

Supplemental Information for

A Synchrotron-based Hydroxyl Radical Footprinting Analysis of Amyloid Fibrils and Pre-fibrillar Intermediates with Residue-specific Resolution

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Table S1. Modification rates for A β 40 fragments (units of s⁻¹).

Modified residue	Residue segment in which the modified residue was identified										
	4-10	10-17	11-19	20-33	21-31	21-33	21-34	24-34	34-40	35-40	36-40
F4	5.5										
Y10	5.5	9.4									
H13		4.6	4.7								
H14		5.7	5								
L17			4.5								
F19			6.2								
F20				4.5							
V24				5.1	4.8		4.9	5			
K28				11.3	11.5	10	8.2	10			
I31				7.5	7.9	7.7	7.2	7.1			
I32				8	7.6	7.5	7.6	7.1			
L34							6.9	5.4	3.4		
M35									10	19	
V36,V39,V40*									14.8		17.5

* Fragments containing three C-terminal valine residues were not chromatographically resolved.

Table S2. Modification rates for LWM A β 40 (units of s⁻¹).

Modified residue	Residue segment in which the modified residue was identified									
	4-19	4-17	10-19	11-19	1-17	20-33	20-34	21-34	34-40	35-40
F4	2				4.2					
Y10	3.1	3.1	2.3		3.7					
H13	2.1	3.2	2.3	2.3						
H14	2.1	3.4	3	3						
L17			2.7							
F19	2.4		3	2.3						
F20							4.1			
V24							4.7			
K28						1.5	1.2	1.7		
I31						6	5	6.5		
I32						1.41	0.45	0.47		
L34							1.2	0.55		
M35									12	
V36,V39,V40*									1.9	1.6

* Fragments containing three C-terminal valine residues were not chromatographically resolved.

Table S3. Modification rates for fibrillar A β 40 (units of s⁻¹).

Modified Residue	Residue segment in which the modified residue was identified									
	4-19	4-17	10-19	11-19	1-17	20-33	20-34	21-34	34-40	35-40
F4	1.06				1.6					
Y10	2	1.8	1.3		1.7					
H13	0.14	0.1	0.07	0.11						
H14	0.19	0.4	0.29	0.6						
L17			0.15							
F19	0.07		0.08	0.12						
F20							0.94			
V24							0.31			
K28						0.15	0.14	0.3		
I31						0.37	0.73	0.42		
I32						0.12	0.1	0.18		
L34							0.09	0.04		
M35									2.4	2.1
V36/39/40*									0.04	0.03

* Fragments containing three C-terminal valine residues were not chromatographically resolved.

Table S4. Propagation of error analysis for table 1

Residue	LMW				Fibril			
	PF*	range**	μ_{PF}^\dagger	σ^\ddagger	PF*	range**	μ_{PF}^\dagger	σ^\ddagger
F4	2	(1-4)	2	1.7	4	(3-6)	4	2
Y10	2	(1-4)	2	0.8	4	(2-7)	4	2
H13	2	(1-3)	2	0.5	40	(30-70)	50	24
H14	2	(1-3)	2	0.6	20	(10-30)	20	9
L17	2	--	2	0.5	30	--	30	9
F19	2	(2-3)	2	0.6	80	(70-90)	80	19
F20	2	(1-2)	2	0.9	7	(4-10)	8	4
V24	1	--	1	0.2	20	--	20	4
K28	7	(5-11)	8	2.2	60	(30-100)	70	52
I31	1	(1-2)	1	0.4	20	(10-30)	20	10
I32	10	(6-26)	13	12	60	(40-90)	60	26
L34	6	(3-15)	7	6.0	90	(40-200)	100	82
M35	1	(1-2)	1	0.6	6	(4-10)	7	3
V36/39/40	9	(7-12)	9	2.0	400	(400-800)	600	140

*Protection factor (PF) is defined as k_{frag}/k_{struct} where k_{frag} is the average rate of modification of the given residue in the predigested A β 40 and k_{struct} is the average rate of modification of the residue in LMW A β 40 or fibril A β 40 listed in Table 1.

**The ranges expected for PF's are estimated using the average (k) and standard deviation (σ) of the rates of modification for each amino acid side chain (Table 1). The low end of each range is given by $(k_{frag} - \sigma_{frag}) / (k_{struct} + \sigma_{struct})$ and the high end of the range by $(k_{frag} + \sigma_{frag}) / (k_{struct} - \sigma_{struct})$

†The expected value for the protection factor (μ_{PF}) was calculated using the expression derived for the expected value μ_R of a ratio $R=X/Y$,

$$\mu_R \cong \frac{\mu_X}{\mu_Y} (1 + CV_Y^2),$$

μ_X and μ_Y are the average modification rates, k_{frag} and k_{struct} , respectively and CV_Y is the coefficient of variability ($CV_Y = \sigma_Y / \mu_Y$).

††The standard deviation of the ratio $R=X/Y$ is

$$\sigma_R \cong \left(\frac{\mu_X}{\mu_Y} \right) \sqrt{CV_X^2 + CV_Y^2 + 3CV_Y^2 CV_X^2 + 8CV_Y^2}$$

as derived in (Holmes DT, Buhr KA. Error propagation in calculated ratios. *Clinical Biochemistry* 2007;40:728-734.

Figure S1. (a) Electron micrograph of LMW A β 40 spotted on a glow-discharged carbon-coated grid and negative stained with methylamine tungstate, showing the characteristic globular oligomeric forms. (b) Silver stained SDS-PAGE analysis of the same LMW preparation of A β 40 after PICUP. The band at the bottom is monomeric A β 40 (mwt = 4330), and the bands above it represent dimers and higher-order oligomers that are not observed in sham cross-linking experiments.

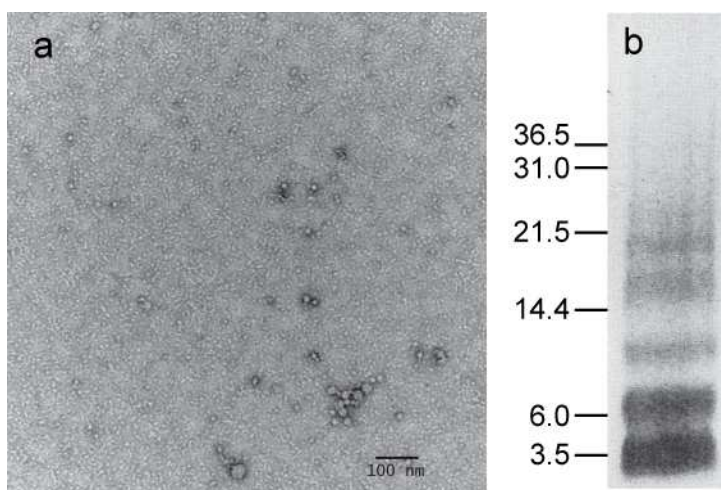


Figure S2. (a-c) Superimposed conformational isomers of full length A β 40 NMR models and d) A β (1-28) as deposited in the PDB files indicated. Side chains are shown for residues with experimentally determined protection factors.

