uses, phytochemistry and pharmacology of *Abrus precatorius* L.: a comprehensive review. *Journal of Ethnopharmacology*, 296, 115463.
- Qu, G., Liu, Y., Ma, Q., Li, J., Du, G., Liu, L., & Lv, X. (2023). Progress and prospects of natural glycoside sweetener biosynthesis: A review. *Journal of Agricultural and Food Chemistry*, 71(43), 15926-15941.

- Rajkumar, A. P., Qvist, P., Lazarus, R., et al. (2015). Experimental validation of methods for differential gene expression analysis and sample pooling in RNA-seq. *BMC genomics*, 16, 1-8.
<https://doi.org/10.1186/s12864-015-1767-y>
- Ragasa, C. Y., Lorena, G. S., Mandia, E. H., Raga, D. D., & Shen, C. C. (2013). Chemical constituents of *Abrus precatorius*. *American Journal of Essential Oils and Natural Products*, 1(2), 7-10.
- Schmid, J., Heider, D., Wendel, N. J., Sperl, N., & Sieber, V. (2016). Bacterial glycosyltransferases: challenges and opportunities of a highly diverse enzyme class toward tailoring natural products. *Frontiers in Microbiology*, 7, 182.
- Seki, H., Tamura, K., & Muranaka, T. (2015). P450s and UGTs: key players in the structural diversity of triterpenoid saponins. *Plant and Cell Physiology*, 56(8), 1463-1471.
- Su, L., Li, S., Qiu, H., Wang, H., Wang, C., He, C., Xu, M., & Zhang, Z. (2021). Full-length transcriptome analyses of genes involved in triterpenoid saponin biosynthesis of *Psammosilene tunicoides* hairy root cultures with exogenous salicylic acid. *Frontiers in Genetics*, 12, 657060.
- Takahashi, H., Abo, C., Suzuki, H., Romsuk, J., Oi, T., Yanagawa, A., Gorai, T., Tomisaki, Y., Jitsui, M., Shimamura, S., Mori, H., Kaga, A., Ishimoto, M., Seki, H., Muranaka, T., & Nakazono, M. (2023). Triterpenoids in aerenchymatous phellem contribute to internal root aeration and waterlogging adaptability in soybeans. *New Phytologist*, 239(3), 936-948.
<https://doi.org/10.1111/nph.18975>
- Tammi, M. T. (2023). Bioinformatics Education and Tutorials: Understanding RefSeq. Bioinformaticshome.com.
https://bioinformaticshome.com/edu/Bioinformatics/Biological_Databases/Sequence_Databases/refseq.html
- Tang, H., Hu, J., Zhao, M., Cao, L., & Chen, Y. (2023). Comparative study of the physiological responses, secondary metabolites, and gene expression of medicinal plant *Prunella vulgaris* L. treated with exogenous methyl jasmonate and salicylic acid. *Acta Physiologiae Plantarum*, 45(2), 20.

- Taylor, S. C., Laperriere, G., & Germain, H. (2017). Droplet Digital PCR versus qPCR for gene expression analysis with low abundant targets: from variable nonsense to publication quality data. *Scientific reports*, 7(1), 2409.
- Thanh, H. N., Zhao, L., & Liu, Q. (2014). De novo transcriptome sequencing analysis and comparison of differentially expressed genes (DEGs) in *Macrobrachium rosenbergii* in China. *PloS one*, 9(10), e109656.
- ThermoFisher Scientific. (n.d.). PCR Troubleshooting Guide | Thermo Fisher Scientific - ID. Thermofisher.com. Retrieved June 6, 2025, from <https://www.thermofisher.com/id/en/home/life-science/cloning/cloning-learning-center/invitrogen-school-of-molecular-biology/pcr-education/pcr-reagents-enzymes/pcr-troubleshooting.html>
- Toscano, S., Trivellini, A., Cocetta, G., Bulgari, R., Francini, A., Romano, D., & Ferrante, A. (2019). Effect of preharvest abiotic stresses on the accumulation of bioactive compounds in horticultural produce. *Frontiers in Plant Science*, 10, 1212.
- Tutar, O., Marín-Guirao, L., Ruiz, J. M., & Procaccini, G. (2017). Antioxidant response to heat stress in seagrasses. A gene expression study. *Marine Environmental Research*, 132, 94-102.
- Uhomoibhi, J. O. O., Shode, F. O., Idowu, K. A., & Sabiu, S. (2022). Molecular modelling identification of phytocompounds from selected African botanicals as promising therapeutics against druggable human host cell targets of SARS-CoV-2. *Journal of Molecular Graphics and Modelling*, 114, 108185.
- Vijayan, S., & Thirumal, M. (2024). Systematic review on *Abrus precatorius* Linn. since 1871: ethnobotanical uses, phytochemistry and pharmacological properties. *Phytochemistry Reviews*, 1-30.
- Wang, S. (2013). Synthesis and biological evaluation of neutral glycosyltransferase inhibitors (Doctoral dissertation, Université Claude Bernard-Lyon I).

