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Structural Files for the ETR1 Ethylene-Receptor Dimer Based on Computational Modeling

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Structural models for the ETR1 homodimer were generated with AlphaFold-Multimer. Coppers were modeled under two potential coordinations involving Cys65 and His69 of the ETR1 homodimer, one in which the two coppers are bound independently and do not share an interaction with each other, and another where they are closely bonded.

See the following publication for details: Azhar, B.J., Abbas, S., Aman, S., Yamburenko, M.V., Chen, W., Müller, L., Uzun, B., Jewell, D.A., Dong, J., Shakeel, S.N., Groth, G., Binder, B.M., Grigoryan, G., Schaller, G.E. (2023) Basis for high-affinity ethylene binding by the ethylene receptor ETR1 of Arabidopsis. Proc. Natl. Acad. Sci. USA. 120:e2215195120. doi: 10.1073/pnas.2215195120

Supplement 1: PDB file for ETR1_AlphaFoldDimer_Cu_interacting
Supplement 2: PDB file for ETR1_AlphaFoldDimer_CU_notinteracting
Supplement 3: PyMOL file for ETR1_AlphaFoldDimer