Self-Assembling Multidomain Peptide Fibers with Aromatic Cores

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SUPPORTING INFORMATION

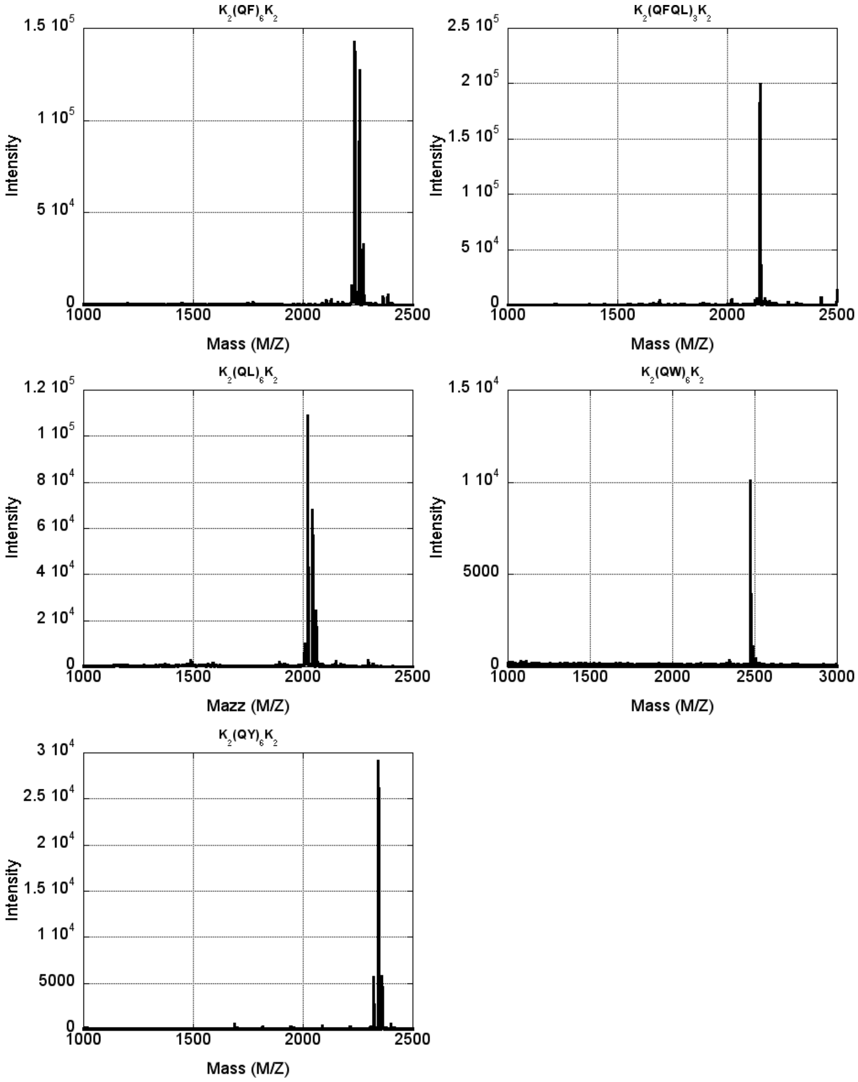

Figure S1. MALDI-TOF mass spectrometry of multidomain peptides. $K_2(QF)_6K_2$: Expected Mass: 2222.2, Observed Mass: 2221.2 $(M+H)^+$. $K_2(QFQL)_3K_2$: Expected Mass: 2121.5, Observed Mass: 2126.0 $(M+H)^+$. $K_2(QL)_6K_2$: Expected Mass: 2019.5, Observed Mass: 2019.8 $(M+H)^+$. $K_2(QW)_6K_2$: Expected Mass: 2457.8, Observed Mass: 2458.7 $(M+H)^+$. $K_2(QY)_6K_2$: Expected Mass: 2319.6, Observed Mass: 2319.9 $(M+H)^+$ and 2342.0 $(M+Na)^+$.

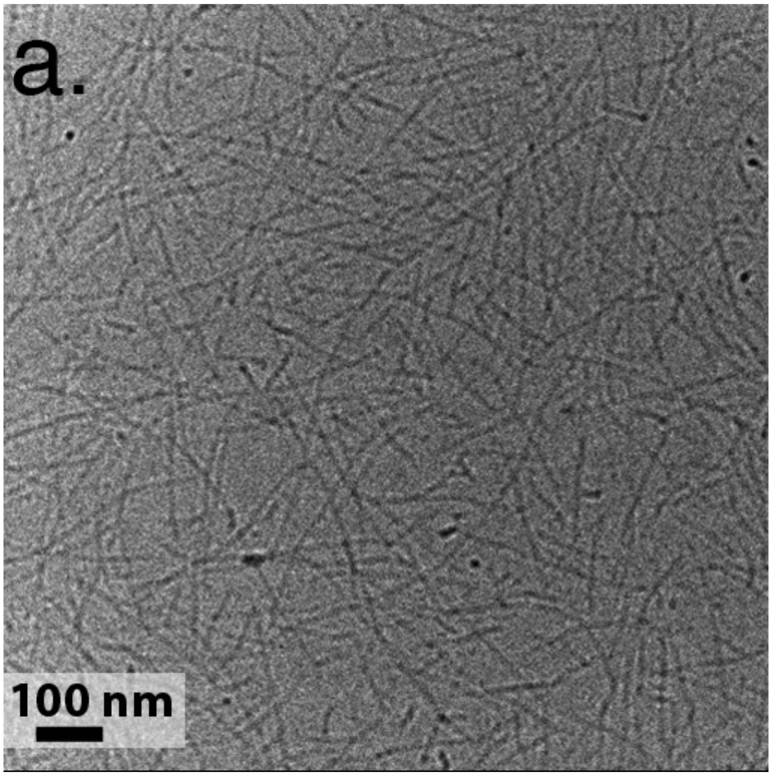

Figure 6a presented at a larger size.