- Wang, F., Wan, C., Wu, W., Zhang, Y., Pan, Y., Chen, X., Li, C., Pi, J., Wang, Z., Ye, Y., & Chen, X. (2023). Methyl jasmonate (MeJA) enhances salt tolerance of okra (*Abelmoschus esculentus* L.) plants by regulating ABA signaling, osmotic adjustment substances, photosynthesis and ROS metabolism. *Scientia Horticulturae*, 319, 112145.
- Wang, R., Xu, S., Wang, N., Xia, B., Jiang, Y., & Wang, R. (2017). Transcriptome analysis of secondary metabolism pathway, transcription factors, and transporters in response to methyl jasmonate in *Lycoris aurea*. *Frontiers in Plant Science*, 7, 1971.
- Wang, Y., Xu, H., Liu, W., Wang, N., Qu, C., Jiang, S., ... & Chen, X. (2019). Methyl jasmonate enhances apple cold tolerance through the JAZ–MYC2 pathway. *Plant Cell, Tissue and Organ Culture (PCTOC)*, 136, 75-84.
- Widianto, E., Santoso, D. B., Kardiman, K., & Nugraha, A. E. (2020). Pemberdayaan masyarakat tentang pemanfaatan tanaman saga (*Abrus precatorius* L) di Desa Tanahbaru Pakisjaya Karawang. *Aksiologi: Jurnal Pengabdian Kepada Masyarakat*, 4(1), 63-69.
- Wilson, A. E., & Tian, L. (2019). Phylogenomic analysis of UDP-dependent glycosyltransferases provides insights into the evolutionary landscape of glycosylation in plant metabolism. *The Plant Journal*, 100(6), 1273-1288.
- Wongwicha, W., Tanaka, H., Shoyama, Y., & Putalun, W. (2011). Methyl jasmonate elicitation enhances glycyrrhizin production in *Glycyrrhiza inflata* hairy roots cultures. *Zeitschrift für Naturforschung C*, 66(7-8), 423-428.
- Wu, K., Li, C., Li, Z., Li, Z., Gu, Z., Ban, X., & Kong, H. (2024). Highly-branched modification of starch: An enzymatic approach to regulating its properties. *Food Hydrocolloids*, 147, 109433.
- Yang, Q., Zhang, Y., Qu, X., Wu, F., Li, X., Ren, M., Tong, Y., Wu, X., Yang, A., Chen, Y., & Chen, S. (2023). Genome-wide analysis of UDP-glycosyltransferases family and identification of UGT genes involved in abiotic stress and flavonol biosynthesis in *Nicotiana tabacum*. *BMC plant biology*, 23(1), 204.

- Yao, Y., Zhang, H., Guo, R., Fan, J., Liu, S., Liao, J., Huang, Y., & Wang, Z. (2023). Physiological, cytological, and transcriptomic analysis of magnesium protoporphyrin IX methyltransferase mutant reveal complex genetic regulatory network linking chlorophyll synthesis and chloroplast development in rice. *Plants*, 12(21), 3785.
- Yu, X., Zhang, W., Zhang, Y., Zhang, X., Lang, D., & Zhang, X. (2018). The roles of methyl jasmonate to stress in plants. *Functional Plant Biology*, 46(3), 197-212. <https://doi.org/10.1071/FP18106>
- Zhang, H. X., Sun, G., Gu, J. L., & Du, Z. Z. (2017). New sweet-tasting oleanane-type triterpenoid saponins from “Tugancao”(*Derris eriocarpa* How). *Journal of Agricultural and Food Chemistry*, 65(11), 2357-2363.
- Zhou, G., Wei, Q., Li, B., Zeng, X., & Liu, G. (2019). Establishment and optimization of a hydroponic system for root morphological and nutritional analysis of citrus. *Scientia Agricola*, 77(4), e20180261.
- Zhu, Y., Li, Y., Xin, D., Chen, W., Shao, X., Wang, Y., & Guo, W. (2015). RNA-Seq-based transcriptome analysis of dormant flower buds of Chinese cherry (*Prunus pseudocerasus*). *Gene*, 555(2), 362-376.