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-Mg$^{2+}$ and PA1611REC-Ca$^{2+}$. The PA1611REC with Mg$^{2+}$ in the active-site cleft is colored green, whereas the protein with Ca$^{2+}$ 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. Mg$^{2+}$ is shown as a yellow-green sphere, and Ca$^{2+}$ is shown as a cyan sphere. The main (β/α)$_5$ architecture is well superimposed, including the discontinuous helix α4.