Table 1. Comparison between β(1,3)-glucan binding residues in GNBPs.

	β(1,3)-glucan binding residue					
	I	II	III	IV	V	VI
N. graveolus GNBP-2	E	R	E	W	F	Y
D. rubriceps GNBP-2	E	R	E	W	F	Y
M. darwiniensis GNBP-2	E	R	E	W	Y	Y
N. graveolus GNBP-1	E	R	D	W	E	Y
D. rubriceps GNBP-1	E	R	D	W	E	Y
M. darwiniensis GNBP-1	E	R	D	W	E	Y
T. castaneum GNBP	E	V	Δ	Y	P	Q
D. melanogaster GNBP-2	D	H	N	M	Y	F
D. melanogaster GNBP-1	D	S	E	L	W	Y
B. mori GNBP	E	T	I	L	K	Y
H. cunea GNBP	E	T	K	L	K	Y
A. gambiae GNBP-A	E	T	T	Y	F	Y
A. gambiae GNBP-B	E	R	S	W	A	H
B. circulans β(1,3)-glucanase	D	N	D	W	V	Y

SUPPORTING TABLE LEGEND

Table 1

Comparison between β(1,3)-glucan binding residues in GNBPs. Protein sequences were aligned with ClustalW and positions I-VI were extrapolated from computational model. Residue positions (in *N. graveolus* sequence) are: I 56, II 143, III 146, IV 172, V 179, VI 308. Color coding: red=acidic, ochre=hydrophobic, blue=basic, light blue=N/Q, purple=Y, peach=W. Δ represents a deletion in the specified residue.