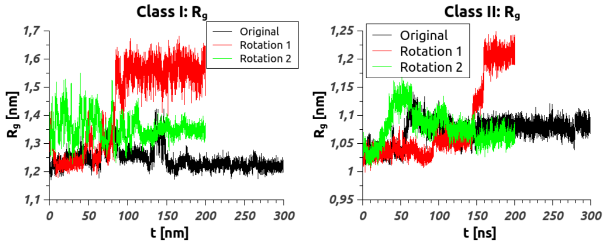
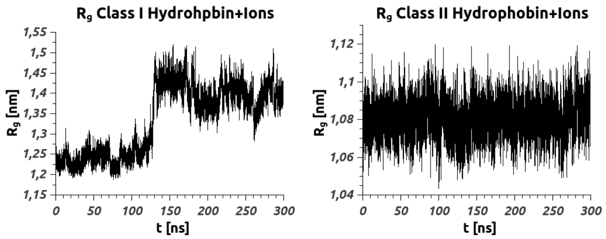
1 Supplementary Information



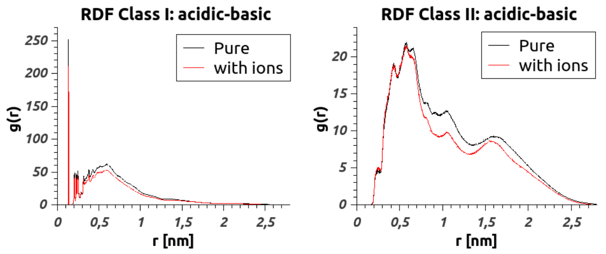
(a) EAS (b) HFBII

Fig. 1 Radius of gyration for both proteins at the interface with varied initial orientations.



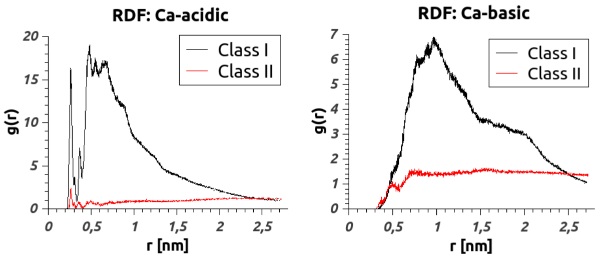
(a) EAS (b) HFBII

Fig. 2 Radius of gyration for both proteins at the interface after the addition of ions.

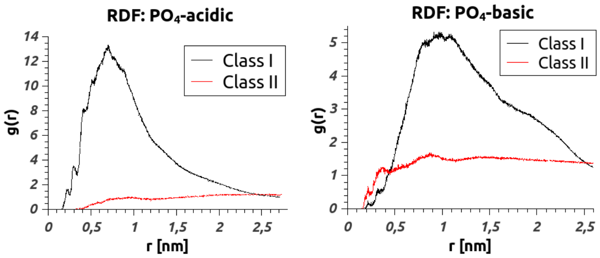


(a) EAS (b) HFBII

Fig. 3 Radial distridbution function (RDF) of acidic against basic residues for both proteins with and without ions.



(a) Calcium-acidic residues (b) Calcium-basic residues



(c) Phosphate-acidic residues (d) Phosphate-basic residues

Fig. 4 Radial distribution functions for the ions against the charged residues.

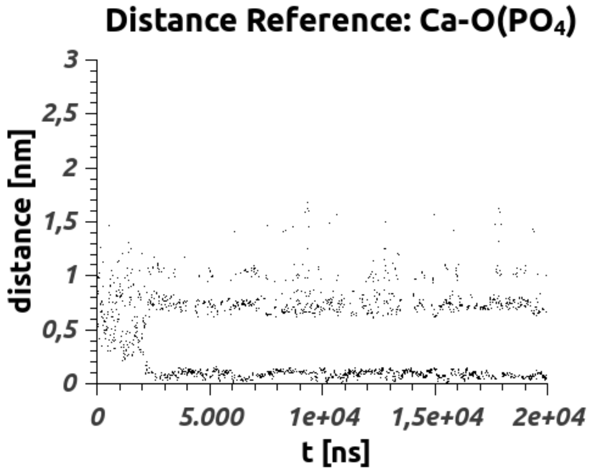
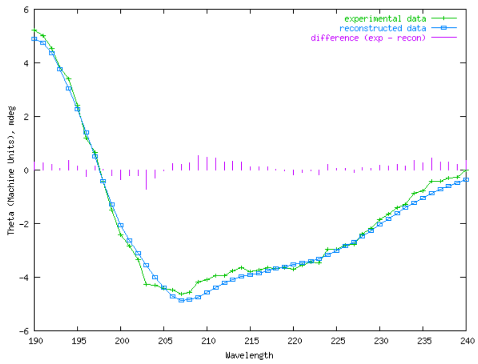
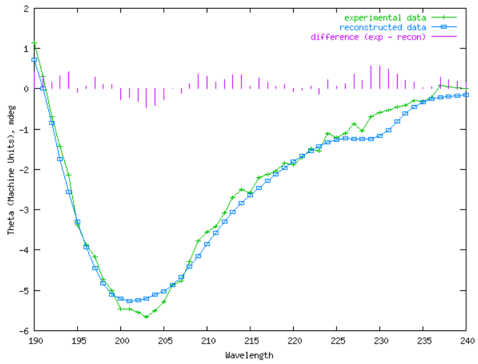


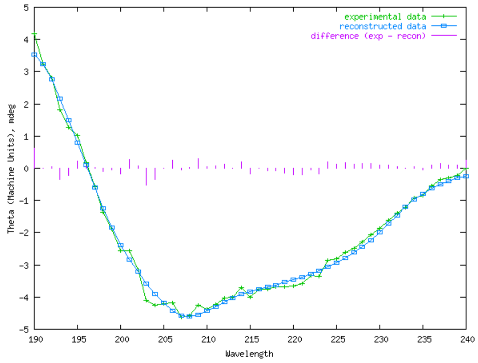
Fig. 5 Mean distance between all Ca^{2+} and all oxygens of HPO_4^{2-} for a reference simulation containing only water and the ions.



