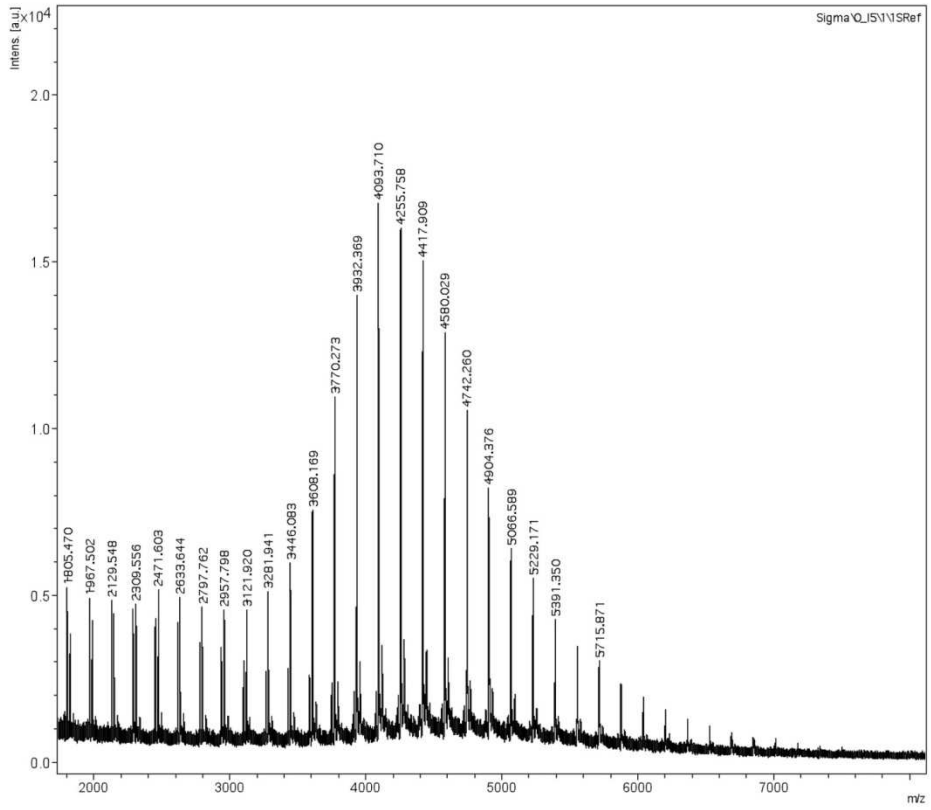
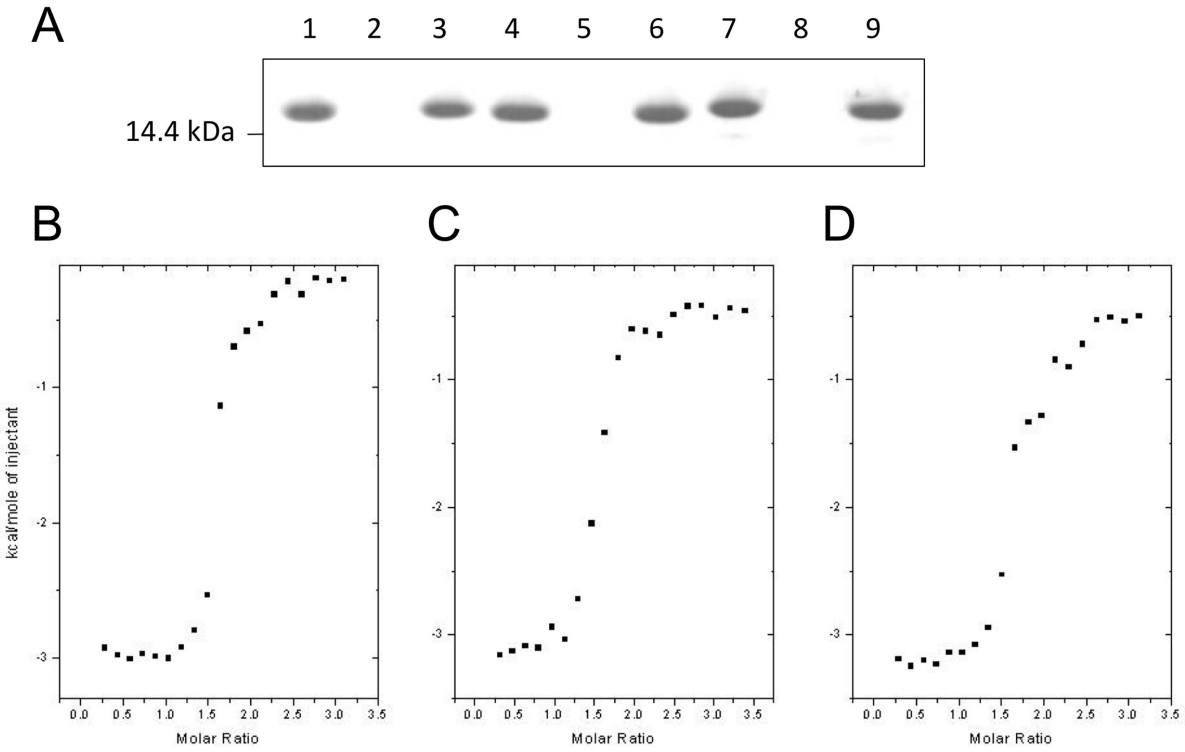
Supplementary Table 1. Statistics for a structural ensemble of 20 lowest-energy structures of *Plodia interpunctella* N-βGRP (residue 6-118).

