Table 2. Structural statistics for EAS

Experimental input	Value
Total NOE restraints	1,623
Total unambiguous restraints	1,441
Intraresidue	747
Sequential	409
Medium range (2–4 residues)	59
Long range ($\geq$5 residues)	226
Total ambiguous restraints	182
Torsion angle constraints	
Dihedrals ϕ	63
Dihedrals ψ	27
Hydrogen-bond restraints (between residues 15–61, 59–17, 57–19, 62–79, 60–81)	10
Disulfide bond restraints (between residues 9–60, 18–54, 19–45, 61–80)	4
Quality control	
PROCHECK statistics: residues in most favored regions (residues 2–5,13–20,42–63,72-81)	82.5%
Residues in allowed regions	15.7%
Residues in generously allowed regions	1.3%
Residues in disallowed regions	0.5%
rms deviation of backbone atoms	
2–5,13–20,42–63,72-81	0.67 ± 0.14
2–20,42–63,72-81	0.79 ± 0.16
rms deviation of all heavy atoms	
2–5,13–20,42–63,72-81	1.00 ± 0.12
2–20,42–63,72-81	1.13 ± 0.16
Mean deviations from ideal geometry	
Bond lengths, Å	0.0035 ± 0.0001
Bond angles	0.42 ± 0.02°