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

Beenish J. Azhar
Dartmouth College

Safdar Abbas
Dartmouth College

Sitwat Aman
Dartmouth College

Maria V. Yamburenko
Dartmouth College

Wei Chen
Dartmouth College

See next page for additional authors

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Authors

Beenish J. Azhar, Safdar Abbas, Sitwat Aman, Maria V. Yamburenko, Wei Chen, Lena Muller, Buket Uzun, David A. Jewell, Jian Dong, Samina N. Shakeel, Georg Groth, Brad M. Binder, Gevorg Grigoryan, and G. Eric Schaller

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

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