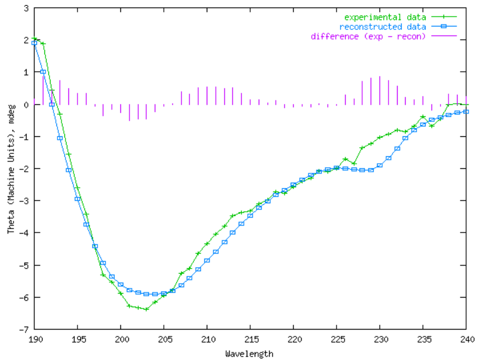
(a) H*B



(b) HFBII

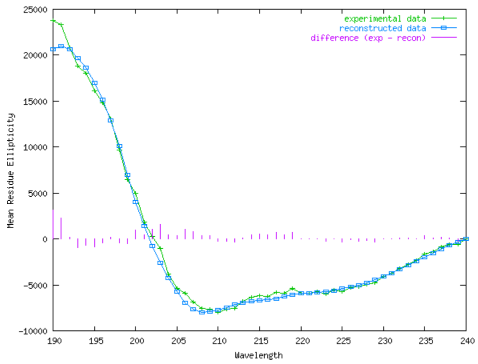


(c) H*B with hexane

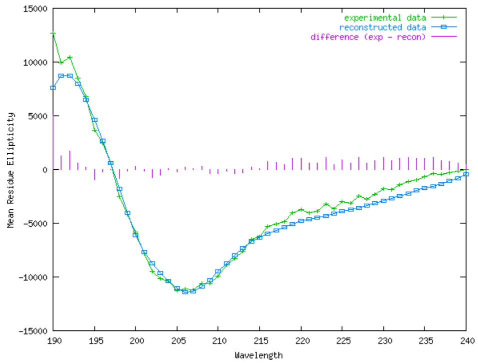


(d) HFBII with hexane

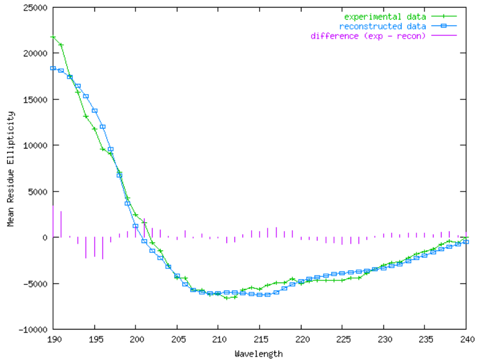
Fig. 6 Measured CD-spectra of hydrophobins without HAP together with the CONTIN 3 fit via the Dichroweb server.



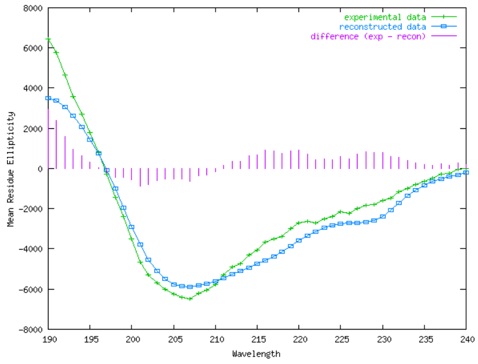
(a) H*B with HAP



(b) HFBII with HAP



(c) H*B with HAP and hexane



(d) HFBII with HAP and hexane

Fig. 7 Measured CD-spectra of hydrophobins with HAP together with the CONTIN 3 fit via the Dichroweb server.

1 SUPPLEMENTARY INFORMATION

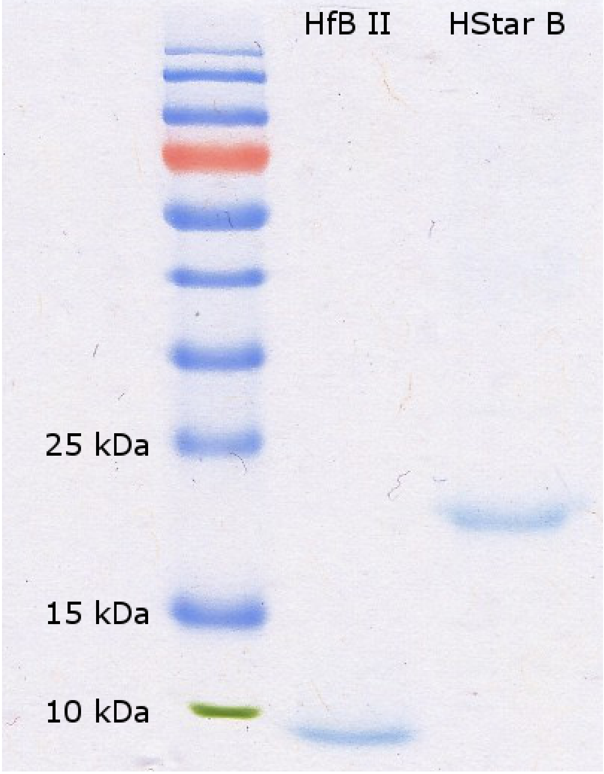


Fig. 8 SDS Gel of both hydrophobins measured in CD.