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Supporting information for article:

Implementation of wedged-serial protein crystallography at PROXIMA-1

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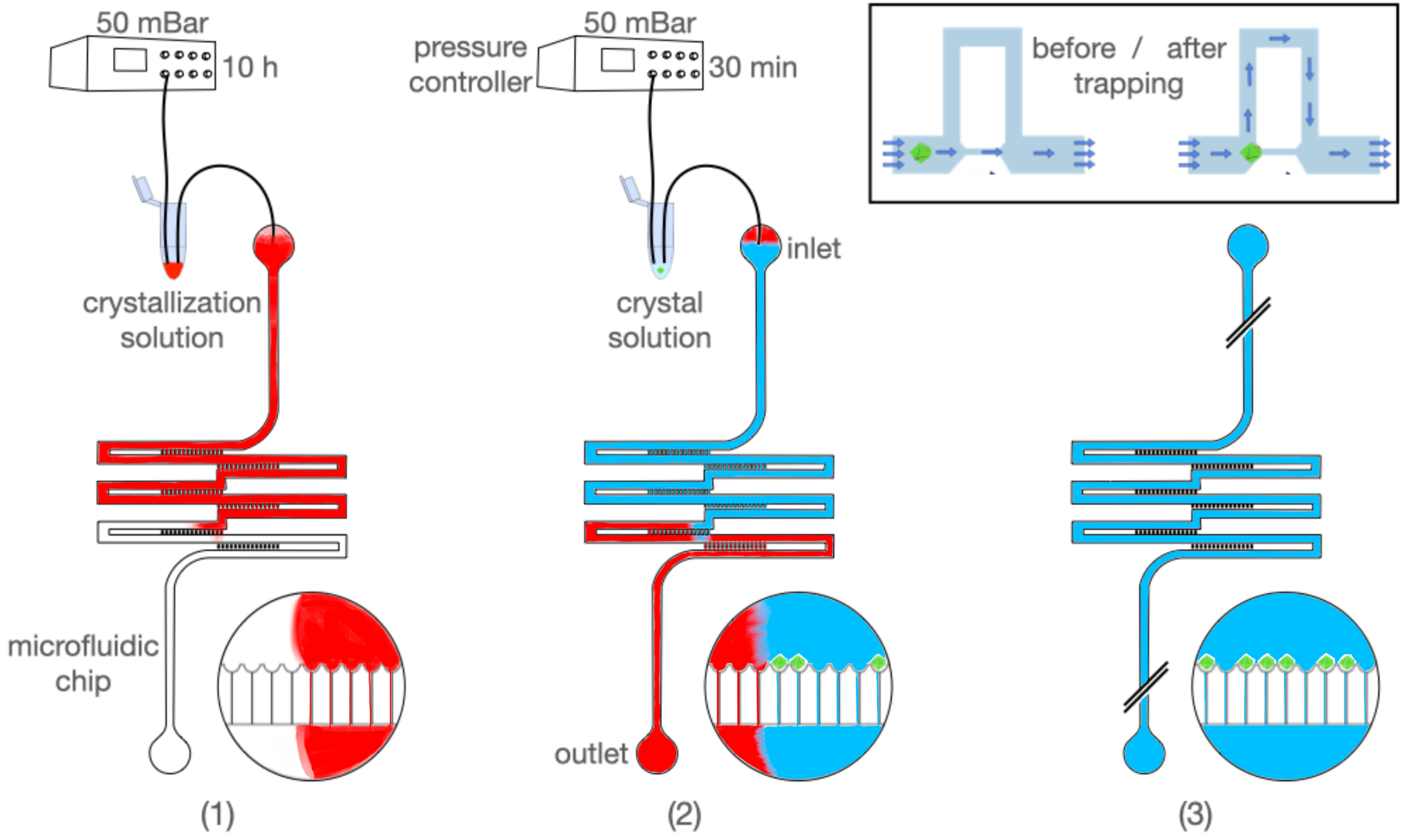

Figure S1. Schematic explanation of the sample loading process. The crystallization solution is first loaded for 10 h (pressure of 50 mBar) to assure that the microfluidic chip is fully wet and without air bubbles *(1)*. Crystals in solution are then injected for 30 min or for the full volume of sample stock *(2)* and the chip is sealed *(3)*. ***Inlet:*** crystal trapping principle, illustrating the liquid flow favored path based on the resistivity of the channels.

