

Supplementary Information

Radically different amyloid conformations dictate the seeding specificity of a chimeric

Sup35 prion

Catherine K. Foo, Yumiko Ohhashi, Mark J. S. Kelly, Motomasa Tanaka, Jonathan S. Weissman

Correspondence should be addressed to J.S.W. (weissman@cmp.ucsf.edu).

Supplementary Methods

Assignment of Chimera spectrum. Sequence specific assignments of the backbone Hn and ^{15}N resonances were transferred from pre-existing assignments for corresponding SC residues²³ where possible. Verification of transferred assignments and new assignments were obtained by using the following 3D triple resonance experiments on uniformly labeled ^{13}C -, ^{15}N -Chimera: HNCO, HN(CA)CO, CBCA(CO)NH, HNCACB, HN(CA)NH, HNCA, HN(CO)CA. HNCO, HN(CA)CO, HNCA, and HN(CO)CA experiments used semi-constant time ^{15}N evolution and HNCA and HN(CO)CA additionally used constant time $^{13}\text{C}\alpha$ evolution to increase resolution^{30,31}. All spectra were recorded on Bruker Avance 800 MHz or DRX 500 MHz spectrometers equipped with cryoprobes with actively shielded Z gradients at 298K. All NMR spectra were processed with nmrPipe³² and assignments were performed using the program CcpNmr Analysis³³.

Supplementary References

- 30 Yamazaki, T. *et al.* (1994). An HNCA Pulse Scheme for the Backbone Assignment of ¹⁵N,¹³C,²H-Labeled Proteins: Application to a 37-kDa Trp Repressor-DNA Complex. *Journal of the American Chemical Society* **116**, 6464-6465.
- 31 Sun, Z.-Y. J., Frueh, D. P., Selenko, P., Hoch, J. C. & Wagner, G. (2005). Fast assignment of ¹⁵N-HSQC peaks using high-resolution 3D HNCocaNH experiments with non-uniform sampling. *J Biomol NMR* **33**, 43-50.
- 32 Delaglio, F. *et al.* (1995). NMRPipe: a multidimensional spectral processing system based on UNIX pipes. *J Biomol NMR* **6**, 277-293.
- 33 Vranken, W. F. *et al.* (2005). The CCPN data model for NMR spectroscopy: development of a software pipeline. *Proteins* **59**, 687-696.

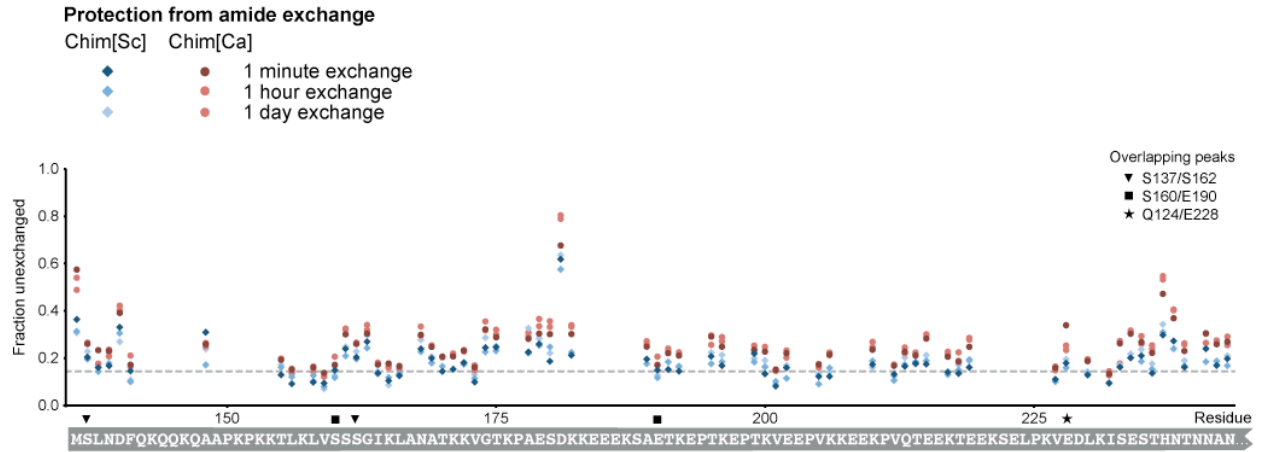


Figure S1. Protection from amide exchange for residues in the middle domain. Fractions unexchanged for Chimera residues 137-243 as described in the text.

