Supplementary Table 3

NMR and refinement statistics for protein structures	
	mRIPK1(BMRB 36547 , PDB 8IB0)
Inter-residue distances and dihedral angle constraints	
Distance restraints	
range ($\|i-j\|=2$)	66
range ($\|i-j\|\geq 3$)	28
Total dihedral angle restraints(phi/ psi)	30
Unambiguous intramolecular residues contacts	94
Ambiguous intramolecular residues contacts	29
Parallel intermolecular constraints	16
Structure statistics	
Violations (mean ± s.d.)	
Distance constraints (Å)	0
Dihedral-angle constraints (°)	0
Deviations from idealized geometry	
Bond lengths (Å)	0
Bond angles (°)	0
Average pairwise r.m.s. deviation (Å)[a]	
Backbone N, Cα, C′ (Å)	0.62
All atom (Å)	1.06

a: Average RMSD was generated using VMD (http://www.ks.uiuc.edu/Research/vmd).