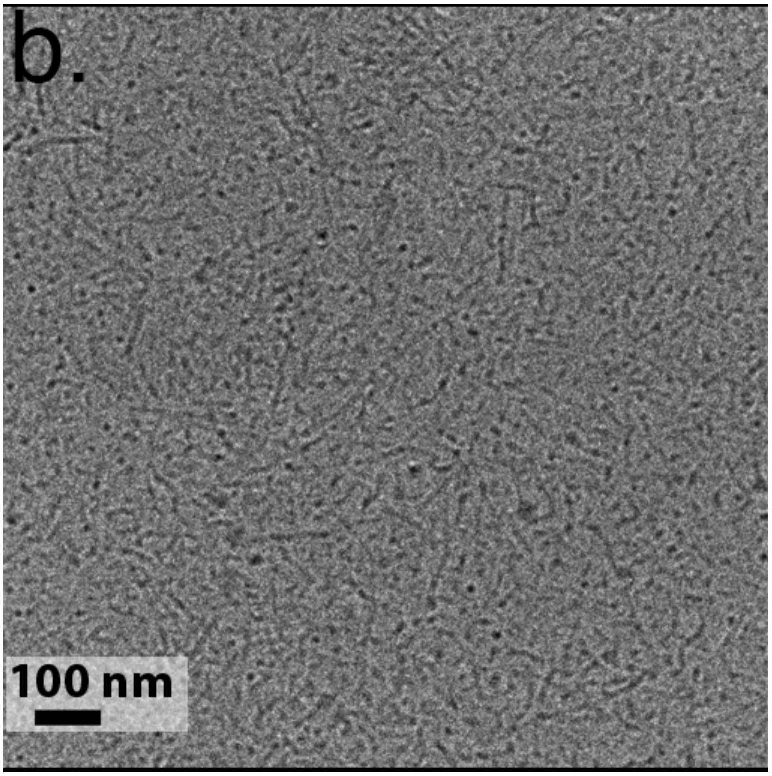

Figure 6b presented at a larger size.

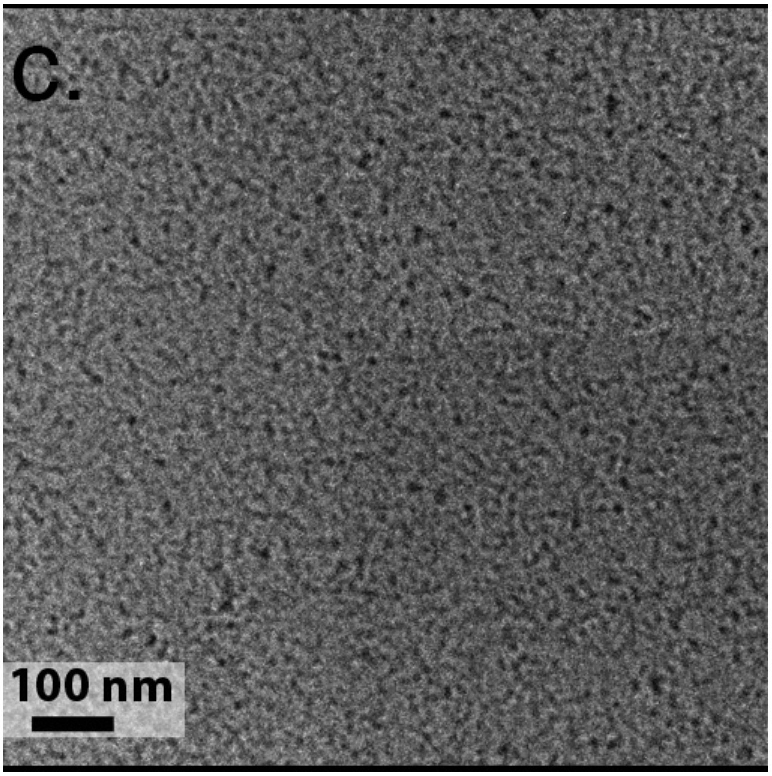

Figure 6c presented at a larger size.

