

## MS6. Membrane proteins and signal transduction pathways

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### MS6-P1 Crystal structure of the catalytic domain of the ethylene receptor ETR1 from *Arabidopsis thaliana*

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Plants employ ethylene to regulate many developmental processes such as seed germination, root growth, fruit ripening, and senescence (1). *Arabidopsis thaliana* perceives ethylene by a group of five partly redundant, membrane bound receptors (ETR1, ETR2, ERS1, ERS2, EIN4). Ethylene binds at the N-terminal hydrophobic domain of the receptors and initiates the signalling events via its cytosolic domain. The receptor cytosolic domain contains several different domains which are triggering the signalling events by interacting with different proteins such as CTR-1 kinase (2). In case of ETR1, the cytosolic domain is made of a GAF domain followed by a histidine kinase dimerization (dHp) and catalytic domain (CA) and a receiver domain (RD).

Sequence analysis of ethylene receptors indicated similarity to bacterial two-component systems (TCS) by their C-terminal cytosolic histidine kinase (HK) and receiver domains. Based on the integrity of signature motifs in the catalytic domain of the HK, the receptors are further assigned to two subfamilies. Members of subfamily 1 (ETR1 and ERS1) possess all sequence motifs of canonical HK domains and also histidine kinase activity. Subfamily 2 receptors (ETR2, ERS2 and EIN4) have incomplete motifs and lack histidine kinase activity. While all receptors participate in ethylene signal transduction, members of subfamily 1 seem to play a predominant role.

To understand the kinetic and regulatory mechanism of ethylene receptors, we have successfully crystallized and solved the structure of the catalytic domain of ETR1. The protein was crystallized with various nucleotides. Crystals obtained in the presence of ADP belong to space group  $I2_12_1$  with one molecule per asymmetric unit and diffract x-ray radiation to beyond 1.85 Å resolution. The overall structure assumes an  $\alpha/\beta$  sandwich fold and closely resembles the CA domain of HK853. The crystal structure reveals the flexibility of the ATP lid and the metal specificity of subfamily 1 receptors through the unusual binding of a metal ion with the adenine moiety of ADP and residue C573 from the G3 motif (3).

References:

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