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Note	

Supporting information for

Structure of human serum albumin at a foam surface

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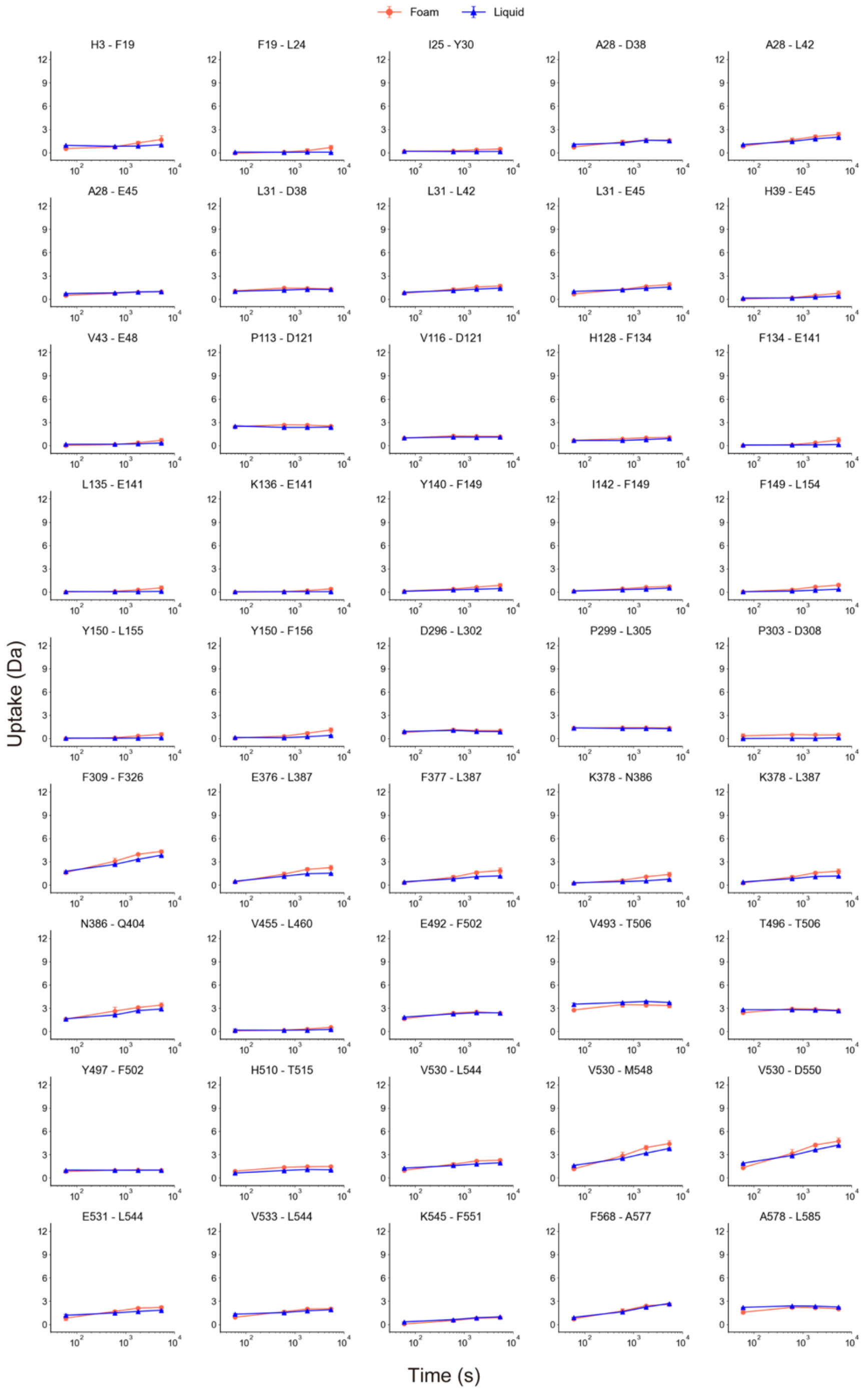


Figure S1. Deuterium uptake plots of peptides that did not show significant differences between the foam and liquid samples.

