UV Resonance Raman Structural Characterization of an (In)soluble Polyglutamine Peptide

Supporting Information

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UVRR Curve-Fitting

Grams software (version 8.0, Thermo Fisher Scientific, Inc.) was used to model the Q20 UVRR spectra as a sum of Gaussian and Lorentzian bands:

$$f(x) = \sum_i (1-M)\left(He^{-(\frac{x-x_0}{w})^2(4\ln(2))}\right) + (M)\left(\frac{H}{4(\frac{x-x_0}{w})^2+1}\right) \qquad \text{S1}$$

where H is the peak height, x_0 is the center peak frequency, w is the full width at half height, M=1 if the band is Lorentzian, and M=0 if the band is Gaussian for the ith UVRR band. The $AmIII_3^S$ bands where modeled as Gaussians because they are inhomogenously broadened by the Ψ angle distribution of the peptide.[1]

Ramachandran Ψ Angle Calculation

Methodologies for determining the relationship between the $AmIII_3^S$ frequency and Ψ angle are reported by Mikhonin et al.[2] The procedure used to determine the Ψ angle distribution from the inhomogeneous width of the $AmIII_3^S$ band was previously reported by Asher et al.[1] We assume that the inhomogeneous broadening of the $AmIII_3^S$ band results from only the Ψ angle distribution of the peptide. The Gaussian $AmIII_3^S$ bands where modeled as a sum of Lorentzian bands with identical homogenous linewidths:

$$AmIII_3^S = \frac{1}{\pi}\sum_i^M \frac{p_i\Gamma^2}{\Gamma^2+(v-v_i)^2} \qquad \text{S2}$$

where p_i is the probability that the ith band occurs at center frequency v_i and Γ is the homogenous linewidth of the $AmIII_3^S$ band. The $AmIII_3^S$ homogenous linewidth was previously estimated to be ~7.5 cm^{-1} for small crystalline peptides.[1] The Ψ angle for each Lorentzian band

was calculated using the appropriate equation derived by Mikhonin et al.[2] to obtain a Ψ angle distribution.

The following equation was developed by Mikhonin et al.[2] to calculate Ψ from the $AmIII_3^S$ frequency for a peptide backbone completely solvated by water:

$$v_i = 1256\ (cm^{-1}) - 54(cm^{-1})\sin(\Psi + 26) - 0.11(\frac{cm^{-1}}{°C})(T - T_0) \qquad S3$$

where v_i is the frequency of the ith Lorentzian band, T is the sample temperature (°C), and T_0 = 0^0C. We use this equation to calculate Ψ angles for the PPII and 2.5_1-helix conformations of DQ20 and the NDQ20 supernatant, which have peptide backbones that are completely solvated in water.

The following equation is used to calculate the Ψ angle distribution for a peptide backbone in an unknown solvation environment:

$$v_i = 1250\ (cm^{-1}) - 54(cm^{-1})\sin(\Psi + 26) - 0.06(\frac{cm^{-1}}{°C})(T - T_0) \qquad S4$$

where the variables are the same as discussed above for equation S3. This equation was used to calculate the Ψ angle distribution for the turn-like structures found in DQ20 where the peptide backbone can engage in either peptide-peptide and/or peptide-water hydrogen bonds.

To calculate the Ψ angle of Q20 powder and NDQ20 in water, we used the following equation by Mikhonin et al.[2] to calculate Ψ for crystalline peptides:

$$v_i = 1260\ (cm^{-1}) - 54(cm^{-1})\sin(\Psi + 26) \qquad S5$$

This equation is used to calculate the Ψ angle for solid, anhydrous peptides.

To calculate Ψ for NDQ20 fibrils, we use the equation developed by Mikhonin et al.[2] for anhydrous β-sheet and α-helix conformations.

$$v_i = 1239\ (cm^{-1}) - 54(cm^{-1})\sin(\Psi + 26) \quad \text{S6}$$

This equation is used for anhydrous peptide backbones involved peptide-peptide hydrogen bonding of canonical β-sheet and/or α-helical structures.

