



*Supplementary Materials*

# Aggregation Condition–Structure Relationship of Mouse Prion Protein Fibrils

Jēkabs Fridmanis <sup>1</sup>, Zigmantas Toleikis <sup>1,2</sup>, Tomas Sneideris <sup>2,†</sup>, Mantas Ziaunys <sup>2</sup>, Raitis Bobrovs <sup>1</sup>,  
Vytautas Smirnovas <sup>2</sup> and Kristaps Jaudzems <sup>1,\*</sup>

<sup>1</sup> Department of Physical Organic Chemistry, Latvian Institute of Organic Synthesis, Aizkraukles 21, LV-1006 Riga, Latvia; fridmanis.jekabs@osi.lv (J.F.); zigmantas.toleikis@gmc.vu.lt (Z.T.); raitis.bobrovs@osi.lv (R.B.)

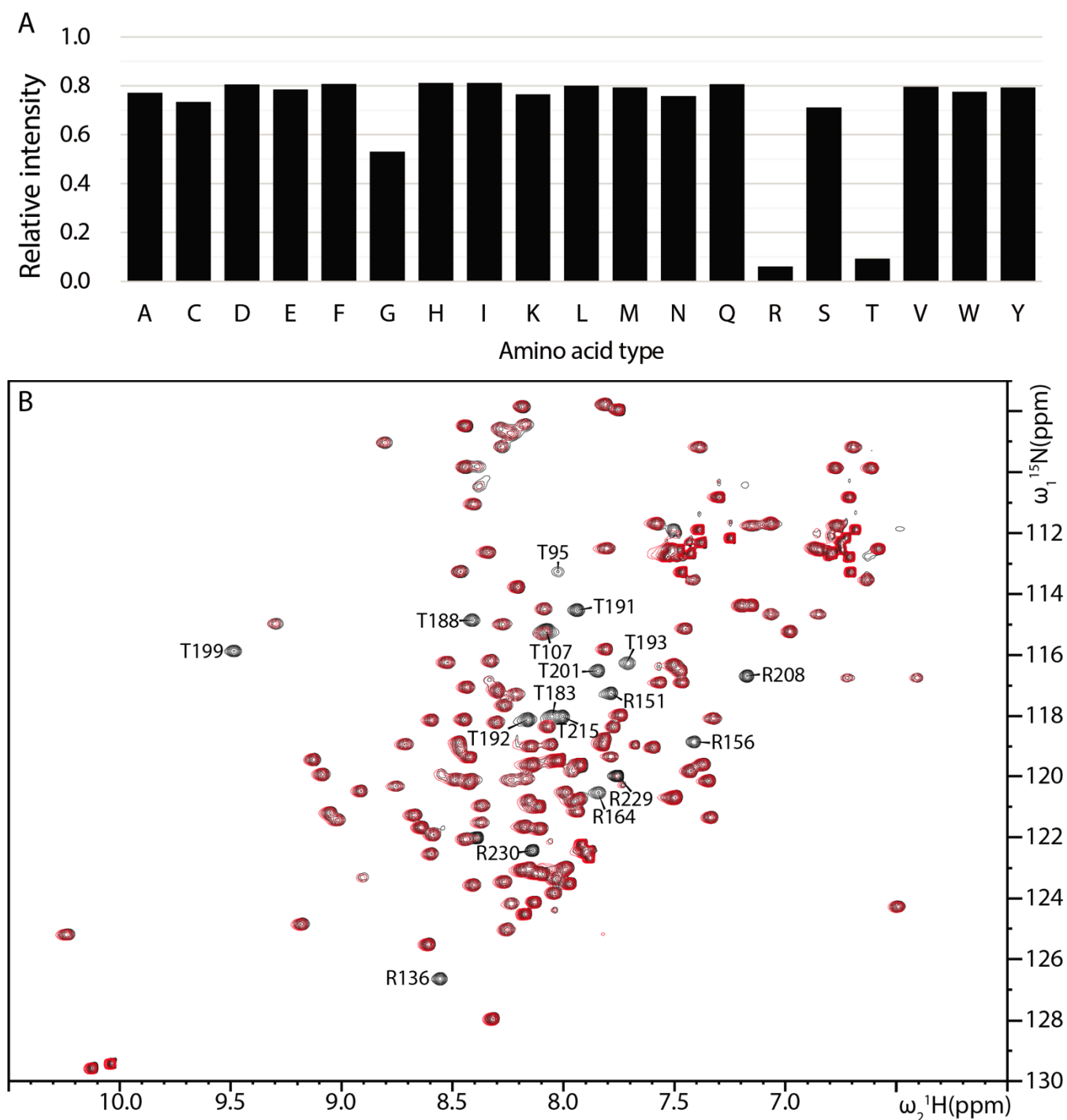
<sup>2</sup> Institute of Biotechnology, Life Sciences Center, Vilnius University, LT-10257 Vilnius, Lithuania; sneideris.t@gmail.com (T.S.); mantas.ziaunys@gmc.vu.lt (M.Z.); vytautas.smirnovas@bti.vu.lt (V.S.)

