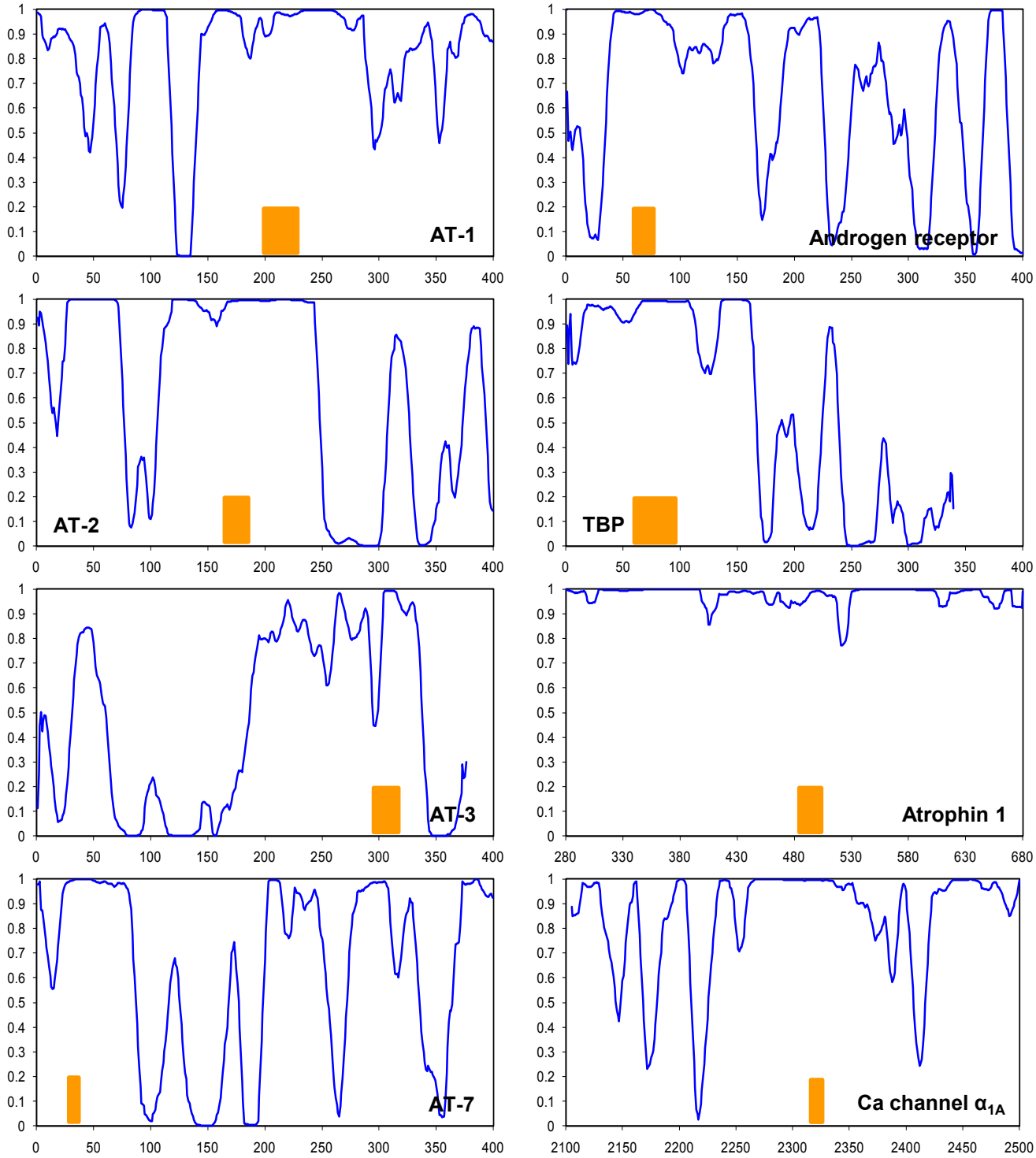
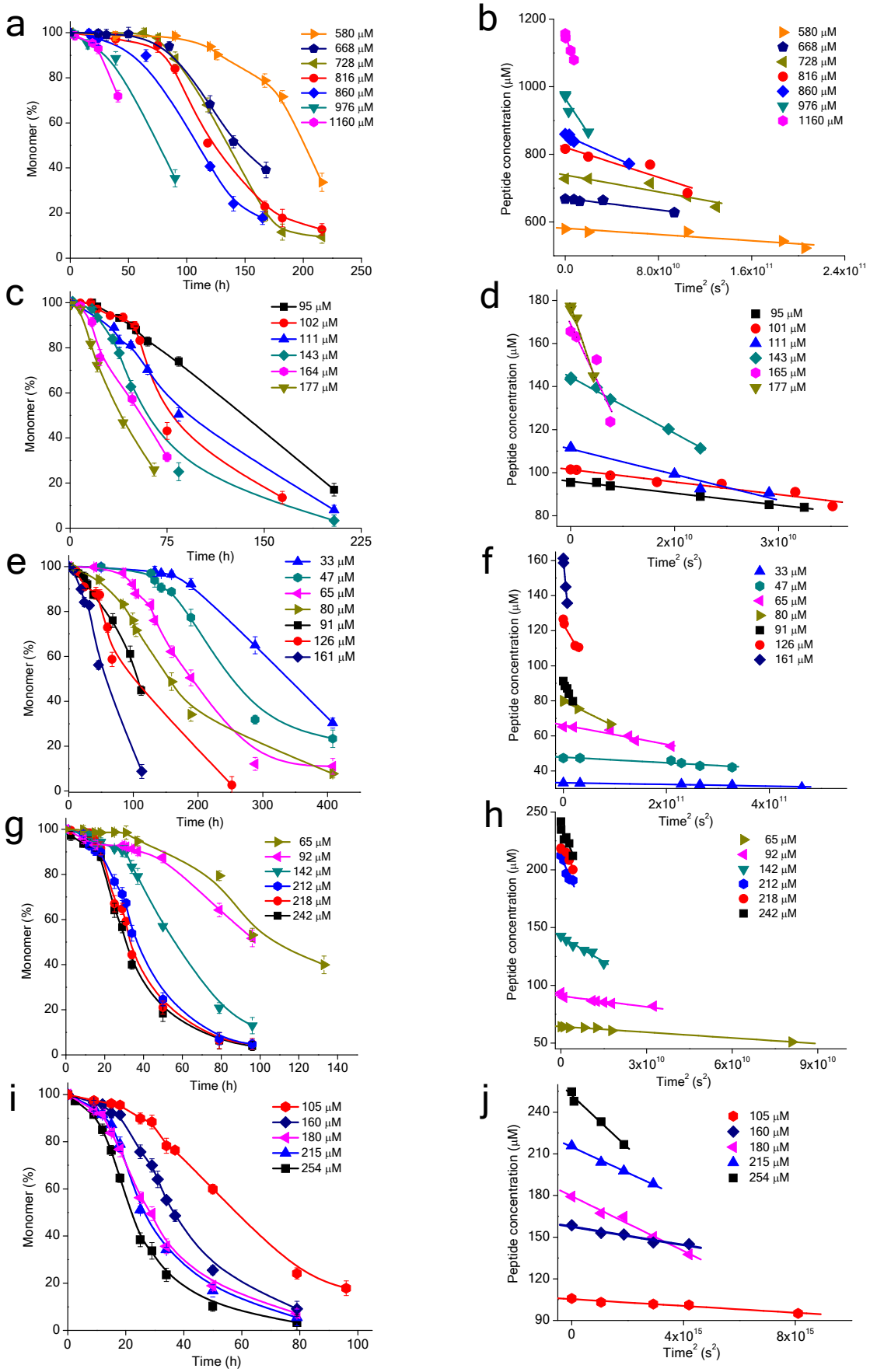
Name or identifier	Sequence
$K_2Q_{18}K_2$, Q_{18}	KKQQQQQQQQQQQQQQQQQQKK
$K_2Q_{23}K_2$, Q_{23}	KKQQQQQQQQQQQQQQQQQQQQQQQKK
$K_2Q_{24}K_2$, Q_{24}	KKQQQQQQQQQQQQQQQQQQQQQQQQKK
$K_2Q_{25}K_2$, Q_{25}	KKQQQQQQQQQQQQQQQQQQQQQQQQQKK
$K_2Q_{26}K_2$, Q_{26}	KKQQQQQQQQQQQQQQQQQQQQQQQQQQKK
$K_2Q_{27}K_2$, Q_{27}	KKQQQQQQQQQQQQQQQQQQQQQQQQQQQKK
$K_2Q_{30}K_2$, Q_{30}	KKQQQQQQQQQQQQQQQQQQQQQQQQQQQQQKK
$K_2Q_{37}K_2$, Q_{37}	KKQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQKK
$SFQ_{37}P_{10}K_2$	SFQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQPPPPPPPPPPKK
$htt^{NT}Q_{37}P_{10}K_2$	MATLEKLMKAFESLKSFQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQPPPPPPPPPPKK
$AT7^{NT}Q_{30}K_2$	MSERAADDVRGEPRRAAAAAGGAAAAAARQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQKK
biotinyl-$K_2Q_{29}K_2$	biotinyl-KKQQQQQQQQQQQQQQQQQQQQQQQQQQQQQKK

