Table 4. Average torsion angles in the NMR structure of TTR(105–115) in the fibrillar state

Residue	Angle	Angle, °*
Y105	ψ	163 ± 3
	χ^1	–80 ± 10
	χ^2	94 ± 16
T106	ϕ	–115 ± 10
	ψ	133 ± 5
	χ^1	–49 ± 6
I107	ϕ	–128 ± 12
	ψ	138 ± 1
	χ^1	–75 ± 2
	χ^2	163 ± 7
A108	ϕ	–123 ± 11
	ψ	130 ± 6
A109	ϕ	–131 ± 8
	ψ	126 ± 9
L110	ϕ	–119 ± 9
	ψ	124 ± 9
	χ^1	179 ± 4
	χ^2	59 ± 5
L111	ϕ	–120 ± 11
	ψ	120 ± 1
	χ^1	–60 ± 1
	χ^2	–177 ± 2
S112	ϕ	–115 ± 9
	ψ	106 ± 1
P113	ψ	140 ± 4

Residue	Angle	Angle, °*
Y114	ϕ	–124 ± 12
	ψ	138 ± 10
	χ^1	–112 ± 28
	χ^2	96 ± 18
S115	ϕ	–116 ± 76

All peptide bond torsion angles, ω, were within 2º of ω = 180º and are not listed. Torsion angles were evaluated by using MOLMOL (1).

1. Koradi, R., Billeter, M. & Wuthrich, K. (1996) *J. Mol. Graphics* **14,** 51–55.