

- Qi H., Han X., Huang J.-F., Wu X., and Han J., 2026, Integrated transcriptomic, proteomic, and metabolomic analysis of a chromosome segment substitution line reveals the regulatory mechanism governing fatty acids and storage proteins in soybean seeds, *Genes*, 17(4): 432.
<https://doi.org/10.3390/genes17040432>
- Sarkar S., Sagan V., Bhadra S., Rhodes K., Pokharel M., and Fritsch F.B., 2023, Soybean seed composition prediction from standing crops using PlanetScope satellite imagery and machine learning, *ISPRS Journal of Photogrammetry and Remote Sensing*, 204: 257-274.
<https://doi.org/10.1016/j.isprsjprs.2023.09.010>
- Sun J., Li W., Wei X., Shou H., Tran L.-S.P., Feng X., and Wang S., 2025, Mechanistic roles of *GmSWEET10a/b* and *GmSUT1* in the oil-protein balance in soybean mature seeds at transcriptional and metabolic levels, *The Plant Journal*, 123(4): e70435.
<https://doi.org/10.1111/tpj.70435>
- Tamagno S., Sadras V.O., Aznar-Moreno J., Durrett T.P., and Ciampitti I.A., 2022, Selection for yield shifted the proportion of oil and protein in favor of low-energy seed fractions in soybean, *Field Crops Research*, 279: 108446.
<https://doi.org/10.1016/j.fcr.2022.108446>
- Van Der Laan L., Parmley K.A., Saadati M., Pacin H.T., Panthulugiri S., Sarkar S., Ganapathysubramanian B., Lorenz A.J., and Singh A.K., 2025, Genomic and phenomic prediction for soybean seed yield, protein, and oil, *The Plant Genome*, 18(1): e70002.
<https://doi.org/10.1002/tpg2.70002>
- Wang J., Zhang L., Wang S., Wang X., Li S., Gong P., Bai M., Paul A., Tvedt N., Ren H., Yang M., Zhang Z., Zhou S., Sun J., Wu X., Kuang H., Du Z., Dong Y., Shi X., Guan Y., and collaborators, 2025, AlphaFold-guided bespoke gene editing enhances field-grown soybean oil contents, *Advanced Science*, 12(23): 2500290.
<https://doi.org/10.1002/adv.202500290>
- Xu W., Wang Q., Zhang W., Zhang H., Liu X., Song Q., Zhu Y., Cui X., Chen X., and Chen H., 2022, Using transcriptomic and metabolomic data to investigate the molecular mechanisms that determine protein and oil contents during seed development in soybean, *Frontiers in Plant Science*, 13: 1012394.
<https://doi.org/10.3389/fpls.2022.1012394>
- Yang M., Du C., Li M., Wang Y., Bao G., Huang J., Zhang Q., Zhang S., Xu P., Teng W., Li Q., Liu S., Song B., Yang Q., and Wang Z., 2024, The transcription factors GmVOZ1A and GmWRI1 synergistically regulate oil biosynthesis in soybean, *Plant Physiology*, 197(2): kiae485.
<https://doi.org/10.1093/plphys/kiae485>
- Yang Y., Zhang L., Zuo H., Yang Y., Hu D., Zhang S., Yuan W., Zhai X., He M., Xu M., Wang J., Lu W., Hu D., Yu D., Huang F., and Zhang D., 2025, *GmGASA12* coordinates hormonal dynamics to enhance soybean water-soluble protein accumulation and seed size, *Journal of Integrative Plant Biology*, 67(9): 2401-2415.
<https://doi.org/10.1111/jipb.13952>
- Yuan X., Jiang X., Zhang M., Wang L., Jiao W., Chen H., Mao J., Ye W., and Song Q., 2024, Integrative omics analysis elucidates the genetic basis underlying seed weight and oil content in soybean, *The Plant Cell*, 36(6): 2160-2175.
<https://doi.org/10.1093/plcell/koae062>
- Zhang M., Liu S., Wang Z., Yuan Y., Zhang Z., Liang Q., Yang X., Duan Z., Liu Y., Kong F., Liu B., Ren B., and Tian Z., 2022, Progress in soybean functional genomics over the past decade, *Plant Biotechnology Journal*, 20(2): 256-282.
<https://doi.org/10.1111/pbi.13682>
- Zhang S., Du H., Li H., Kan G., and Yu D., 2021, Linkage and association study discovered loci and candidate genes for glycinin and β -conglycinin in soybean (*Glycine max* L. Merr.), *Theoretical and Applied Genetics*, 134(4): 1201-1215.
<https://doi.org/10.1007/s00122-021-03766-6>



Disclaimer/Publisher's Note

The statements, opinions, and data contained in all publications are solely those of the individual authors and contributors and do not represent the views of the publishing house and/or its editors. The publisher and/or its editors disclaim all responsibility for any harm or damage to persons or property that may result from the application of ideas, methods, instructions, or products discussed in the content. Publisher remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.