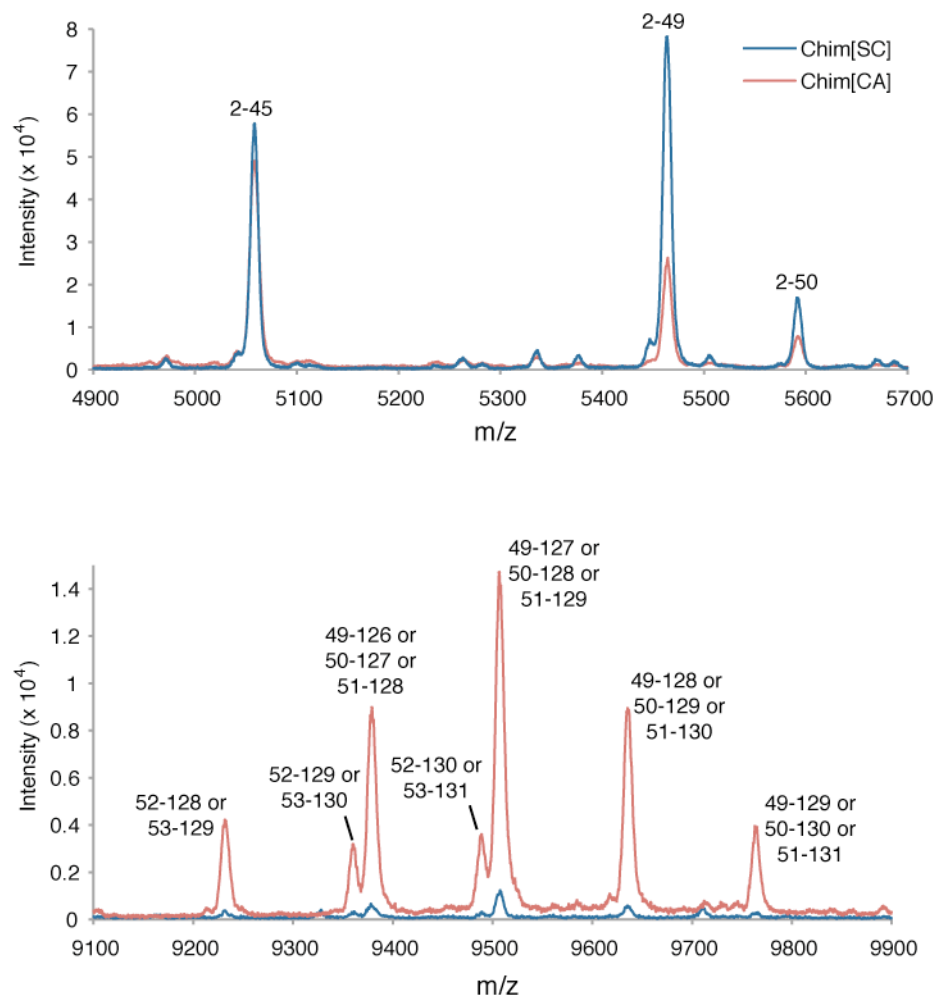


Figure S2. Limited proteolysis and MALDI-TOF MS. Shown here are the mass spectrometry data for proteolysis-resistant peptides from Chim[SC] and Chim[CA]. The peak for 2-50 is labeled here but due to the low intensity of the signal was not included in the schematic in Fig. 3b.