Hydrogen exchange mass spectrometry of proteins at Langmuir monolayers

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SUPPORTING INFORMATION

Figures S1, S2, S3

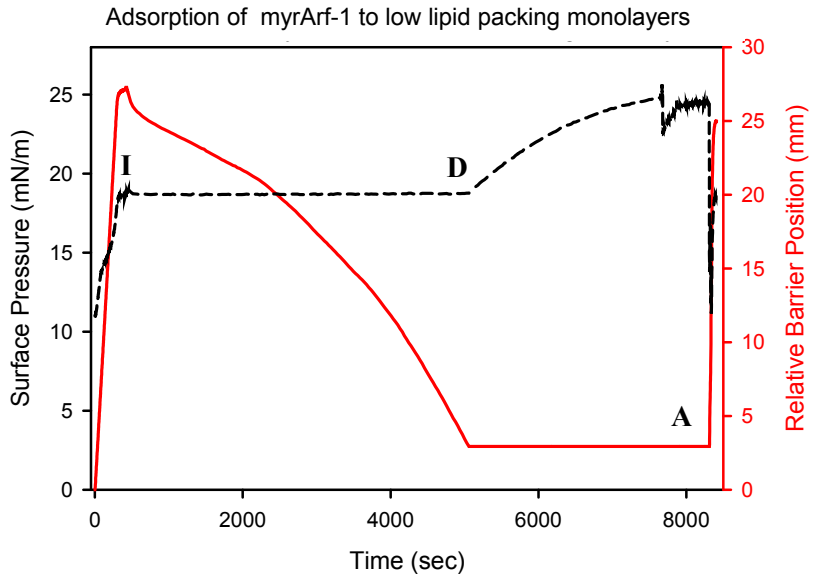

Figure S1.
Change in surface pressure (black) and barrier position (red) in the trough during adsorption of myrArf-1 at low lipid packing monolayers. "I" represents when protein was injected underneath the monolayer, "D" represents the subphase exchange with D_2O, and "A" represents aspiration of the sample.

The surface pressure was held constant after addition of protein. The barrier gradually moved back as more protein associated and inserted residues into the monolayer. The barrier was stopped within a few millimeters before reaching the end of the trough. The surface pressure rose slightly after the barrier was stopped indicating that protein was still associating with the monolayer. Aspiration dropped the surface pressure quickly and the barrier rapidly moved forward in order to reestablish the preset surface pressure.

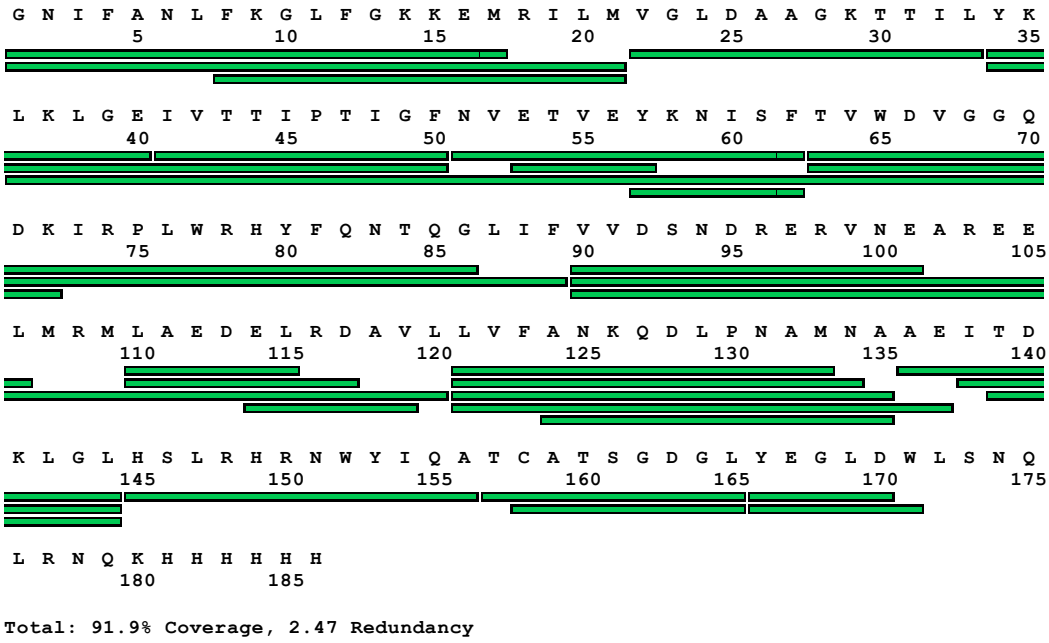

Figure S2.
Coverage maps of identified peptides (green bars) from myrArf-1 generated using a mixture of pepsin and aspergillopepsin, and followed during HX MS experiments. Reproducible peptides were found at least three times in quadruplicate runs. The sequence coverage and redundancy are indicated below the map.