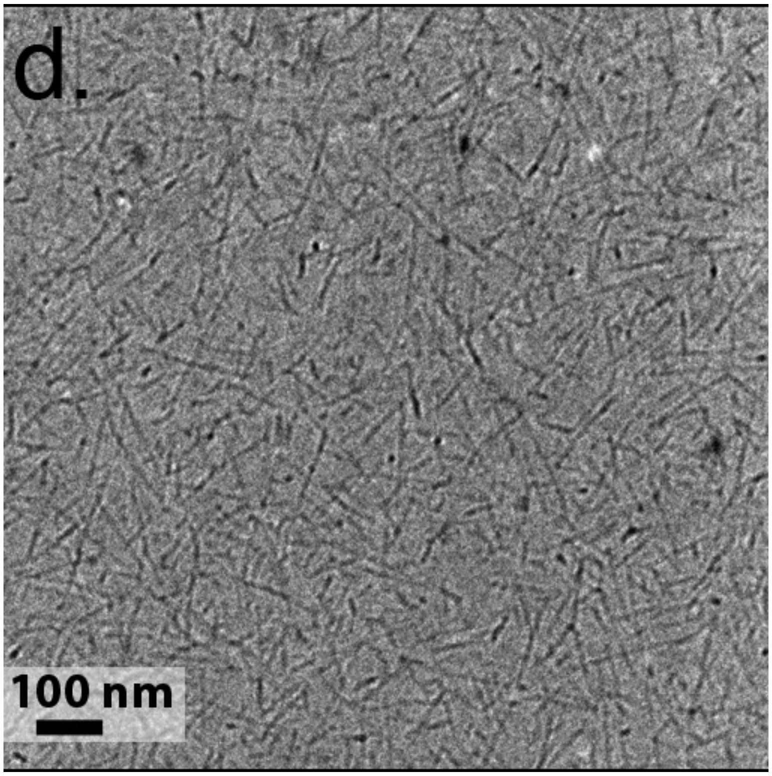

Figure 6d presented at a larger size.

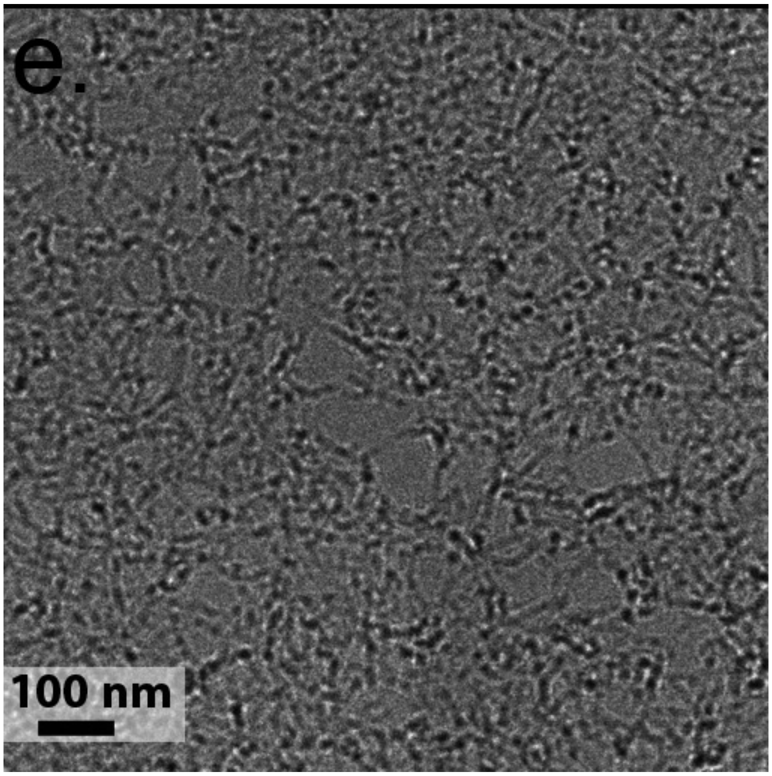

Figure 6e presented at a larger size.

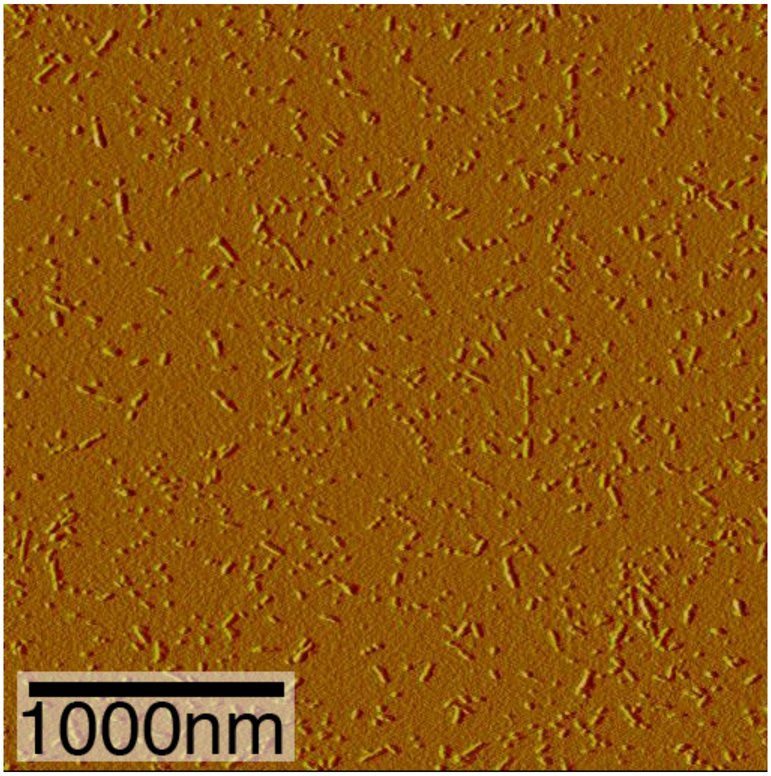

Figure S2. AFM of peptide $K_2(QL)_6K_2$ under non-gelling conditions (no phosphate anion and low ionic strength).