\* Correspondence: kristaps.jaudzems@osi.lv

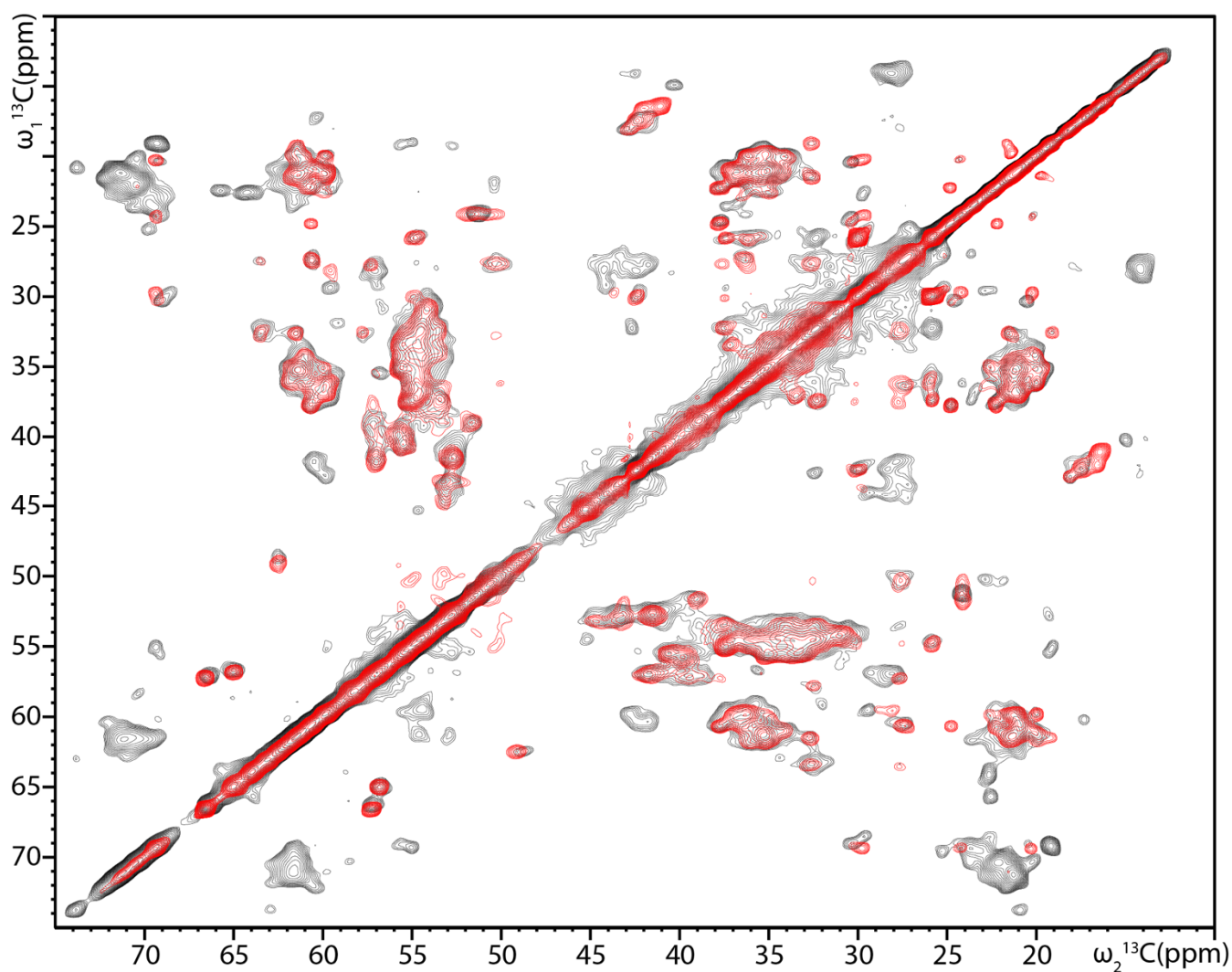
† Present Address: Yusuf Hamied Department of Chemistry, University of Cambridge, Cambridge CB2 1EW, UK.