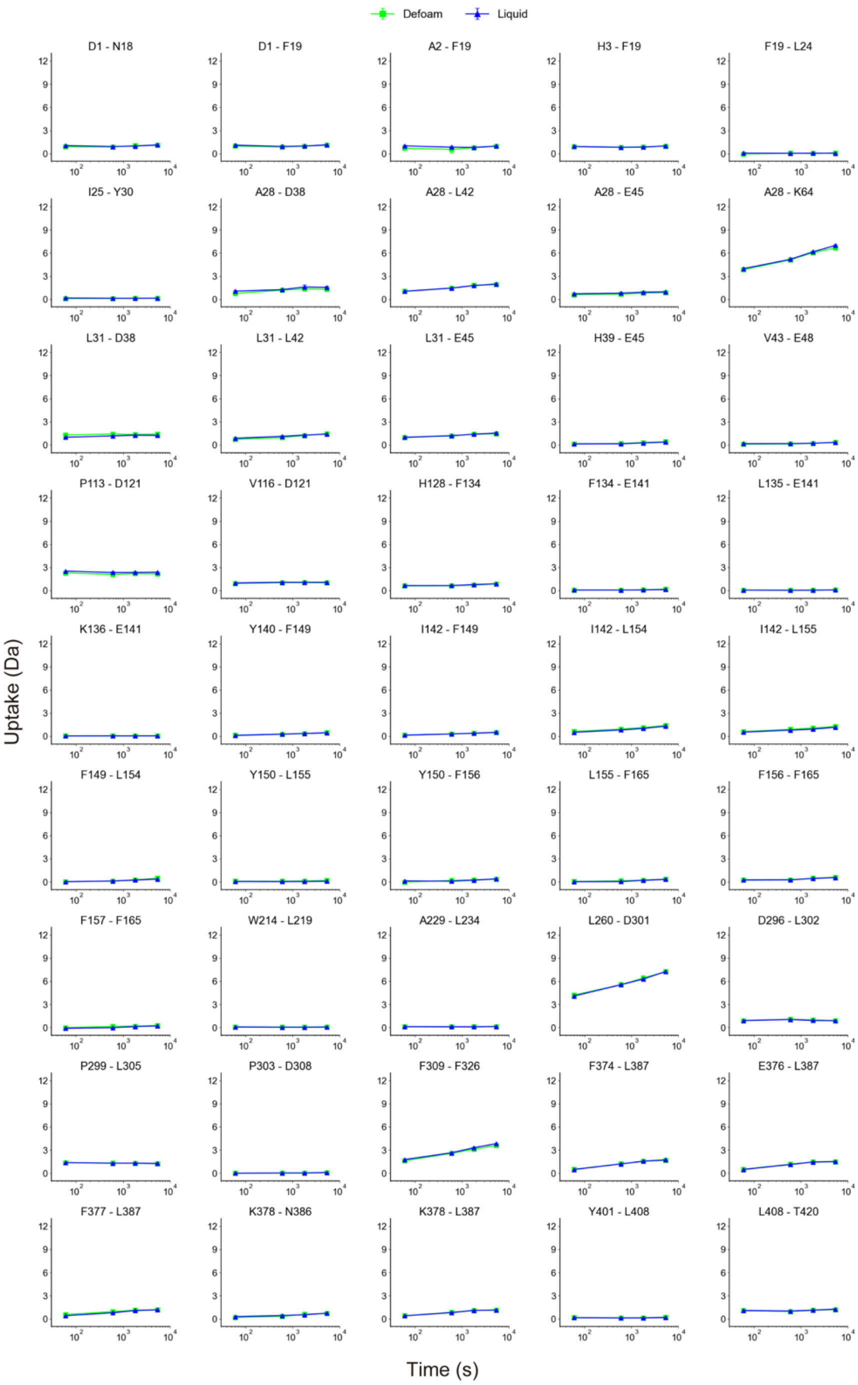


Figure S2. Deuterium uptake plots of peptides that did not show significant differences between the defoamed and liquid samples.

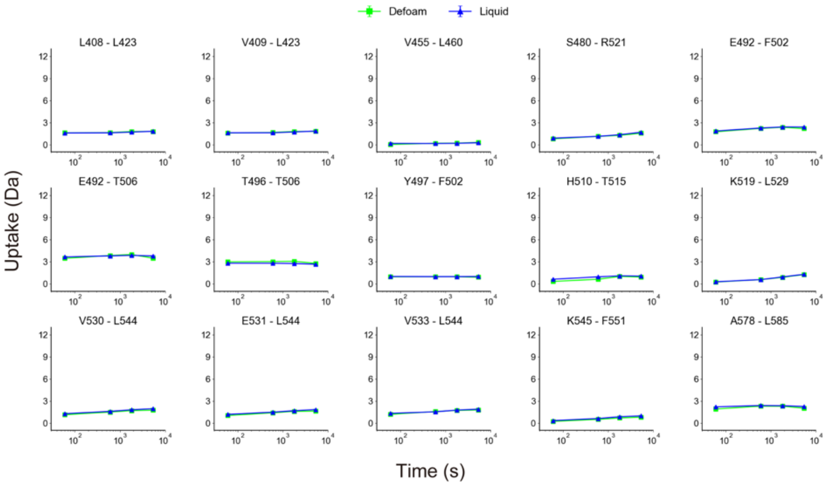


Figure S2 (continued). Deuterium uptake plots of peptides that did not show significant differences between the defoamed and liquid samples.