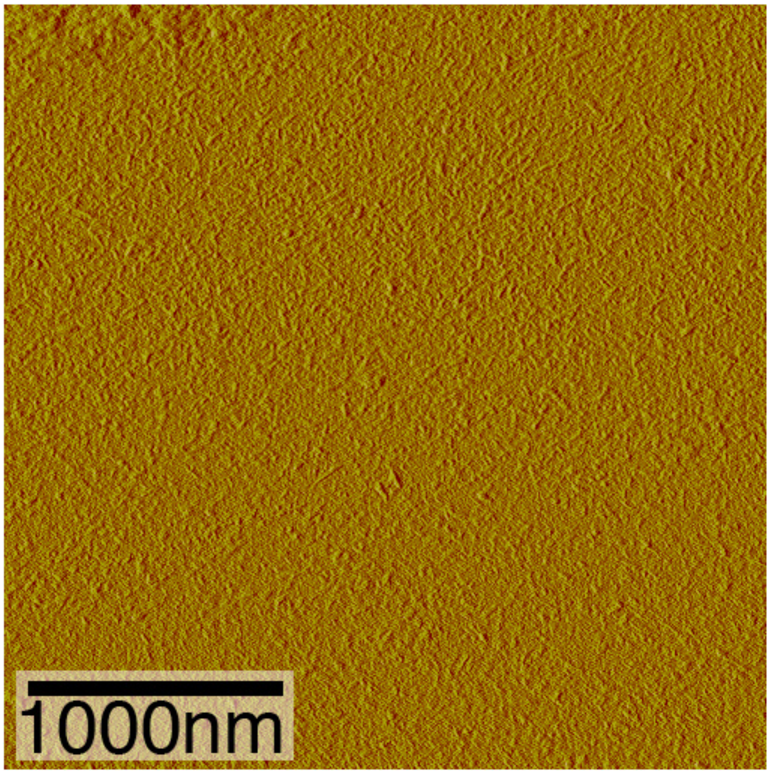

Figure S3. AFM of peptide $K_2(QFQL)_3K_2$ under non-gelling conditions (no phosphate anion and low ionic strength).

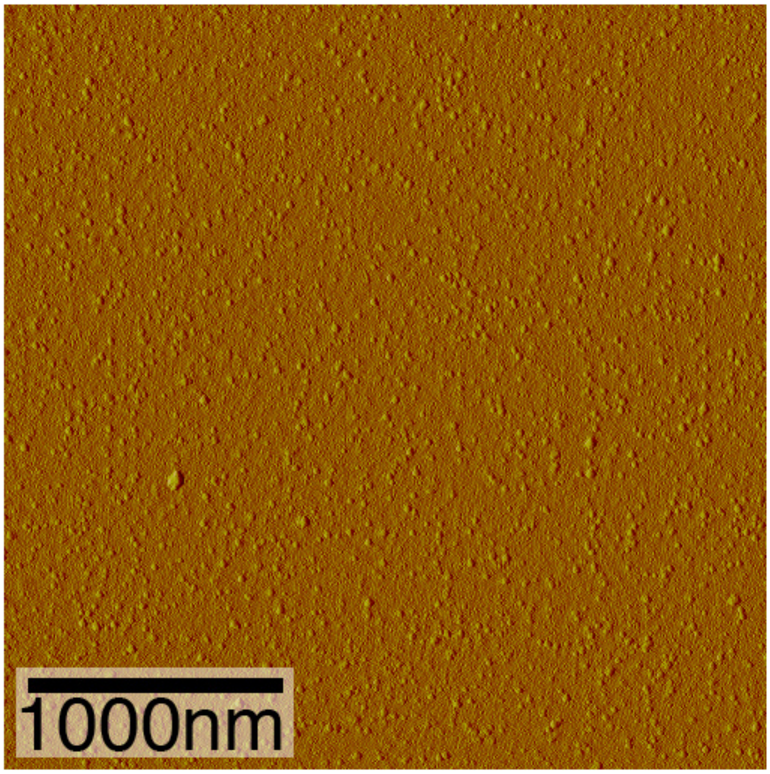

Figure S4. AFM of peptide $K_2(QF)_6K_2$ under non-gelling conditions (no phosphate anion and low ionic strength).

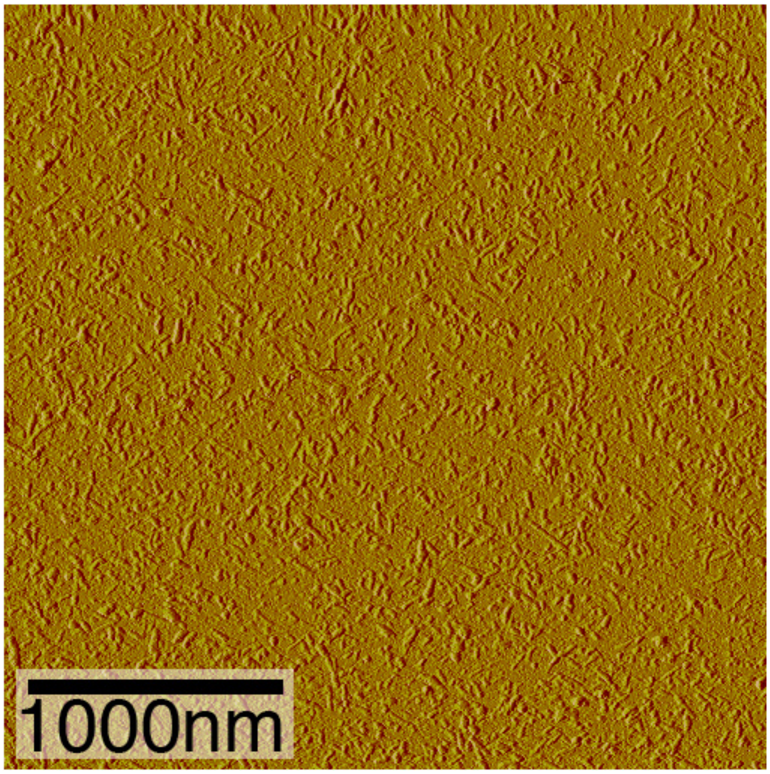

Figure S5. AFM of peptide $K_2(QW)_6K_2$ under non-gelling conditions (no phosphate anion and low ionic strength).