## Table of Contents

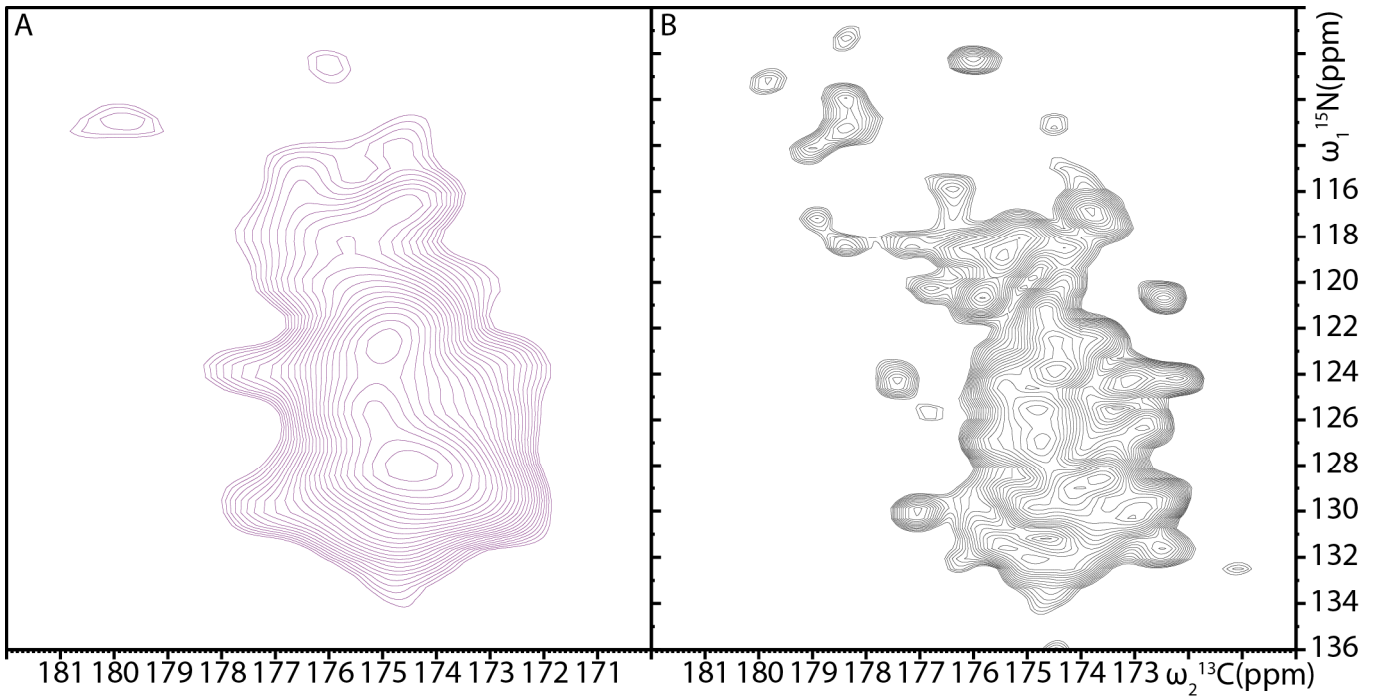
Figure S1.....	2
Figure S2.....	3
Figure S3.....	4
Figure S4.....	5
Figure S5.....	6
Figure S6.....	7
Table S1.....	8
Table S2.....	9
Table S3.....	10
Table S4.....	11



