Supplemental Material for

Orientation and Penetration Depth of Monolayer-Bound p40$^{phox}$-PX

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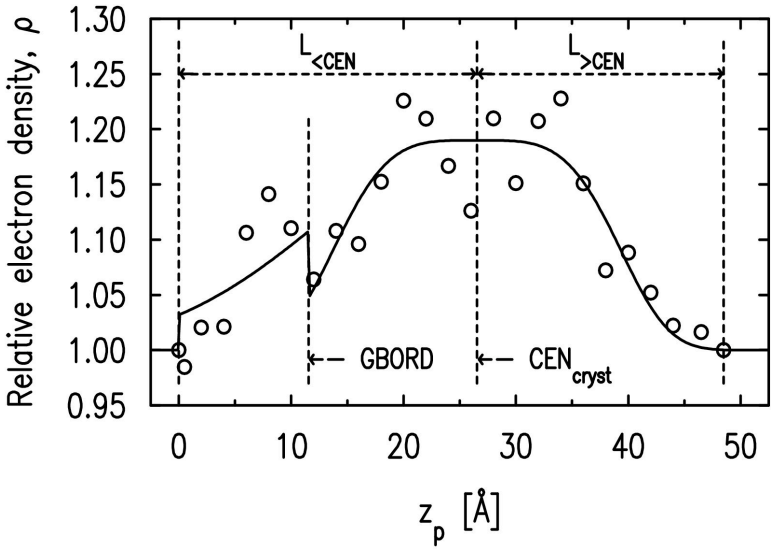


Figure S1. Electron density along the $z_p$ axis of the protein in a box with buffer obtained by slicing the protein in the best fit orientation. Open circles indicate the electron density of each slice for the case of the protein in a box with buffer. The solid line represents the best fit of these electron densities using a model function described in our earlier work (see Ref. 26 in paper). The parameter values are: $L_{<CEN}$=26.5 Å, $L_{>CEN}$=22.0 Å, $CEN_{cryst}$=26.5 Å, $AMPL_{buffer}$=0.19, $AMPL_{empty}$=0.47, WIDTH=13.8 Å, GWIDTH=19.9 Å, and GBORDER – $CEN_{cryst}$= –15 Å.