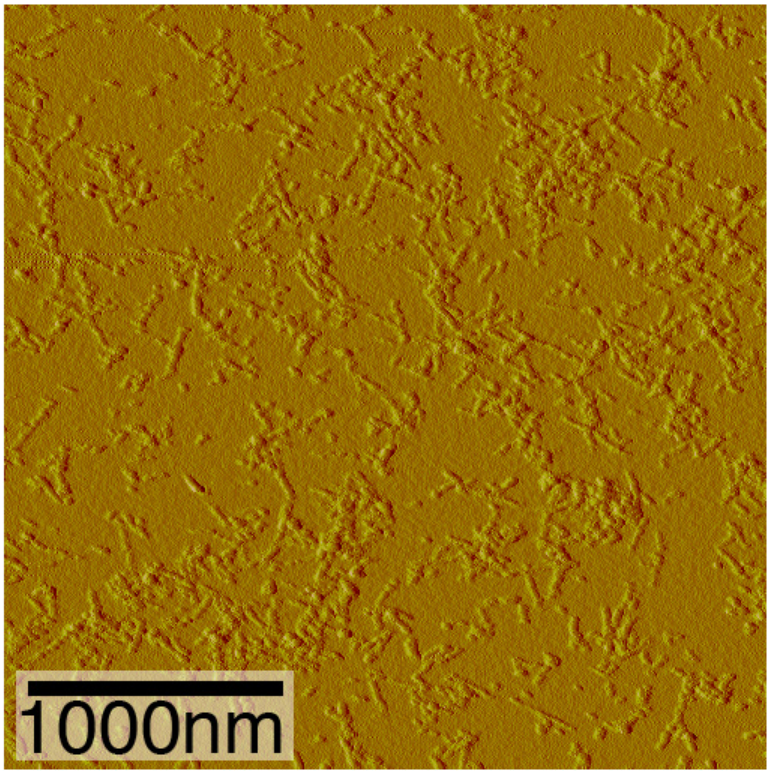

Figure S6. AFM of peptide $K_2(QY)_6K_2$ under non-gelling conditions (no phosphate anion and low ionic strength).

