Electronic Supplementary Information

for

Structure and Kinetics of Chemically Cross-Linked Protein Gels from Small-Angle X-ray Scattering

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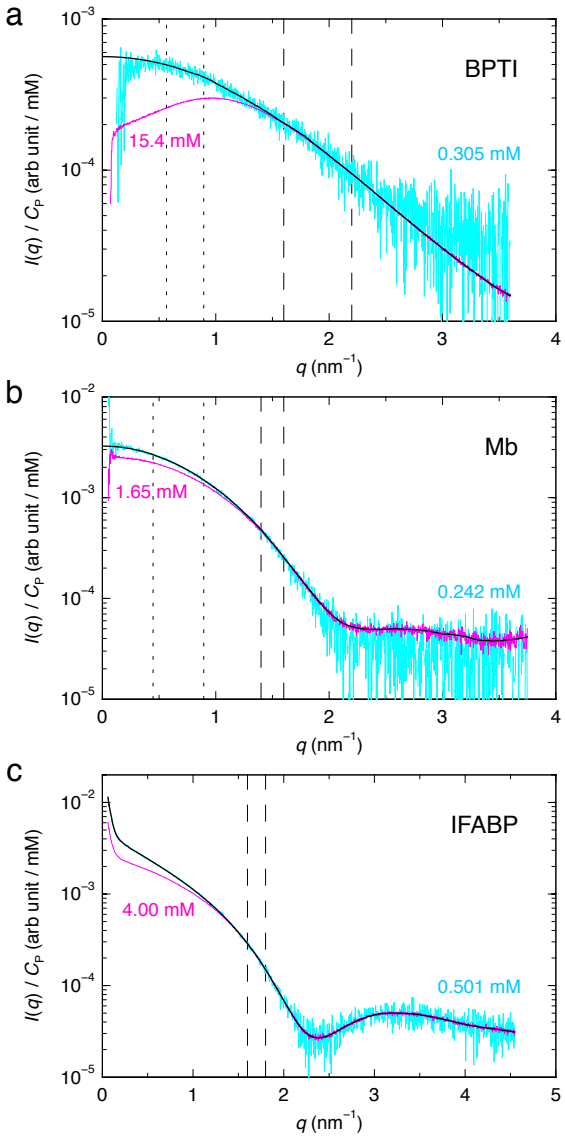

Fig. S1 Apparent form factor (black) and solution SAXS profiles (magenta and cyan) for BPTI (**a**), Mb (**b**) and IFABP (**c**). Dashed and dotted vertical lines indicate the q windows where the two solution scattering files were superimposed and where the Guinier analysis was performed, respectively (Sec. 2.3).

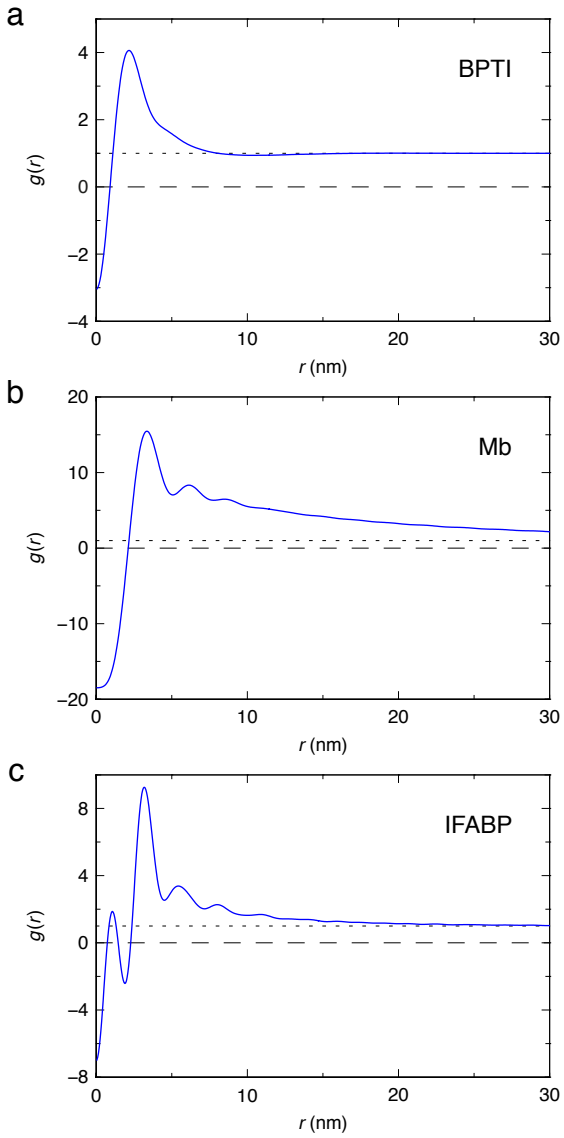

Fig. S2 Pair correlation function, $g(r)$, for cross-linked BPTI (**a**), Mb (**b**), and IFABP (**c**), obtained by fast sine transform of the modified structure factor, $S(q)$ (blue curve in Fig. 3). The dotted line indicates the asymptote $g(r \to \infty) = 1$. The negative $g(r)$ at small r is an artifact caused by setting $S(q) = 1$ at high q.

