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Supporting information for article:

Structural insights into the histidine-containing phosphotransfer protein and receiver domain of sensor histidine kinase suggest a complex model in the two-component regulatory system in *Pseudomonas aeruginosa*

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For

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Supplementary Figure

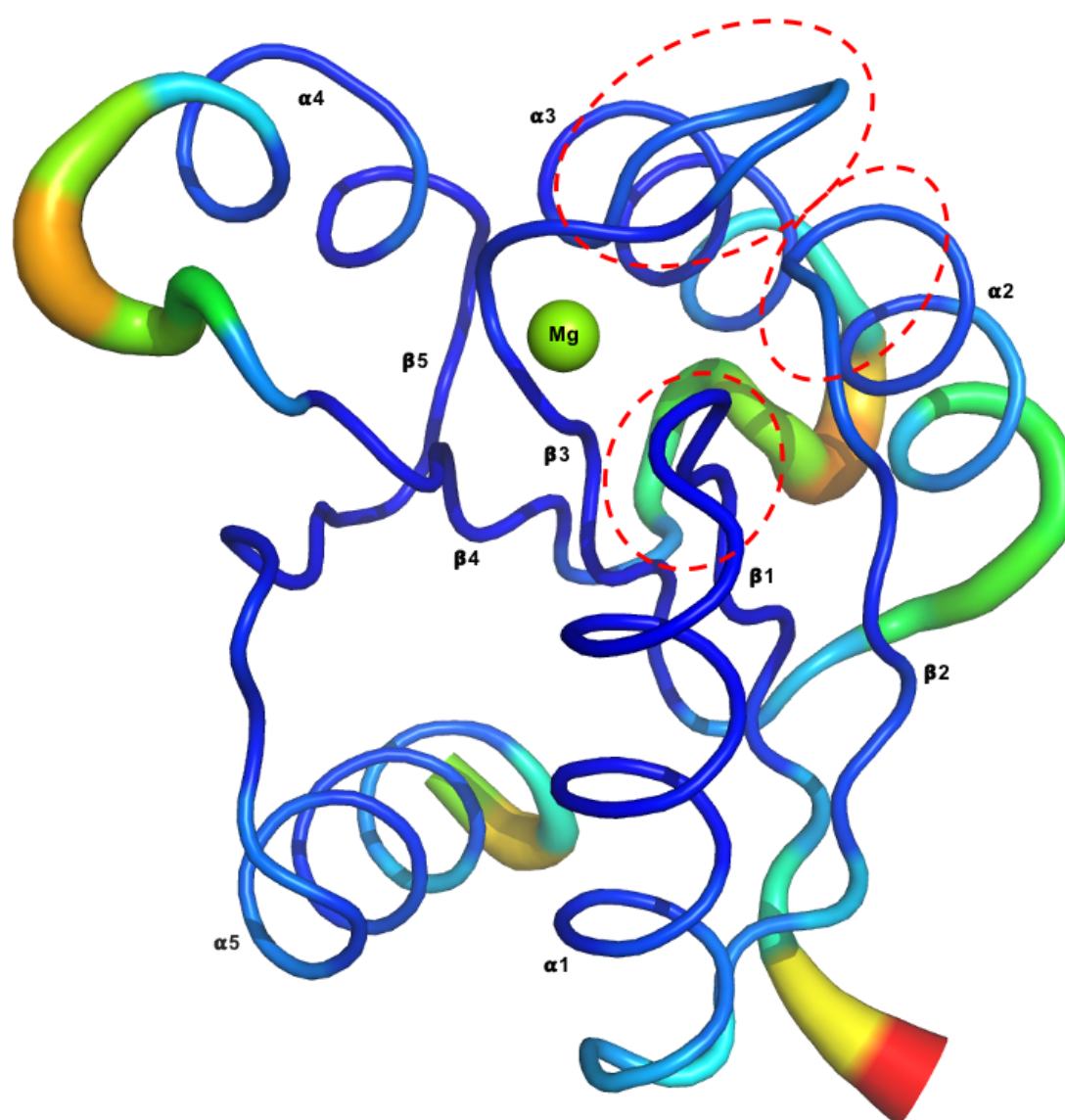


Figure S1. A temperature *B*-factor analysis of PA1611REC. The loops $\beta 1 \rightarrow \alpha 1$ (Glu521 to Asn523), $\beta 2 \rightarrow \alpha 2$ (Ala545 to Asp546) and $\beta 3 \rightarrow \alpha 3$ (Cys566 to Asp572) surrounding the active-site cleft are relatively rigid with low B-factors compared to the loops away from the active site. Mg^{2+} is shown as a green sphere. *B*-factor decrement is presented from red to blue.

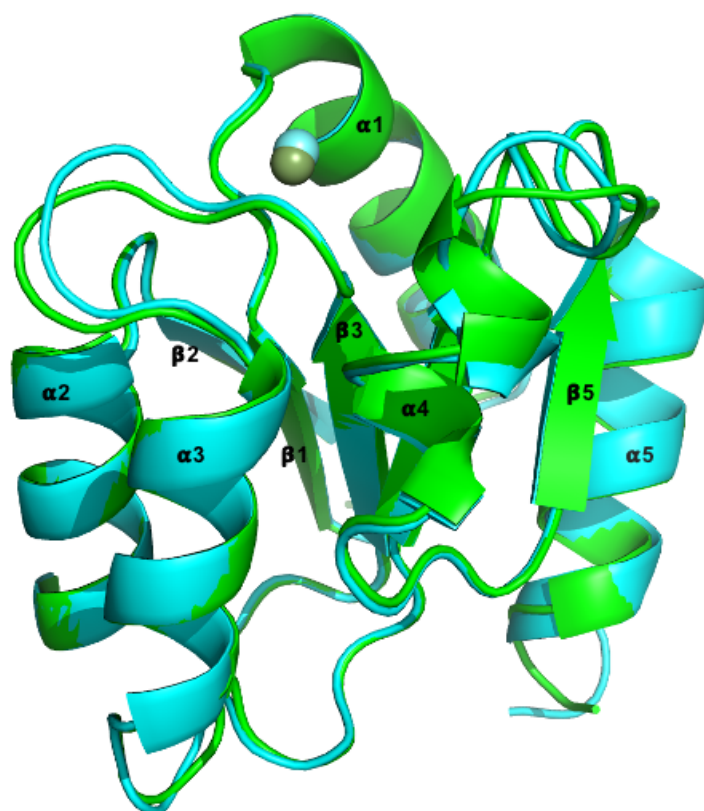


Figure S2. Structural comparison of PA1611REC-Mg²⁺ and PA1611REC-Ca²⁺. The PA1611REC with Mg²⁺ in the active-site cleft is colored green, whereas the protein with Ca²⁺ in the active-site cleft is colored cyan. The β-strands and α-helices are numbered sequentially β1 to β5 and α1 to α5 from the N-terminus to the C-terminus. Mg²⁺ is shown as a yellow-green sphere, and Ca²⁺ is shown as a cyan sphere. The main (β/α)₅ architecture is well superimposed, including the discontinuous helix α4.