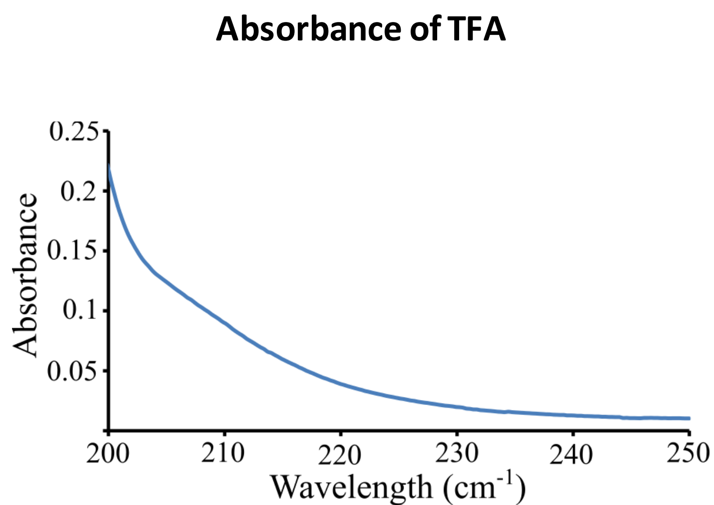

Figure S1: Absorbance spectrum of 1% (v/v) TFA in water.

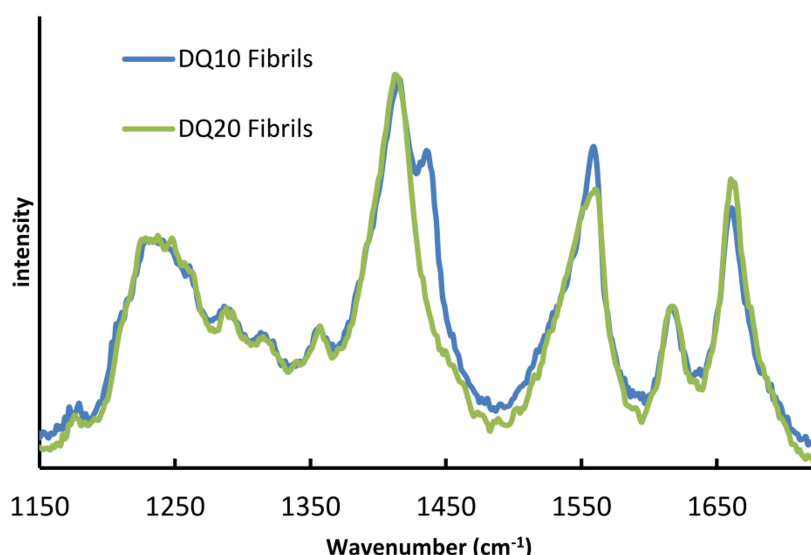

Figure S2: Comparison of 204 nm UVRR spectra of (blue) DQ10 fibrils and (green) DQ20 fibrils. The $AmIII_3^S$ and AmI spectral regions are similar indicating that DQ10 and DQ20 fibrils have similar secondary structure and hydrogen bonding interactions. The only significant difference between the two spectra is the presence of a strong band at ~1435 cm^{-1} in DQ10 fibrils that is not observed in DQ20 fibrils. This band has the same frequency as the C=O stretching band of TFA, which is strongly resonance enhanced at 204 nm excitation (see main text). It is possible that this band arises from TFA in the supernatant of the DQ10 fibrils. When the DQ20 fibrils were prepared they were washed three times with nanopure H_2O to remove any TFA in the supernatant. The UVRR spectrum of DQ10 fibrils was adapted with permission from Punihaole, D. (2016) J. Phys. Chem. B, 120(12), 3012-3026.[3]

References

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(3) Punihaole, D.; Workman, R. J.; Hong, Z.; Madura, J. D.; Asher, S. A. Polyglutamine Fibrils: New

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