Supplementary material:

Table 1: Templates selected for homology modeling of brinjal CC-NBS domains.

Template	Phyre	Modweb	(PS)^2	3D Jury	Swiss-Model	I-Tasser
1	1Z6T-A (12)	1Z6T-A (32)	2A5Y-B (12)	2A5Y-B (11)	none	1Z6TA (15)
2	2A5Y-B (14)	-	1Z6T-A (14)	2A5Y-B (10)	-	2A5YA (14)
3	1QVR-B (12)	-	2A5Y-C (15)	2A5Y-B (1)	-	2A5YB (14)

Values in the parenthesis show percentage identity with the template in the aligned region.

Table 2: Ramachandran plot calculations of non proline non glycine residues on 3D model of CC-NBS.

	I-TASEER		HOMMER		SPDBV	
	Number	%	Number	%	Number	%
Residue in most favoured regions	199	70.6	213	85.2	233	82.6
Residue in the additionally allowed zones	55	19.5	32	12.8	42	14.9
Residue in the generously regions	14	5	4	1.6	5	1.8
Residue in disallowed regions	14	5	1	0.4	2	0.7
Total non-glycine and non-proline residues	282	100	250	100	282	100
	ER* 2, gly15, proline 2, total 301.		ER2, gly 13, proline 0, total 265.		ER 2, gly 15, proline 2, total 301.	

*ER: end residues, gly: glycine