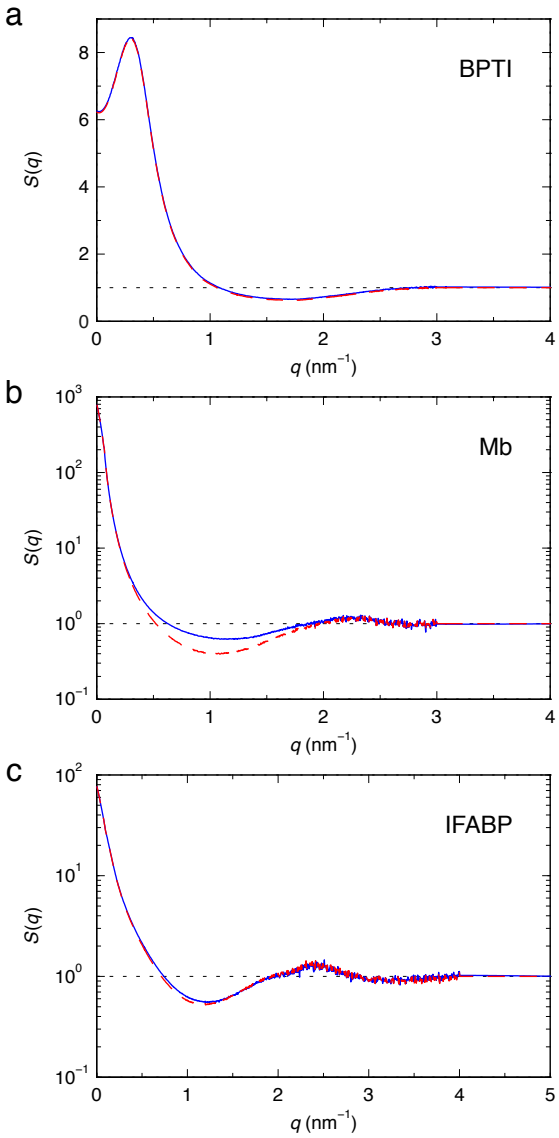

Fig. S3 Back-calculated structure factor, $S(q)$, for cross-linked BPTI (**a**), Mb (**b**) and IFABP (**c**). The red dashed curve is the inverse sine transform of the modified (non-negative) $g(r)$. The blue curve is the original $S(q)$ (blue curves in Fig. 3).

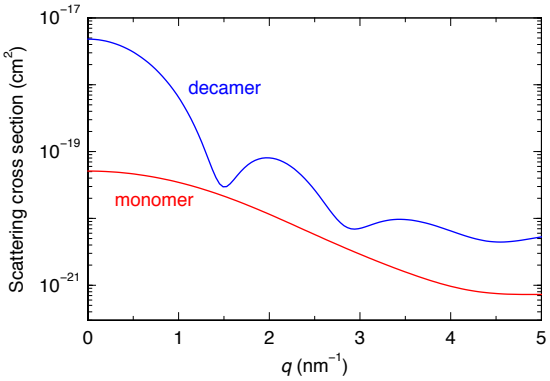

Fig. S4 Scattering cross section for BPTI monomer (red) and decamer (blue). The curves were calculated from the atomic coordinates of the crystal structures 1bpi[1] (monomer) and 1bhc[2] (decamer) using the program CRYSOL[3] without hydration-layer correction.

Table S1 Timing of kinetics series.[a]

	t (min)		
#	BPTI[b]	Mb[c]	IFABP[c]
1	1.5	1.2	1.2
2	6.8	2.2	2.8
3	11.8	3.1	4.3
4	16.9	4.1	5.9
5	27.0	5.1	7.4
6	37.2	6.0	8.9
7	47.3	7.0	10.5
8	62.6	7.9	12.0
9	113.2	8.9	13.6
10	178.9	9.8	15.1
11	239.7	10.8	16.6
12	300.3	11.7	18.2
13	361.1	12.7	19.7
14	421.7	13.6	22.0
15	482.5	14.6	23.6
16	507.9	15.6	25.1

[a] Time elapsed from GA addition to the middle of the irradiation period, including a 1 min dead time.
[b] 60 s irradiation period.
[c] 10 s irradiation period.

References

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