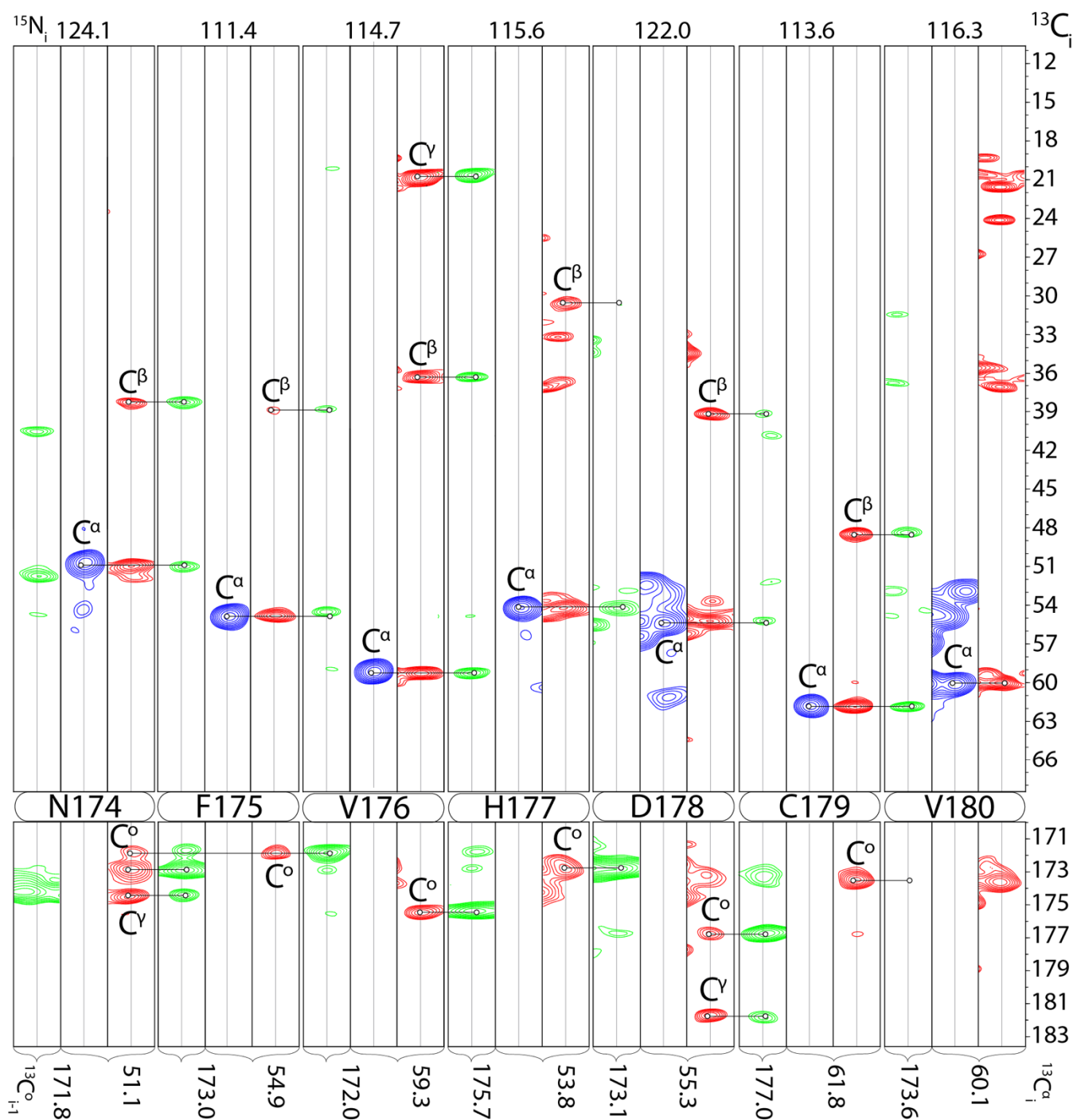
**Figure S1.** Amino acid-selective unlabeled of MoPrP(89-230) analyzed by solution NMR. **(A)** Average peak intensities of each amino acid residue type in  $^{15}\text{N}$ - $^1\text{H}$  HSQC spectra of MoPrP(89-230) samples selectively unlabeled by adding 0.2 g of natural abundance Arg and Thr amino acids per liter of M9 medium relative to uniformly  $^{13}\text{C}$ ,  $^{15}\text{N}$ -labeled samples. **(B)** Overlay of  $^{15}\text{N}$ - $^1\text{H}$  HSQC spectra of fully  $^{13}\text{C}$ ,  $^{15}\text{N}$ -labeled (black) and Thr-, Arg-selectively unlabeled (red) MoPrP(90-230) samples.



