Supplementary

Table S1. NMR restraints and structural statistics for RSV $P_{127-163}$ tetramer.

Number of structures	20
Number of NOE distance restrains per protomer	629
Unambiguous	285
Intra-residue	133
Sequential	155
Medium range	56
Inter-molecular	166
Ambiguous	166
Inter-molecular	166
Number of dihedral angle restraints	28Φ, 28Ψ
Violation statistics	
Distance violation/structure	
Unambiguous	
Viol > 0.5 Å	0.2 ± 0.9
Viol > 0.3 Å	10 ± 5
Ambiguous	
Viol > 0.5 Å	0.2 ± 0.9
Viol > 0.3 Å	6.0 ± 2.4
Dihedral angle violation/structure	
>5°	0
RMS of dihedral angle violation	0°
RMS deviation from ideal covalent geometry	
Number of close contacts	153
Bond angles	1.0°
Bond lengths	0.008 Å
Rmsd	
Backbone, all residues	1.39 Å
Heavy atoms all residues	1.73 Å
Backbone, ordered residues	0.4 Å
Heavy atoms, ordered residues	0.8 Å
Ramachandran plot summary from Procheck	
Most favored regions	99 %
Additionally allowed regions	1 %
Generously allowed regions	0 %
Disallowed regions	0 %