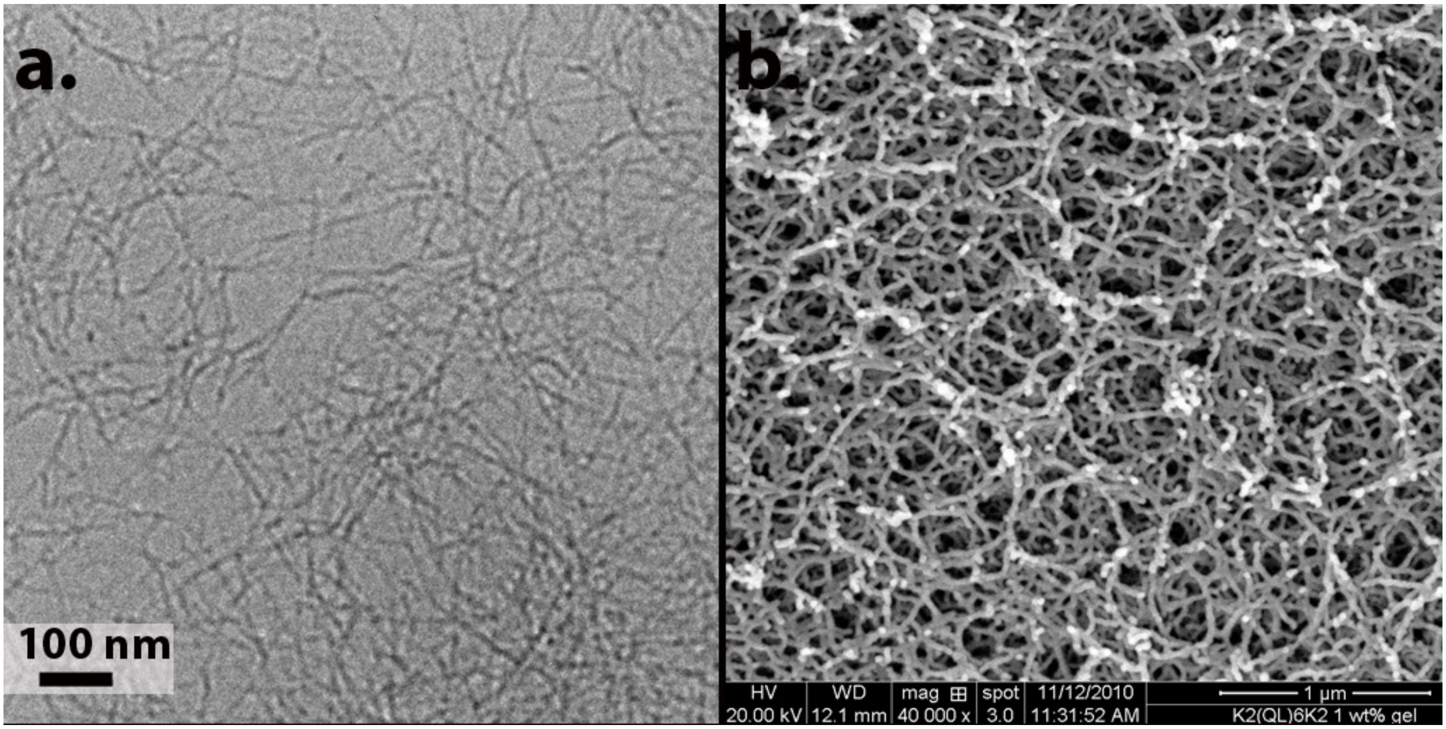

Figure 7a and 7b presented at a larger size.

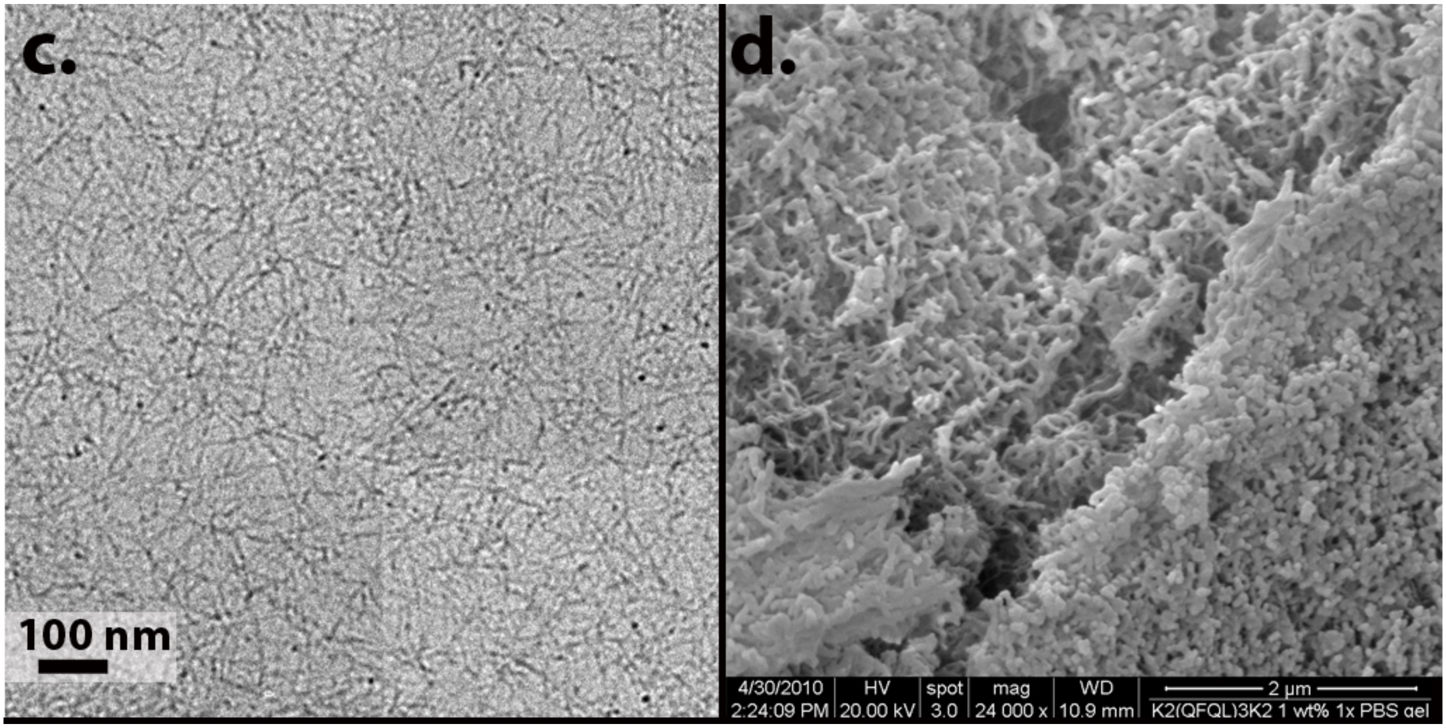

Figure 7c and 7d presented at a larger size.