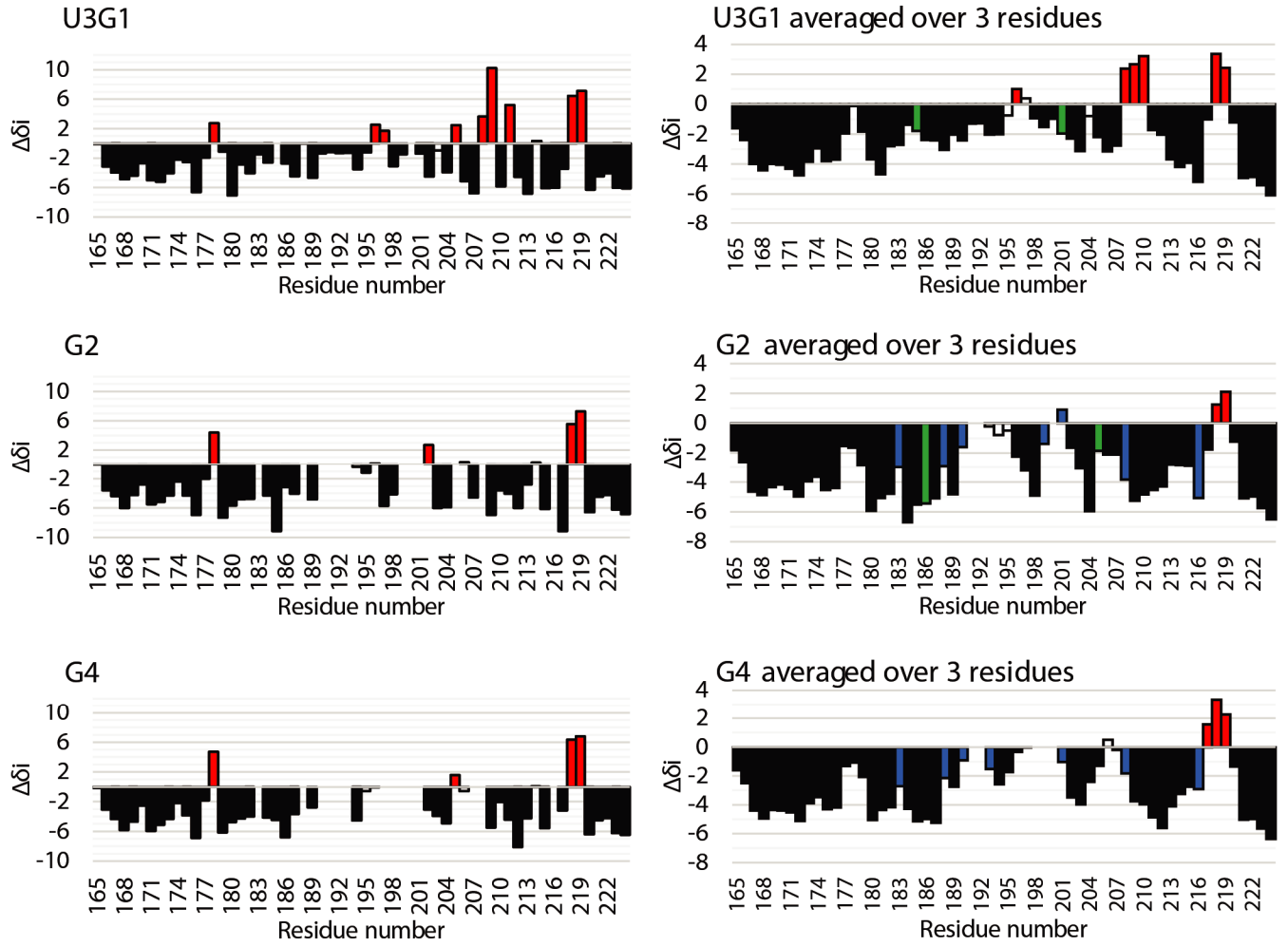
**Figure S2.** Amino acid-selective unlabeled of MoPrP(89-230) analyzed by solid-state NMR. Overlay of 2D DARR MAS NMR spectra of U3G1 fibrils prepared from fully  $^{13}\text{C}$ ,  $^{15}\text{N}$ -labeled (black) and Thr-, Arg-selectively unlabeled (red) MoPrP(90-230) samples. The spectra were recorded at 800 MHz at 273 K with 17 kHz MAS.



