

## Crystal structure of human Evectin-2 PH domain, and its complex structure with O-phospho-L-serine

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Evectin-2, a pleckstrin homology (PH)-domain-containing protein, is implicated to be a regulator of the retrograde transport from plasma membrane to Golgi. Furthermore, it is implicated that Evectin-2 PH domain plays an important role in the retrograde transport by binding to phosphatidylserine (PS) on Recycling Endosomes.

To clarify the detailed binding mode between human Evectin-2 PH domain and PS, the crystal structures of the native and O-phospho-L-serine complex were determined at 1.75 and 1.00 Å resolutions, respectively. The overall structure follows the standard PH domain fold. O-phospho-L-serine binds to positively charged pocket near  $\beta 1/\beta 2$  loop, and this binding mode confers the structural basis of the phosphor lipid binding specificity. Based on these structures, potential functional implications of human Evectin-2 PH domain are discussed.