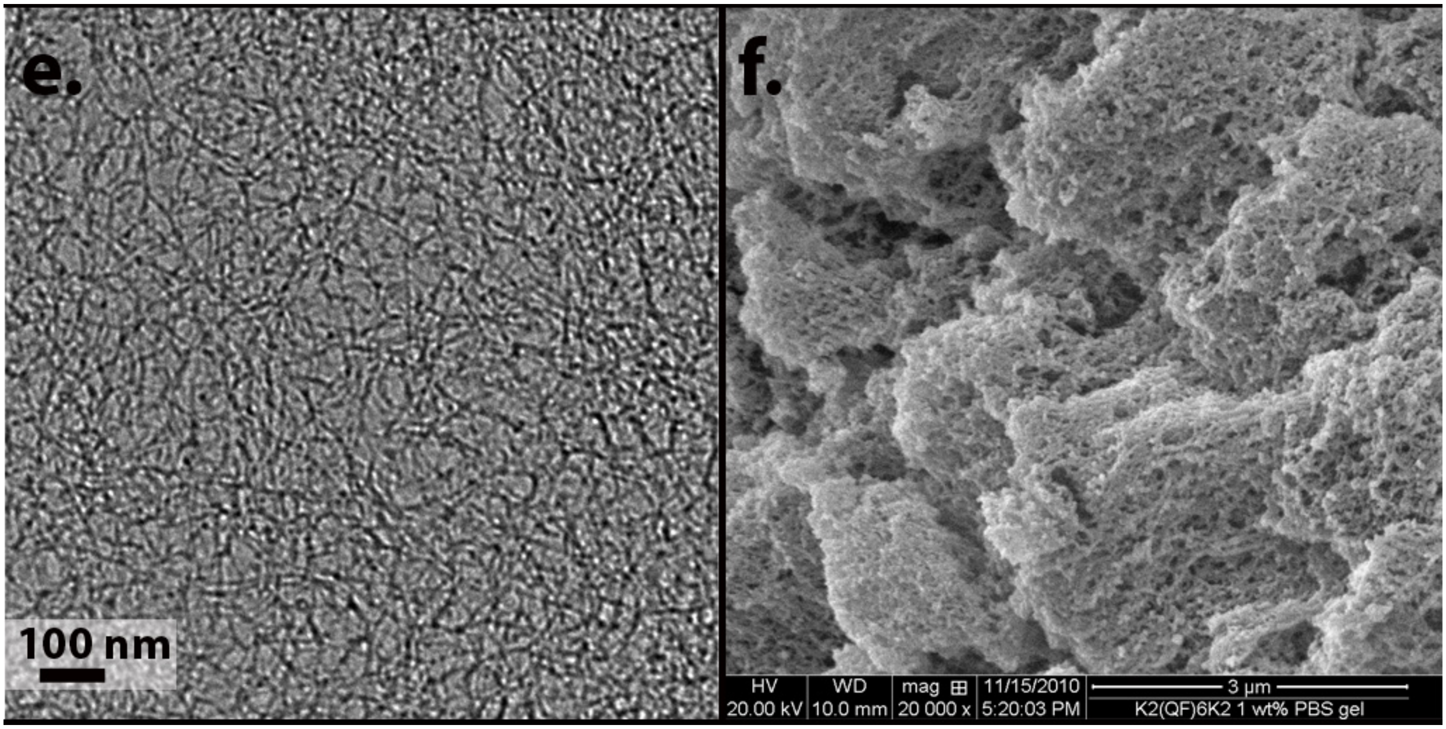

Figure 7e and 7f presented at a larger size.

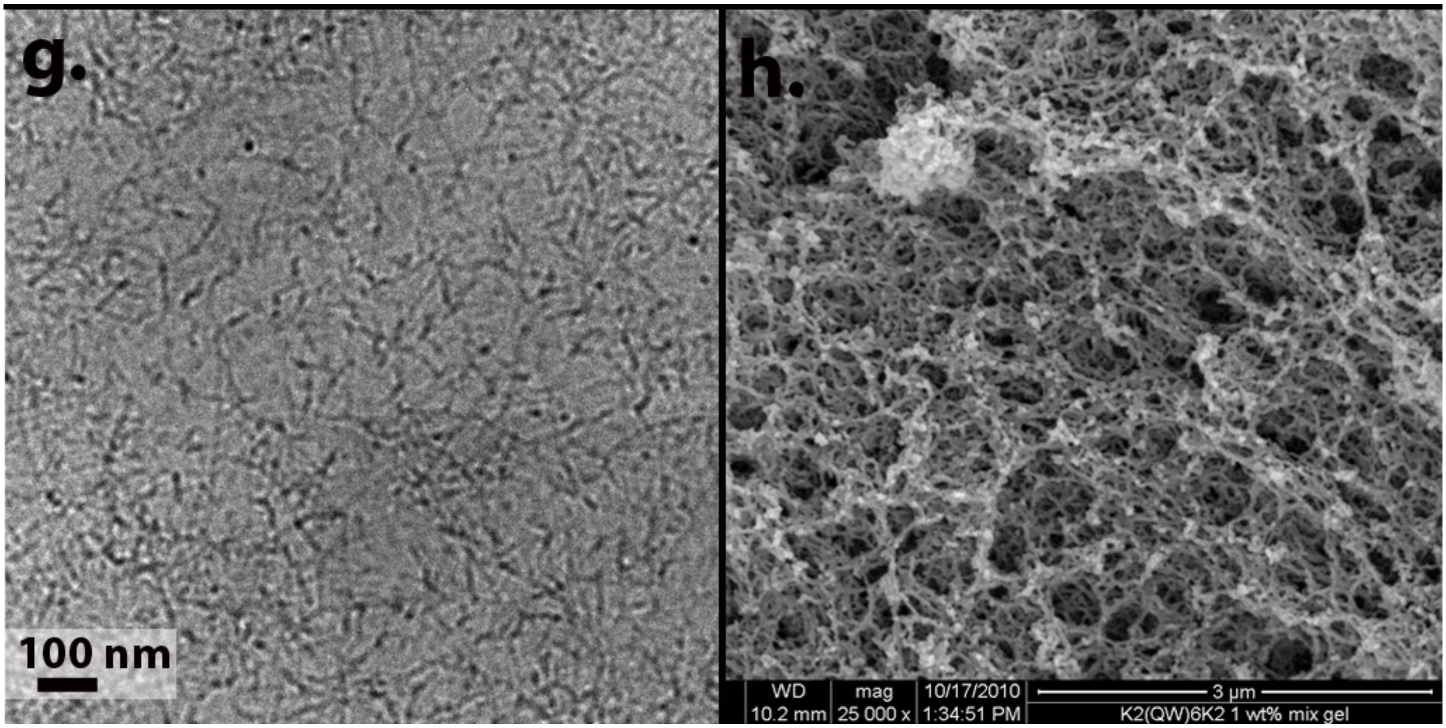

Figure 7g and 7h presented at a larger size.