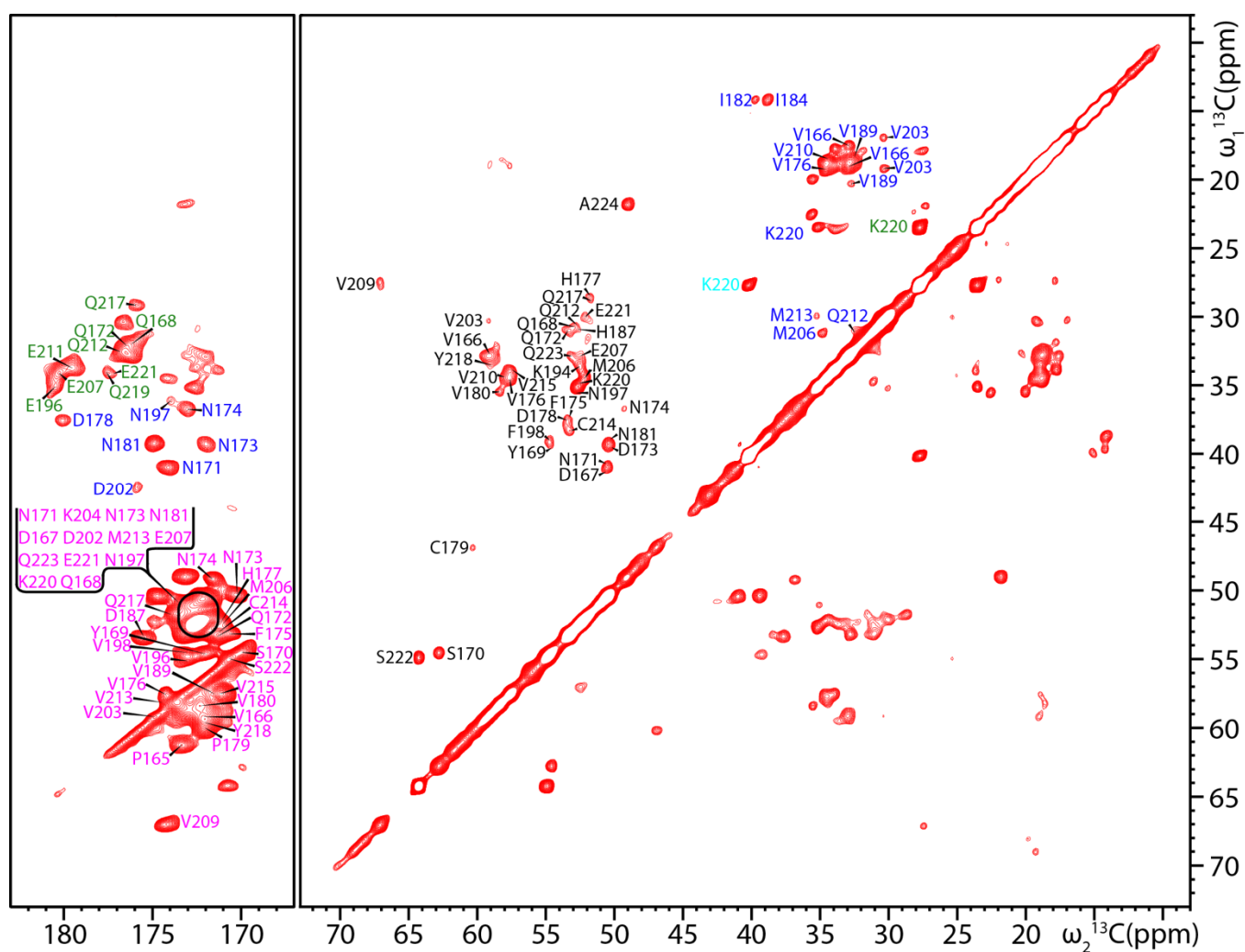
**Figure S3.** Comparison of spontaneously aggregated and sixth-generation reseeded fully  $^{13}\text{C}$ ,  $^{15}\text{N}$ -labeled MoPrP(89-230) U3G1 condition fibrils. **(A)** 2D NCO spectrum of spontaneously aggregated and **(B)** 2D NCO spectrum of sixth-generation fibrils.



