

Supplementary figures

Supplementary Figure 1

Sequences alignment of GGBP3 from 12 *Drosophila* species. The regions are delineated by backgrounds of different colors: green for the signal peptide, blue for the Glucan recognition domain, grey for the N-terminal domain, faint yellow for the Glucanase domain and dark yellow for the O-glycosyl hydrolase (E.C3.2.1) domain. The color code for the amino acids is the following: red for strict conservation, blue for conservative mutations and green for a percentage of conservation higher than 75. The catalytic residues (Glu (E) in bacterial glucanases) that are mutated into Gln (Q) and Tyr (Y) in the GNBP3s are in frame.

Supplementary Figure 2

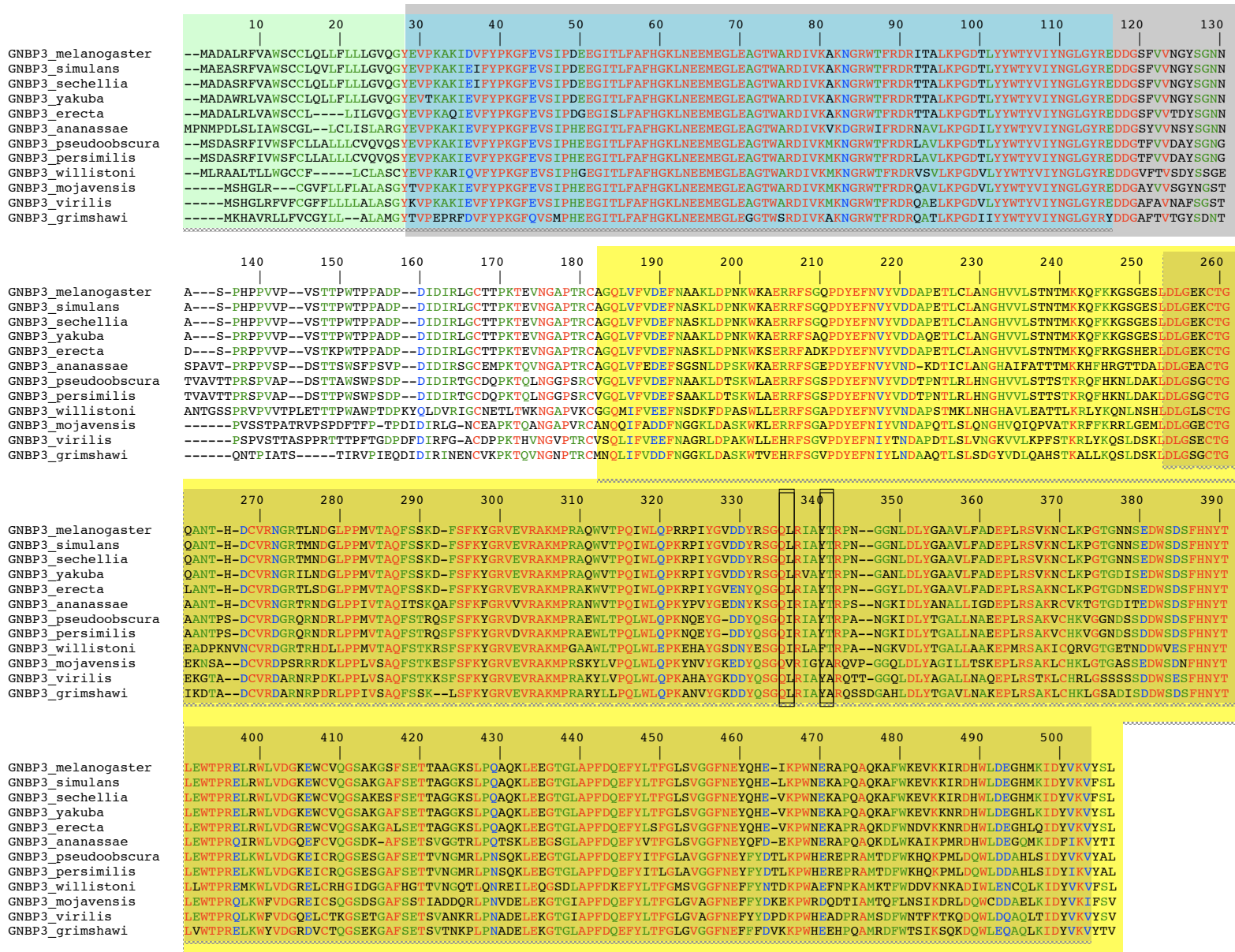
Sequence alignment of the N-terminal domain of GGBP1,2 and 3 of *Drosophila melanogaster* (GNBP1, 2 and 3), *Bombyx mori* and *Hyphantria cunea* GNBP3s. The color code is the same as in supplementary Figure 1

