



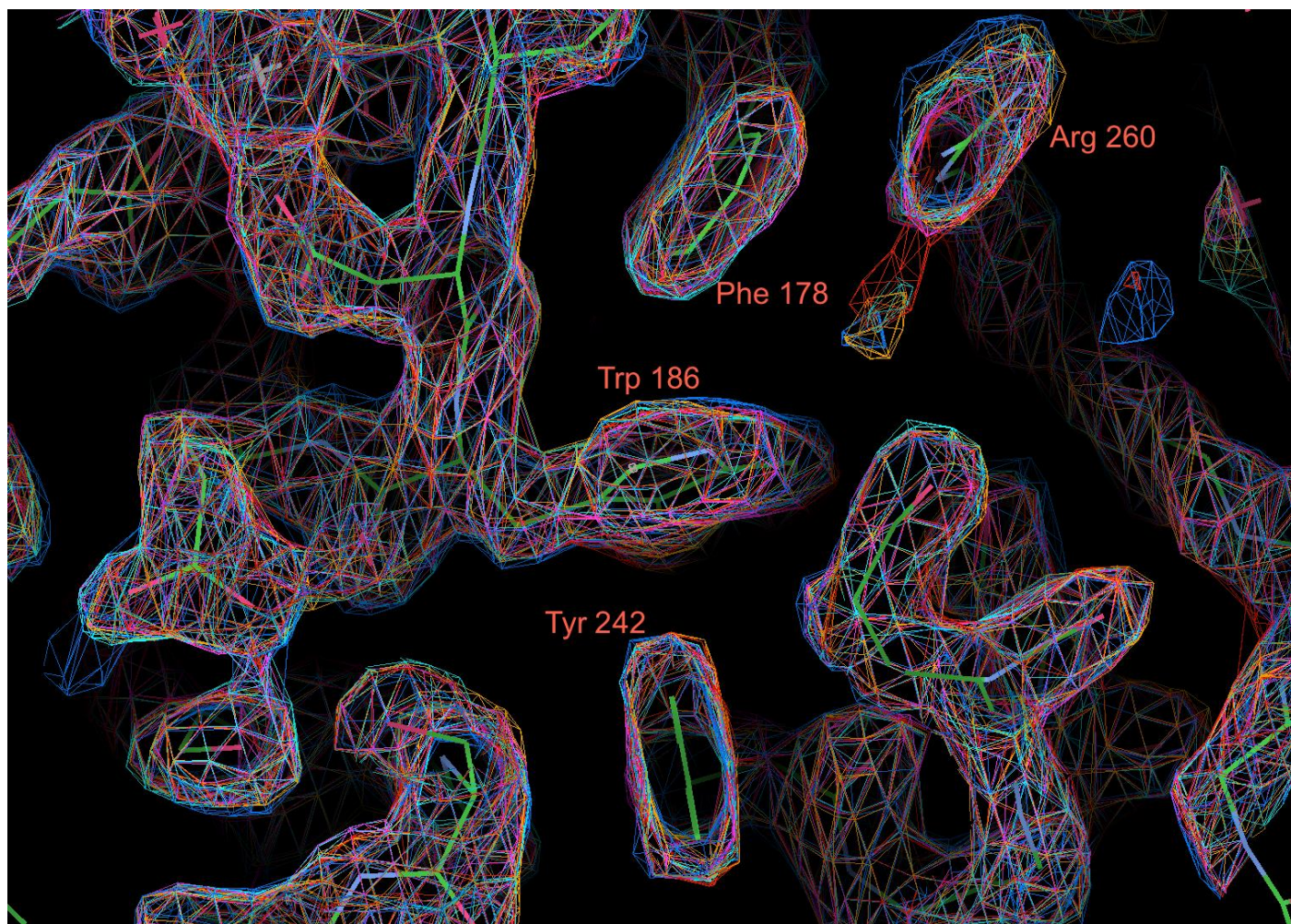
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**Figure S1** Figure S1. Likelihood-weighted electron density maps with coefficients  $2mF_o - DF_c$ . The thermolysin molecular model is refined against data processed with protocol 7POST (Table 1), while electron density maps contoured at  $+1.2\sigma$  are illustrated for all protocols: 4 (blue), 6 (cyan), 6F (orange), 7POST (magenta), and 7F,POST (red). Contours surrounding the amino acid sidechains are in approximate agreement across all data-processing protocols, while the details differ in some locations, including those defining the surrounding solvent atoms.