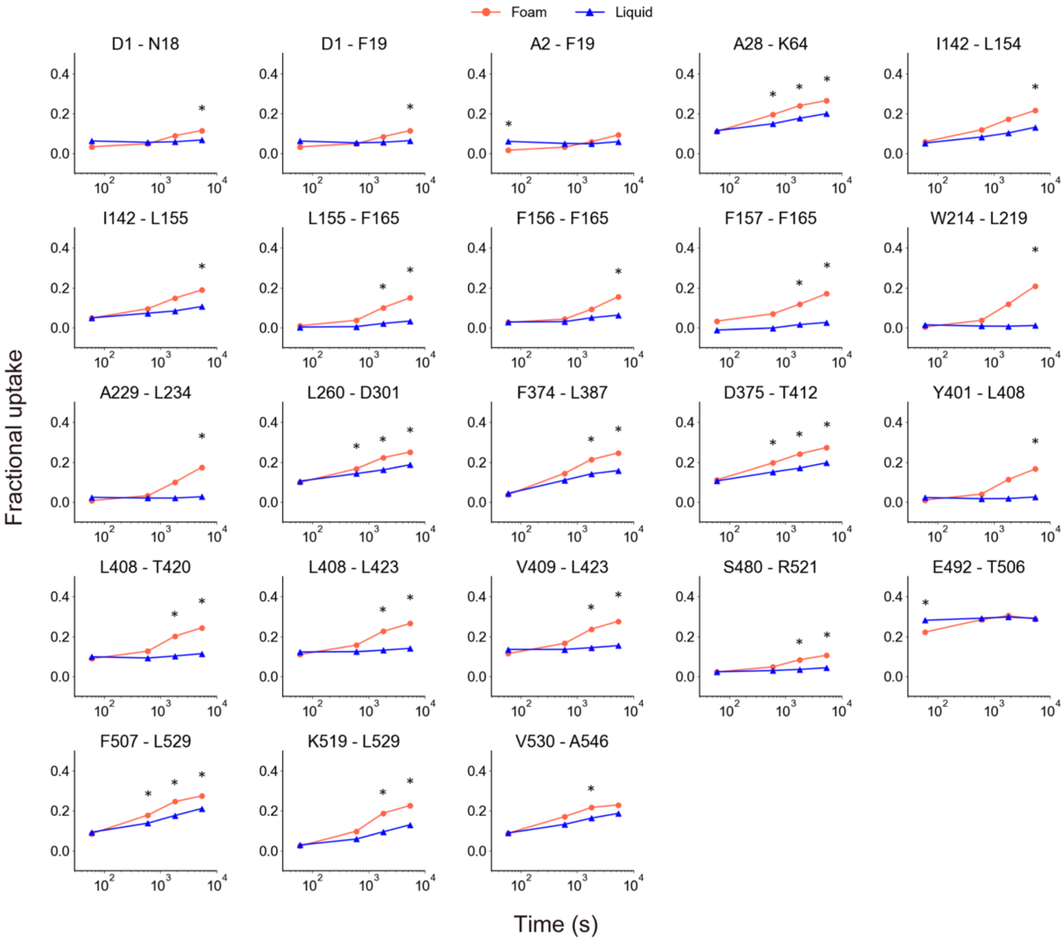
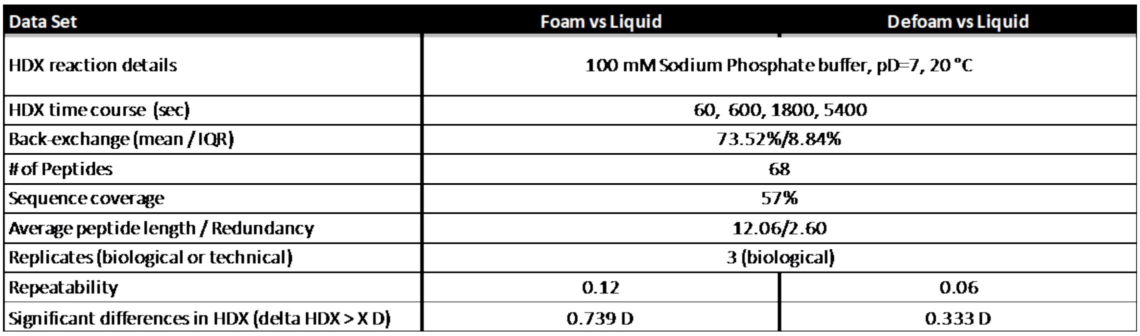


Figure S3. Fractional uptake plots of peptides that showed significant differences in deuterium uptake between the foam and the liquid states.

Table S1. Result of static surface tension measurement.

	HSA solution	Phosphate buffer
Surface tension (mN/m)	50.78	70.87
	50.60	70.82
	50.46	70.78
Average	50.6	70.8
SD	0.16	0.05

Table S2. HDX-MS summary table.[38]



Data Set	Foam vs Liquid	Defoam vs Liquid
HDX reaction details	100 mM Sodium Phosphate buffer, pD=7, 20 °C	
HDX time course (sec)	60, 600, 1800, 5400	
Back-exchange (mean / IQR)	73.52%/8.84%	
# of Peptides	68	
Sequence coverage	57%	
Average peptide length / Redundancy	12.06/2.60	
Replicates (biological or technical)	3 (biological)	
Repeatability	0.12	0.06
Significant differences in HDX (delta HDX > X D)	0.739 D	0.333 D