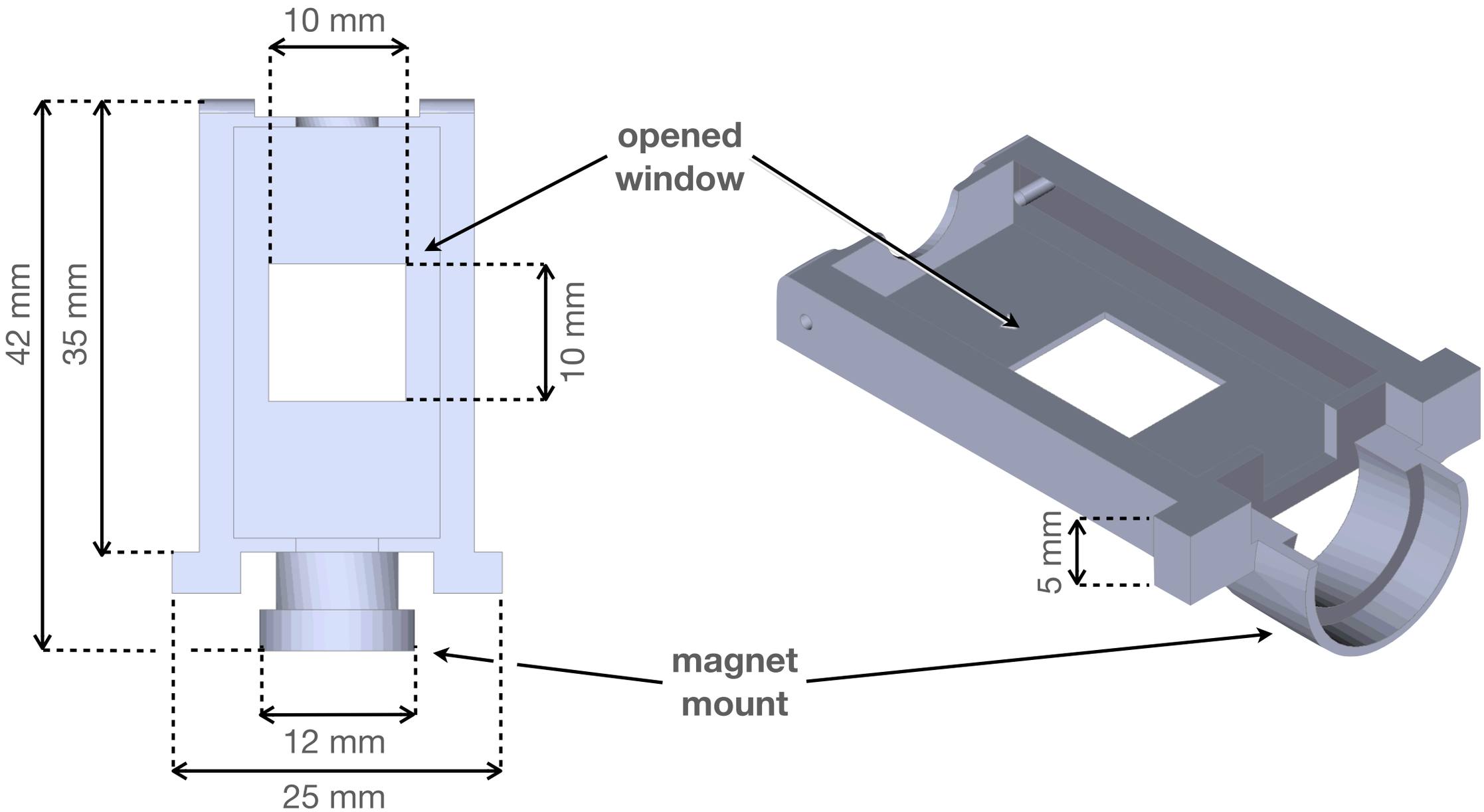

Figure S2. CAD drawing of the 3D-printed chip handling frame. The locations for fixing the magnet mount and the microfluidic chip are indicated.