Total constraints	1,584
NOEs	1,408
Intraresidue (|i-j| = 0)	98
Sequential (|i-j| = 1)	299
Medium-range (2 ≤ |i-j| ≤ 4)	167
Long-range (|i-j| > 4)	844
Dihedral constraints	106
Hydrogen bonds	35
Lennard-Jones potential energy (kcal/mol)	-192.0 ± 16.9
Number of violations	
NOE > 0.5Å	0
Dihedral > 5º	0
Coordinate precision (Å)	
Residues 6-118	
Backbone	1.62 ± 0.42
All non-hydrogen atoms	1.95 ± 0.37
Residues 7-106	
Backbone	0.51 ± 0.08
All non-hydrogen atoms	1.31 ± 0.11

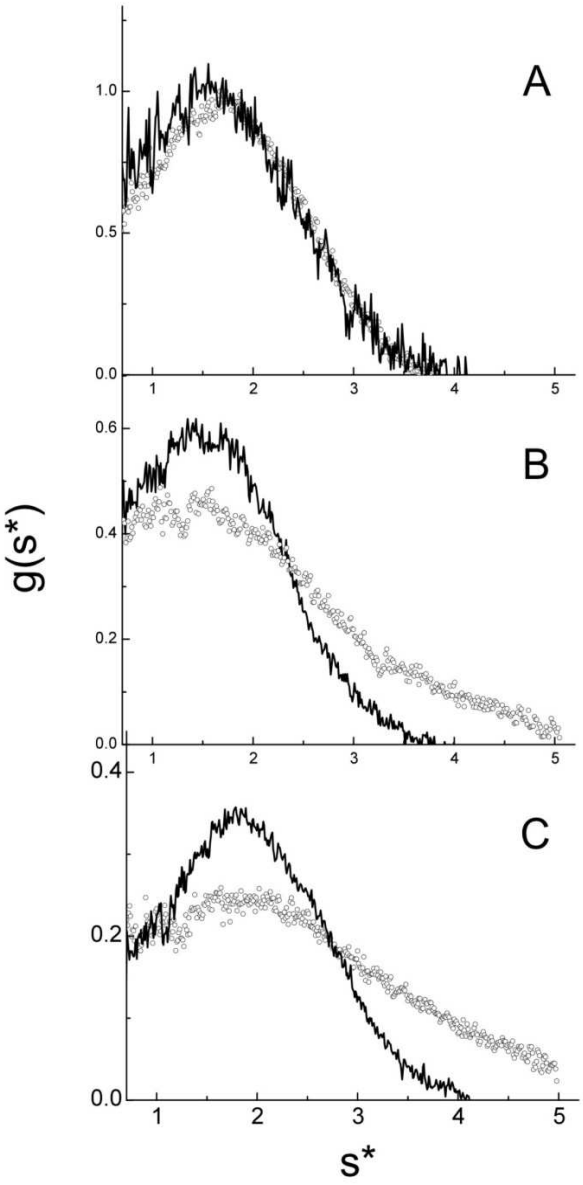
Supplementary Figure 1. MALDI mass spectrum of laminarin. The data were acquired on a Bruker Ultraflex II MALDI-TOF mass spectrometer (Bremen, Germany). 2,5-dihydroxybenzonic acid (DHB) was used as a matrix. The instrument was operated in a positive ion mode.



Supplementary Figure 2. β-1,3-glucan-binding activities of N-βGRP and mutants as measured by curdlan pull-down assay and isothermal titration calorimetry. (A) SDS-PAGE of purified recombinant N-βGRP proteins before and after co-precipitation with curdlan: purified wide type (lane 1), unbound (lane 2), and bound (lane 3); purified D45A mutant (lane 4), unbound (lane 5), and bound (lane 6); purified D45K mutant (lane 7), unbound (lane 8), and bound (lane 9). (B-D) Isothermal titration of laminarin with N-βGRP wild type (B), D45A (C) and D45K (D). The protein concentrations were ~78 μM and the ligand (injectant) concentration was 1.67 mM, in a buffer containing 50 mM Tris-HCl (pH 7.5) and 50 mM NaCl.



Supplementary Figure 3. $g(s^*)$ profiles of sedimentation velocity studies of N-βGRP in the presence of varying amounts of laminarihexaose. Panel A corresponds to 54 μM N-βGRP alone (solid line) and in the presence of 1mM laminarihexaose (dotted line); panel B to 234 μM N-βGRP alone (solid line) and in the presence of 14.1 mM laminalihexaose (dotted line); and panel C to 1.4 mM N-βGRP alone (solid line) and in the presence of 26 mM laminalihexaose (dotted line). Sedimentation experiments were performed at 49,000 rpm and 20°C, using absorption optics at 280 nm (A), 300 nm (B) and 308 nm (C). The shift of the dotted line toward higher s^* values with increasing concentration of laminarihexaose strongly suggests the formation of a weak macro complex of the protein and the hexasaccharide.



Supplementary Figure 4. Sedimentation velocity profiles of N-βGRP:laminarin complex with increasing amounts of laminarin: *L. digitata* laminarin (red); *E. bicyclis* laminarin (blue) added to a constant amount of the protein (26.2 μM). *E. bicyclis* laminarin is more branched with β(1-3)/β(1−6) ratio of 3 than is *L. digitata* laminarin that has a corresponding value of 7.