



Title	Structure of Human Serum Albumin at a Foam Surface
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## **Supporting information for**

### **Structure of human serum albumin at a foam surface**

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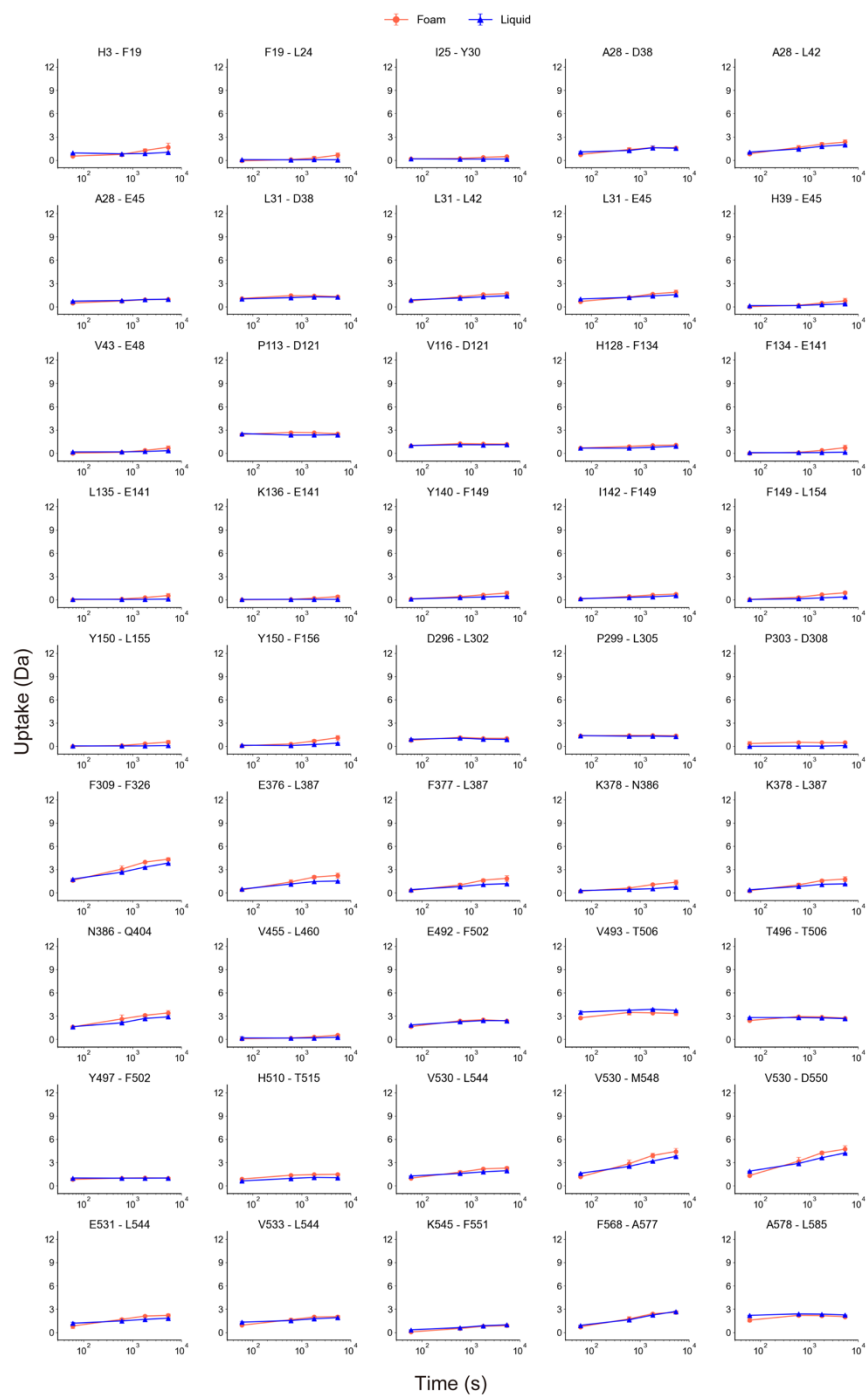