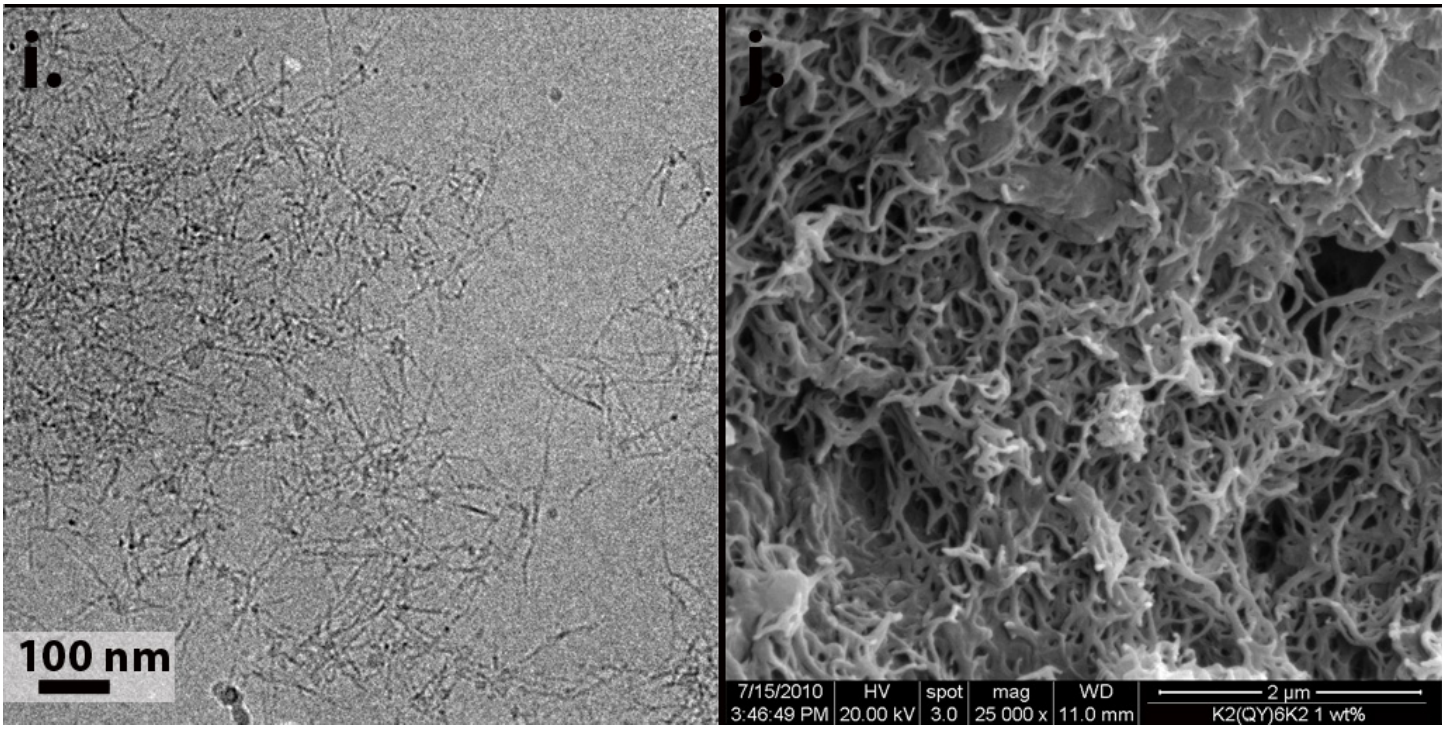

Figure 7i and 7j presented at a larger size.

Assignments from Grazing Angle FT-IR deconvolution.

peak #	approximate position	assignment
1	1695 cm^{-1}	Amide I perpendicular; characteristic of anti-parallel β-sheets
2	1675 cm^{-1}	contribution from lysine side chain
3	1654 cm^{-1}	contribution from glutamine side chain
4	1625 cm^{-1}	Amide I parallel; characteristic of β-sheet
5	1612 cm^{-1}	Amide I parallel; characteristic of extended fiber-like β-sheets
6	1547 cm^{-1}	Amide II
7	1520 cm^{-1}	Amide II

Table S1, peak assignments for deconvoluted grazing angle FT-IR spectra. Frequencies given are approximate and vary by several wave numbers depending on the individual peptide analyzed. Exact Values in table S2.

IR Peak	QL	QFQL	QF	QW	QY
1	1695	1695	1698	-	1696
2	1675	1669	1675	1687	1687
3	1654	1652	1661	1663	1657
4	1625	1625	1628	1632	1625
5	1612	1610	1618	1620	1608
6	1547	1548	1548	1554	1545
7	1521	1519	1517	1530	1516

Table S2. Exact values of decovoluted peaks given in wave numbers, cm^{-1}.