**Figure S4.** Illustration of backbone assignment of MoPrP(89-230) G2 fibrils. Representative strip plot of NCACX (red), CANCO (blue), and NCOCX (green) spectra recorded at 800 MHz and 273 K with 12.5 kHz MAS, mixing time 65 ms (DARR).



**Figure S5.** Secondary chemical shift analysis of MoPrP(89-230) U3G1, G2 and G4 fibrils. Here  $\Delta\delta_i$  is calculated as  $(\Delta\delta C\alpha_i - \Delta\delta C\beta_i)$  on the left and as  $(\Delta\delta C\alpha_i - \Delta\delta C\beta_i) + (\Delta\delta C\alpha_{i-1} - \Delta\delta C\beta_{i-1}) + (\Delta\delta C\alpha_{i+1} - \Delta\delta C\beta_{i+1})$  on the right, where results are averaged over 3 residues. The one-residue values were used for determination of secondary structures for the assigned residues, whereas values calculated over three residues were used to predict the secondary structures for isolated unassigned residues.  $\Delta\delta_i$  values above 1 are indicative of alpha helix (red), and below -1 of beta sheet (black), whereas  $\Delta\delta_i$  values between -1 and 1 indicate non-regular structure (white). Selectively unlabeled residues are indicated with blue bars and residues with missing assignment are indicated with green bars.



**Figure S6.** Assigned 2D RFDR MAS NMR spectrum of Thr-, Arg-selectively unlabeled MoPrP(89-230) U3G1 fibrils. The spectra were recorded at 800 MHz and 273 K with 17 kHz MAS.

**Table S1.** Acquisition and processing parameters for the MAS NMR spectra of fully-labeled MoPrP(89-230) U3G1 fibrils.

Spectrum	MAS Freq. (kHz)	Dec. Field Ampl. (kHz)	Max Indirect Evolution (ms)	Rec. Delay (s)	Scans	Exp. Time	Window Function
2D $^{13}\text{C}$ - $^{13}\text{C}$ DARR (15 ms mixing)	17	83.3	9.9	2.5	32	18 h 15 min	60° shifted sine-bell squared
2D $^{13}\text{C}$ - $^{13}\text{C}$ RFDR (1.6 ms mixing)	17	83.3	7.7	2.5	32	13 h 56 min	60° shifted sine-bell squared
2D C(HH)C (0.3 ms mixing)	17	83.3	5.5	2.3	64	33 h 26 min	60° shifted sine-bell squared
2D NCO	12.5	72.0	14.1	2	64	2 h 18 min	60° shifted sine-bell squared
2D NCA	12.5	72.0	10.6	2	64	1 h 43 min	60° shifted sine-bell
3D CONCA	12.5	72.0	5.9 (CO) 5.3 (N)	2.5	64	28 h 4 min	90° shifted sine-bell
3D NCOCX (65 ms mixing)	12.5	72.0	9.2 (N) 10.8 (CO)	2	192	257 h 33 min	90° shifted sine-bell squared
3D NCACX (65 ms mixing)	12.5	72.0	7.9 (N) 3.9 (CA)	2.5	192	228 h 58 min	90° shifted sine-bell
3D CANCO	12.5	72.0	3.9 (CA) 7.9 (N)	2.5	64	74 h 32 min	90° shifted sine-bell



**Table S2.** Acquisition and processing parameters for the MAS NMR spectra of Thr-, Arg-selectively-unlabeled MoPrP(89-230) U3G1 fibrils.