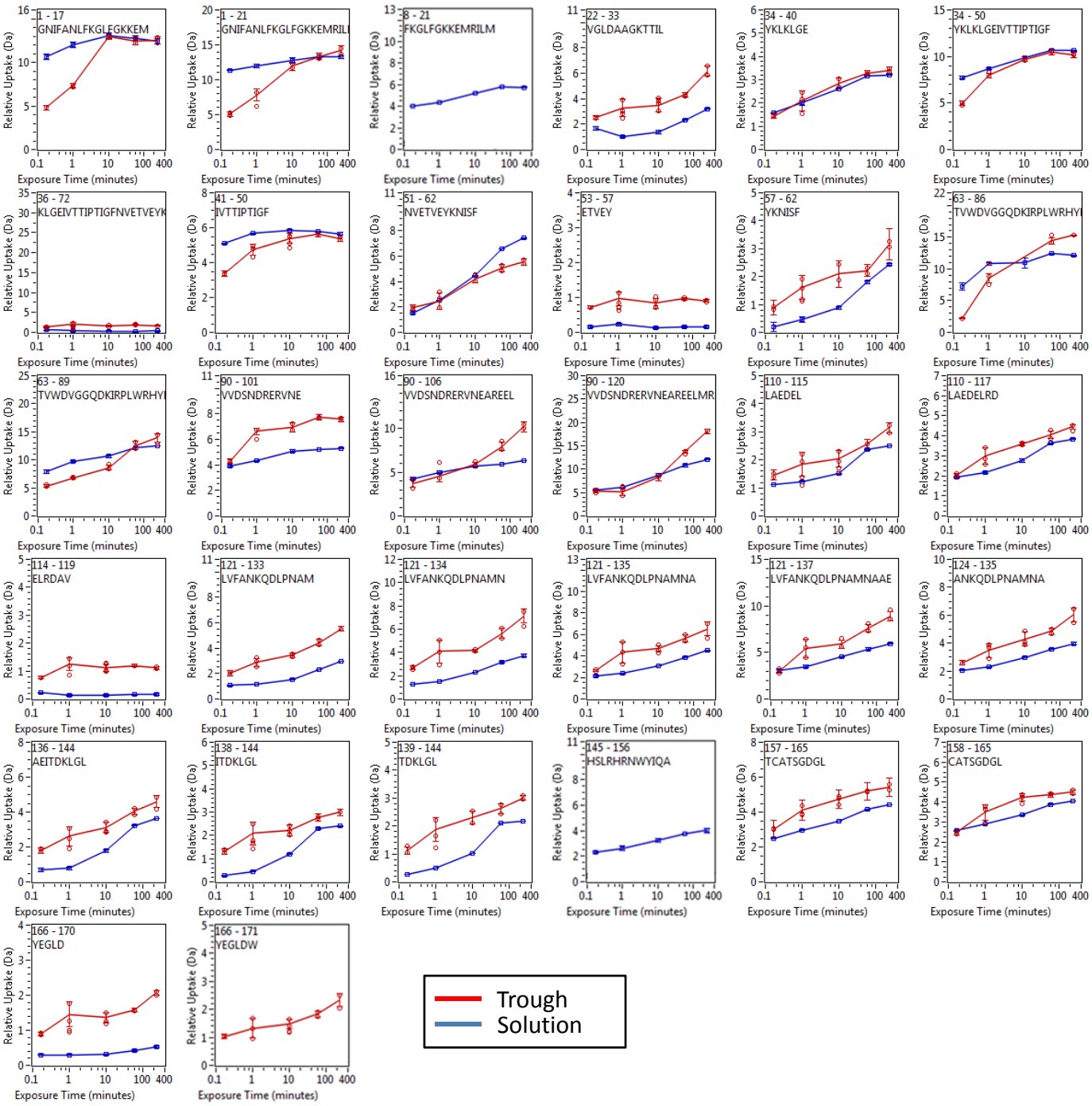

Figure S3.
Deuterium incorporation curves for myrArf-1 comparing trough samples (red) and solution samples (blue). The average deuterium incorporation from at least three independent experiments is plotted with the error bars representing the spread of the measurements.