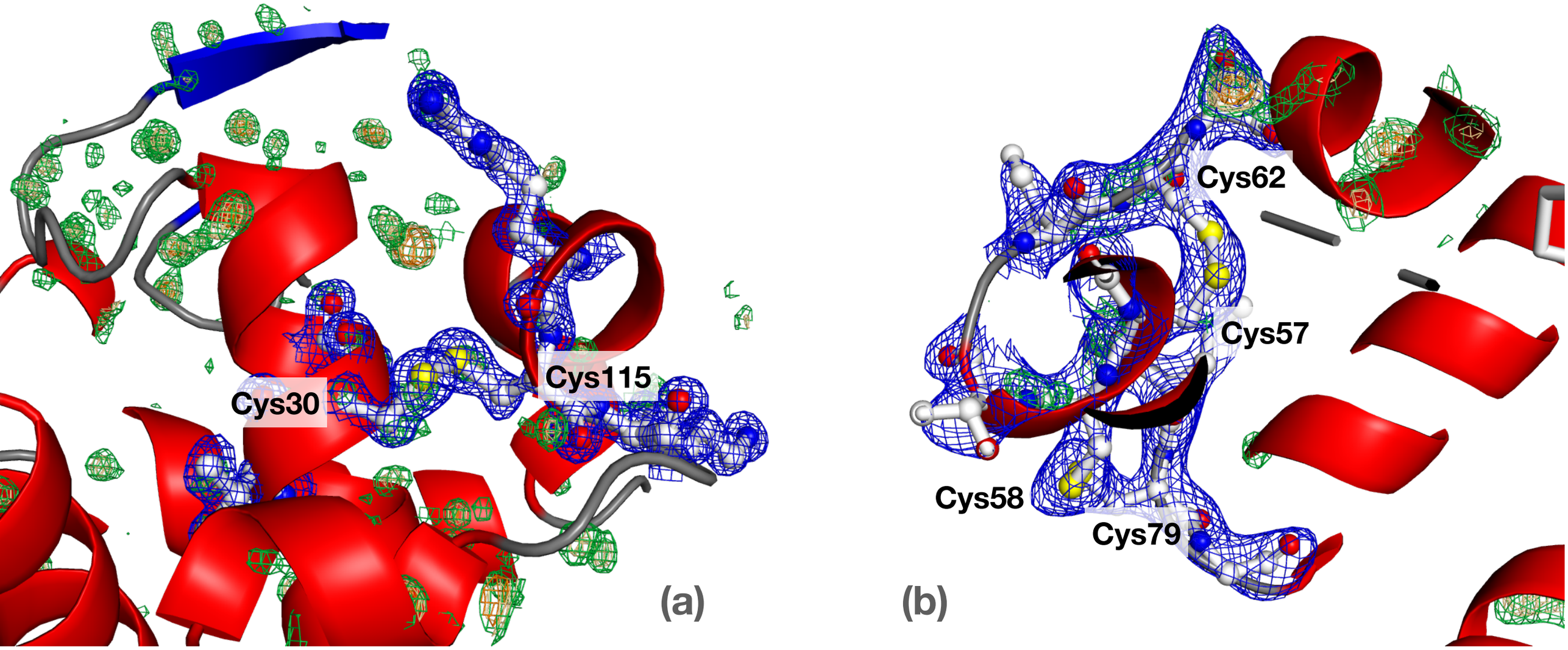

Figure S3. Electron density maps around disulfide bridges. **(a)** Lysozyme structure zoomed around the disulfide bridge Cys30-Cys115. **(b)** Insulin structure zoomed around the double disulfide bridge Cys57-Cys62 and Cys58-Cys79, respectively. The electron density maps are colored in blue for *2Fo-Fc* contoured at 1.2 σ, and green, yellow and orange for *Fo-Fc* contoured at 2.0, 2.5 and 3.0 σ, respectively.