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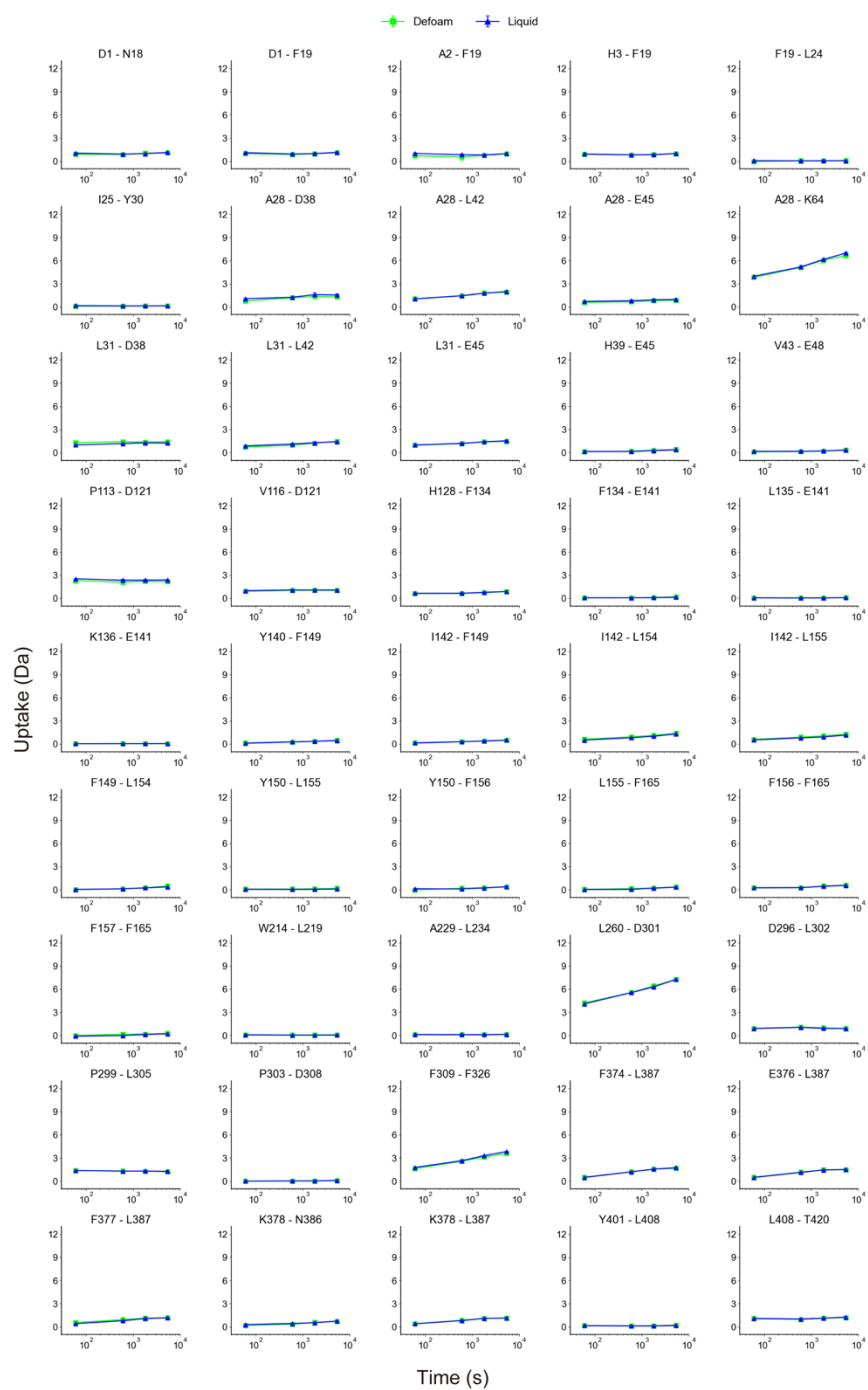
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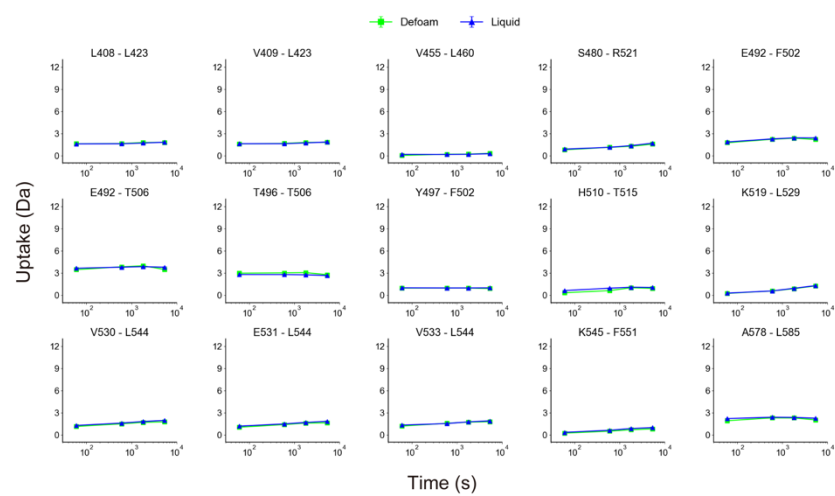
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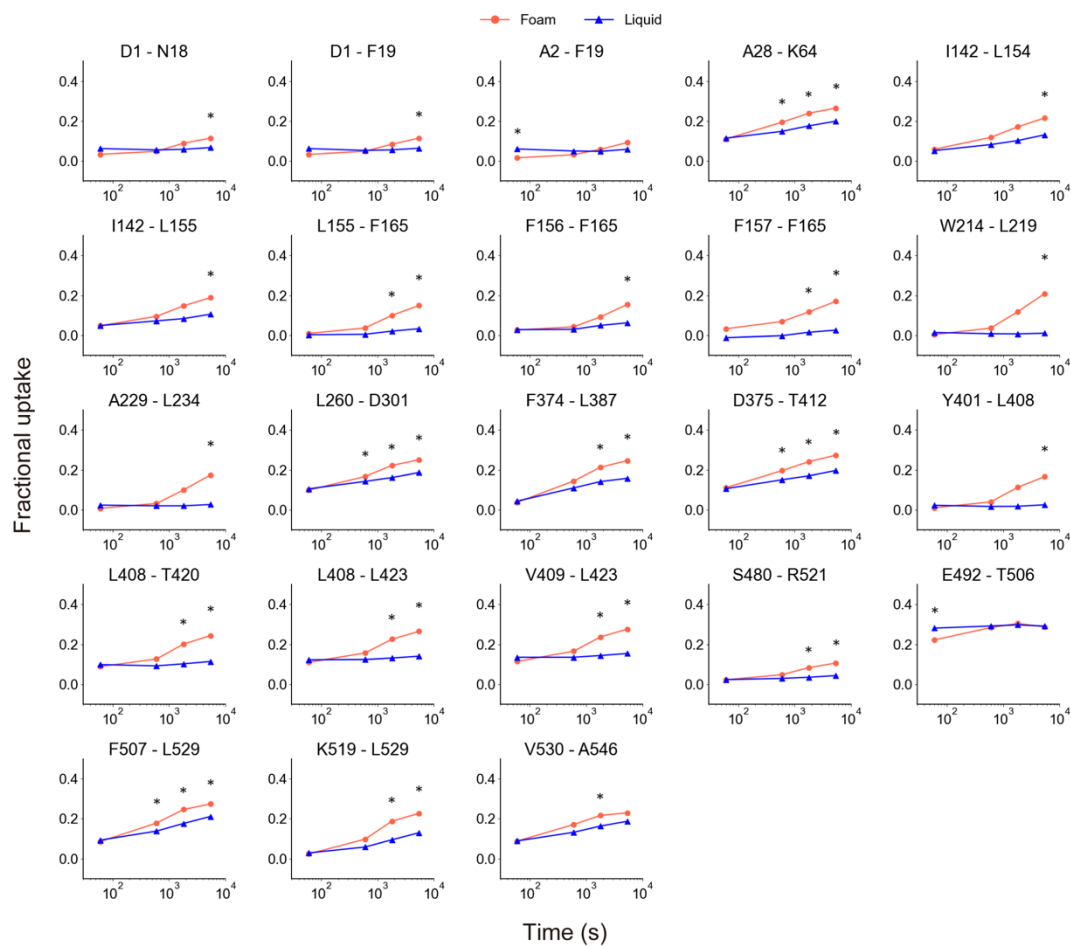
**Figure S1.** Deuterium uptake plots of peptides that did not show significant differences between the foam and liquid samples.



**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.<sup>38</sup>

Data Set	Foam vs Liquid	Defoam vs Liquid
HDX reaction details	100 mM Sodium Phosphate buffer, pH=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