Supplementary Figure 3

(A) Sequence modification in the short-loop mutant.

(B) CD spectra were recorded on a Jasco J-810 spectropolarimeter from 260 to 200 nm using a 1 mm jacketed quartz cell at 20°C, a scan rate of 20 nm.min⁻¹, a response time of 2ms, a band width of 1 nm, and a resolution of 1nm. The contribution of the buffer was subtracted and each spectrum represents the average of five scans. The spectra are presented without smoothing or further data processing. The three curves, corresponding to wild type, W77A and short-loop mutants, display the same minimum at 215 nm and cross the X axis at the same value (205 nm). A slight difference is observed for W77A mutant around 230 nm. This may be due to the removal of the tryptophane residue, which is in strong interaction with an histidine residue in the wild type and short-loop mutant.

Supplementary figure 1



Supplementary figure 2

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          10      20      30      40      50      60      70      80      90      100
GNBP1_Drosophila_melanogaster YKIP TPTV E L L E T - G F S V S I P D E E G V K V V A F N V N R N R N F T S F I N E G Q Y N V R L T E P Q N G R W T T N F S S V P L R S Q D V L Y L W T S V Q H Q K A V Y Q D L A Q P L P V C N L G G E Y R
GNBP2_Drosophila_melanogaster F K V P S I N F E M L K D E G F F E V S I P D E P G I Q R V F Y M F Q I D D T C P A L M D Y - - - - - I T E A V N G S W V S K Q K - M S L Q N N D K L Q I S M L V Q F N E E I F E K S E T R V I I N T R L L T T K
GNBP3_Drosophila_melanogaster Y E V P K A K I D V F Y P K G F F E V S I P D E E G I T L F A F H G K L N E E M E G - L E A G T W A R D I V K A K N G R W T F R D R I T A L K P G D T L Y Y W T Y V I Y N G L G Y R E D D G S F V N G Y S G N N -
GNBP_Hyphantria - Q V P Q V T V Q A L K P R G F K A S I P D S P S V S L F V F Q G N I N R A I S K - S D I G T I S G E I L K A K D G R W T F E D P N V E L K V G D V V N Y Y V V V S N R G G Y I K D N L S F T V S A L - - - - -
GNBP_Bombyx_p50 -- M P D V K I Q A F R P K G L R I S V Q D V P K M T L F A F Q G N L N H K L D S - T S V G T L S A E V L D P V N G R W V Y E E P D L K L K V K D V V Y Y N A V F S I N K K I Y E K T N Q Q F T V T E L - - - - -
Consensus k ! P # l G F e ! S I P D e p g ! v a % # # g i t e a N G r W t L D l y V q # % k ! n
Prim.cons. Y K V P 5 V 2 2 2 A L K P K G F E V S I P D E P G 2 T L F A F Q G N 2 N R 5 5 5 S 2 5 D 5 G T 4 S 4 E I 2 2 A 2 N G R W T F E D P 4 V 5 L K V G D V L Y Y W T V V Q 5 N K 5 2 Y E K D N Q S F T V N 5 L 3 G 3 3 2
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Supplementary Figure 3

A

NEEMEGLEAG

N---AGGEAG

B