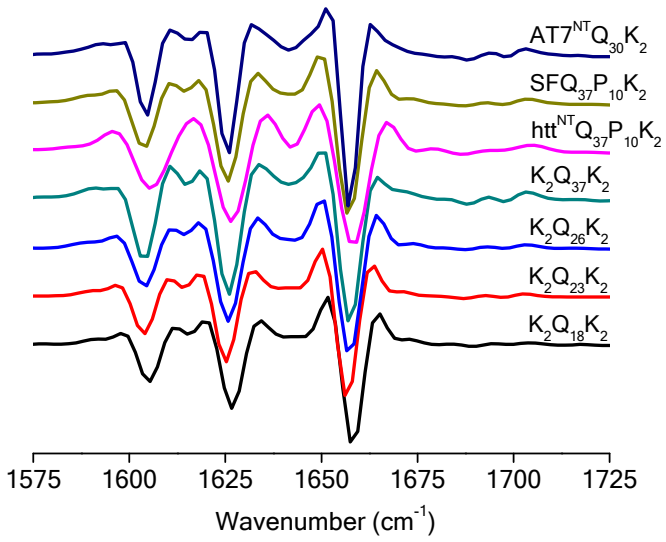
Supplementary Figure 1. Peptide sequences studied discussed in this paper.