Spectrum	MAS Freq. (kHz)	Dec. Field Ampl. (kHz)	Max Indirect Evolution (ms)	Rec. Delay (s)	Scans	Exp. Time	Window Function
2D $^{13}\text{C}$ - $^{13}\text{C}$ DARR (15 ms mixing)	17	83.3	7.7	2.5	32	14 h 8 min	60° shifted sine-bell squared
2D $^{13}\text{C}$ - $^{13}\text{C}$ RFDR (1.6 ms mixing)	17	83.3	7.7	2.5	32	13 h 56 min	60° shifted sine-bell squared
2D C(HH)C (0.3 ms mixing)	17	83.3	7.7	2.5	256	112 h 26 min	60° shifted sine-bell squared
2D NCO	12.5	72.0	14.1	2	128	4 h 37 min	60° shifted sine-bell squared
2D NCA	12.5	72.0	14.1	2	128	4 h 37 min	60° shifted sine-bell
3D CONCA	12.5	72.0	5.9 (CO) 5.3 (N)	2.5	320	140 h 20 min	90° shifted sine-bell
3D NCOCX (65 ms mixing)	12.5	72.0	10.6 (N) 10.8 (CO)	2	256	343 h 24 min	90° shifted sine-bell squared
3D NCACX (65 ms mixing)	12.5	72.0	7.9 (N) 3.9 (CA)	2.5	192	228 h 57 min	90° shifted sine-bell
3D CANCO	12.5	72.0	3.9 (CA) 7.9 (N)	2.5	192	223 h 30 min	90° shifted sine-bell

**Table S3.** Acquisition and processing parameters for the MAS NMR spectra of Thr-, Arg-selectively-unlabeled MoPrP(89-230) G2 fibrils.

Spectrum	MAS Freq. (kHz)	Dec. Field Ampl. (kHz)	Max Indirect Evolution (ms)	Rec. Delay (s)	Scans	Exp. Time	Window Function
2D $^{13}\text{C}$ - $^{13}\text{C}$ DARR (15 ms mixing)	17	83.3	7.7	2.5	32	14 h 8 min	60° shifted sine-bell squared
2D $^{13}\text{C}$ - $^{13}\text{C}$ RFDR (1.6 ms mixing)	17	83.3	7.7	2.5	32	13 h 56 min	60° shifted sine-bell squared
2D C(HH)C (0.3 ms mixing)	17	83.3	7.7	2.5	384	168 h 40 min	60° shifted sine-bell squared
2D NCO	12.5	72.0	14.1	2	128	4 h 37 min	60° shifted sine-bell squared
2D NCA	12.5	72.0	14.1	2	64	2 h 18 min	60° shifted sine-bell
3D CONCA	12.5	72.0	5.9 (CO) 5.3 (N)	2.5	64	28 h 4 min	90° shifted sine-bell
3D NCOCX (65 ms mixing)	12.5	72.0	10.6 (N) 10.8 (CO)	2	64	85 h 54 min	90° shifted sine-bell squared
3D NCACX (65 ms mixing)	12.5	72.0	7.9 (N) 3.9 (CA)	2.5	64	76 h 18 min	90° shifted sine-bell
3D CANCO	12.5	72.0	3.9 (CA) 7.9 (N)	2.5	64	74 h 32 min	90° shifted sine-bell

**Table S4.** Acquisition and processing parameters for the MAS NMR spectra of Thr-, Arg-selectively-unlabeled MoPrP(89-230) G4 fibrils.

Spectrum	MAS Freq. (kHz)	Dec. Field Ampl. (kHz)	Max Indirect Evolution (ms)	Rec. Delay (s)	Scans	Exp. Time	Window Function
2D $^{13}\text{C}$ - $^{13}\text{C}$ DARR (15 ms mixing)	17	83.3	7.7	2.5	64	28 h 17 min	60° shifted sine-bell squared
2D $^{13}\text{C}$ - $^{13}\text{C}$ RFDR (1.6 ms mixing)	17	83.3	7.7	2.5	32	13 h 56 min	60° shifted sine-bell squared
2D C(HH)C (0.3 ms mixing)	17	83.3	7.7	2.5	384	168 h 40 min	60° shifted sine-bell squared
2D NCO	12.5	72.0	14.1	2	64	2 h 18 min	60° shifted sine-bell squared
2D NCA	12.5	72.0	14.1	2	64	2 h 18 min	60° shifted sine-bell
3D CONCA	12.5	72.0	5.9 (CO) 5.3 (N)	2.5	128	56 h 7 min	90° shifted sine-bell
3D NCOCX (65 ms mixing)	12.5	72.0	10.6 (N) 10.8 (CO)	2	256	343 h 20 min	90° shifted sine-bell squared
3D NCACX (65 ms mixing)	12.5	72.0	7.9 (N) 3.9 (CA)	2.5	256	305 h 10 min	90° shifted sine-bell
3D CANCO	12.5	72.0	3.9 (CA) 7.9 (N)	2.5	128	149 h 52 min	90° shifted sine-bell