

<b>NOE restraints</b>	80
Intra-residue	36
Sequential	23
Medium range ( $ i - j  \leq 4$ )	21
Long range ( $ i - j  > 4$ )	0
RMSD from experiment (Å)	$1.16 \pm 0.32$
<b>Structure statistics</b>	21 structures
<b>NOE violations</b>	
Average overall violation (Å)	$0.32 \pm 0.53$
Average intra-residue violation (Å)	$0.14 \pm 0.33$
Average sequential violation (Å)	$0.40 \pm 0.50$
Average medium range violation (Å)	$0.54 \pm 0.69$
<b>Ramachandran analysis</b>	
Most favored regions (%)	58.10
Additional allowed regions (%)	32.90
Generously allowed regions (%)	8.60
Disallowed regions (%)	0.50
<b>Average pairwise RMSD*</b>	
Overall (Å)	1.41
Secondary structure (residues 5-10) (Å)	0.83

Statistics obtained from AQUA3.2 and PROCHECK-NMR analyses.

\* RMSDs computed in UCSF Chimera.