Supplementary Figure 2. PONDR plots for the 400 amino acid residues containing the polyQ sequence (orange blocks) of the nine expanded CAG repeat disease proteins. Protein sequences begin at amino acid #1 except for atrophin 1, huntingtin, and the Ca channel α_{1A}. Sequences shown for AT3 and TBP are of the complete protein; all others are fragments. Values less than 0.5 tend to be ordered; values greater than 0.5, disordered. Values calculated using the VX-LT version (copyright©1999 WSU Research Foundation, all rights reserved) of PONDR® (copyright©2004 Molecular Kinetics, all rights reserved).



Supplementary Figure 3. Kinetics analysis of $K_2Q_NK_2$ polyQ peptides Q_{18} (a, b), Q_{24} (c, d), Q_{25} (e, f) Q_{26} (g, h), Q_{27} (i, j) plotted with respect to time (a, c, e, g, i) or time^2(b, d, f, h, j).



Supplementary Figure 4. Amide I frequency range of the second derivative FTIR spectra of isolated aggregates. The band near 1625 cm^{-1} is diagnostic of β-sheets (Jackson, M. & Mantsch, H.H., *Crit Rev Biochem Mol Biol* **30,** 95-120 (1995)) and the bands near 1605 cm-1 and 1660 cm-1 are associated with glutamine side chains (Venyaminov, S. & Kalnin, N.N., *Biopolymers* **30,** 1259-71 (1990)).

Supplementary Table 1. Membrane filtration test for aggregate formation[a]

Condition	$K_2Q_{37}K_2$	$K_2Q_{23}K_2$
A. Original PBS solution	25.1 µM	215.0 µM
B. After 20 nm filtration of A	25.5 ± 0.5 µM	214.9 ± 2.3 µM
C. After 37 ºC incubation of B	24.9 ± 0.6 µM	215.0 ± 1.1 µM
D. After 20 nm filtration of C	24.7 ± 0.8 µM	214.4 ± 2.0 µM

[a] After the standard disaggregation resulting in peptide dissolved in PBS, samples were filtered through a 20 nm filter (Methods) and the filtrate incubated at 37 ºC. After incubation ($K_2Q_{37}K_2$, 16 hrs; $K_2Q_{23}K_2$, 2 hrs), an aliquot was filtered again through the 20 nm filter. Quantitative analysis of polyQ for each sample before and after filtration was conducted by analytical HPLC (Methods). Comparing aggregate-free monomer concentration at t=0 (sample B) to aggregate-free monomer concentration after incubation (sample D) reveals the extent of formation of aggregates large enough to be trapped by the 20 nm filter. In both experiments, there is no significant aggregation over the incubation period tested.