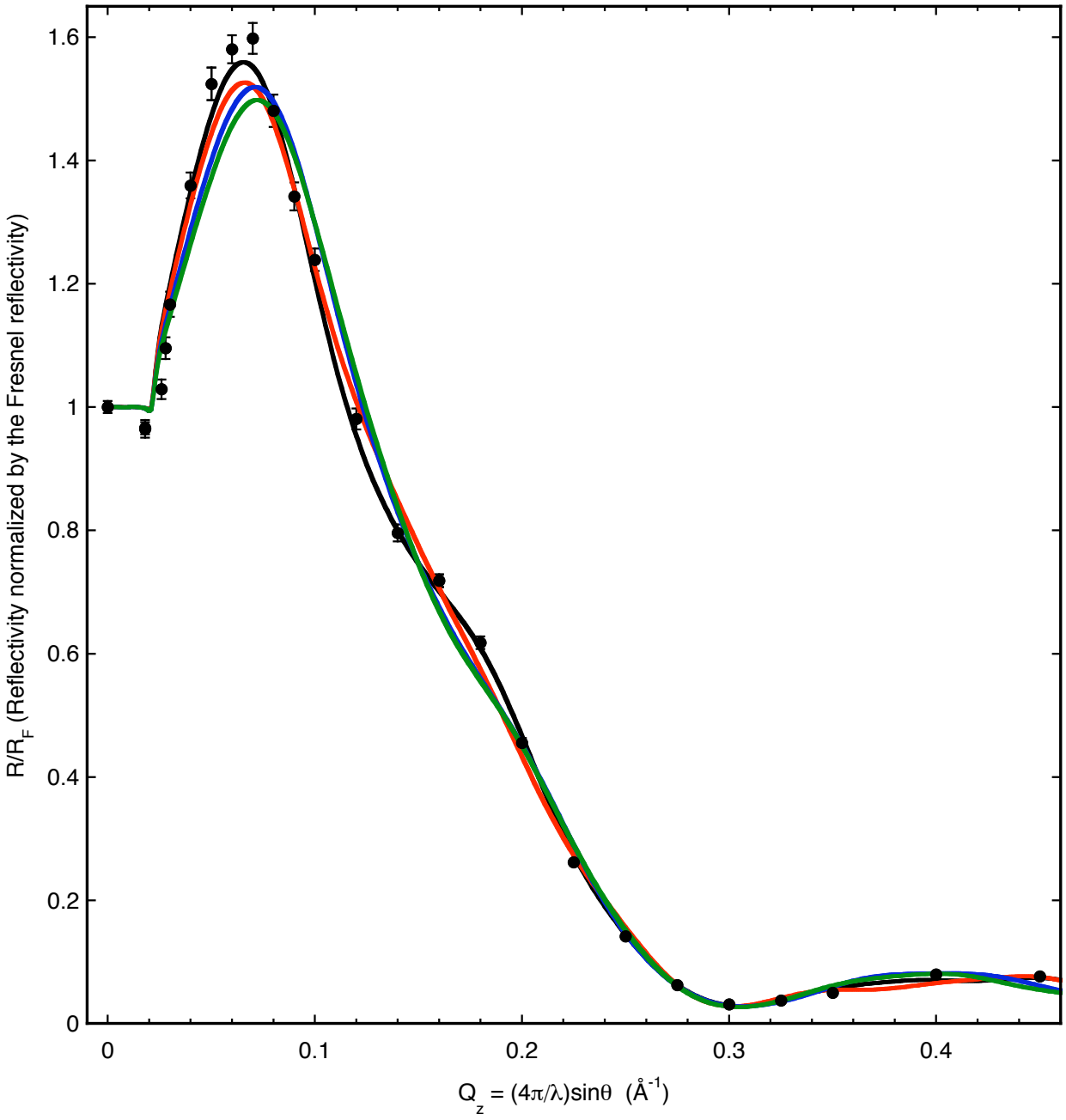


Figure S2. Reflectivity normalized by the Fresnel reflectivity of the SOPC/SOPS/DPPtdIns(3)P monolayer bound $p40^{phox}$-PX system when the initial lipid pressure $\pi_o$=26.3 mN/m (as in Table 2). Dots are the reflectivity data. Curves are fits for different values of the orientation angles. These fits are chosen as representative of fits identified by different colored squares in Figure 6. Black line ($\theta$=30°, $\phi$=140°), best fit (see parameters in the second to last column of Table 1 or first line of Table 2); red line ($\theta$=20°, $\phi$=130°), varies from best fit by 2.2 standard deviations; blue line ($\theta$=20°, $\phi$=110°), varies from best fit by 3.9 standard deviations; green line ($\theta$=30°, $\phi$=80°), varies from best fit by 4.9 standard deviations.

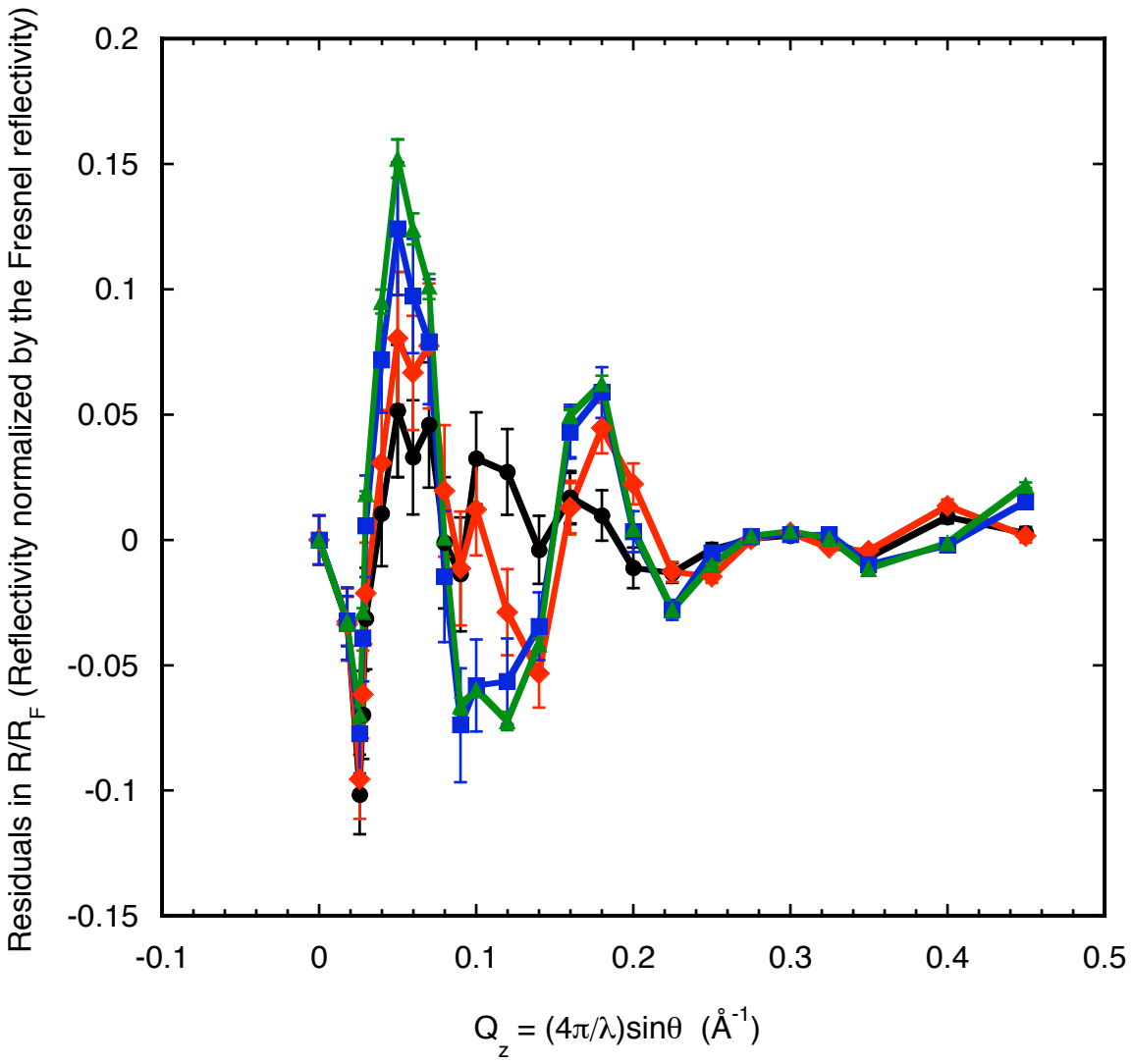


Figure S3. Residuals for fits in Figure S2. Color coding is the same. Black line and black dots ($\theta$=30°, $\phi$=140°), best fit (see parameters in Table 1 or first line of Table 2); red line and red diamonds ($\theta$=20°, $\phi$=130°), varies from best fit by 2.2 standard deviations; blue line and blue squares ($\theta$=20°, $\phi$=110°), varies from best fit by 3.9 standard deviations; green line and green triangles ($\theta$=30°, $\phi$=80°), varies from best fit by 4.9 standard deviations.