

Supplementary Information for

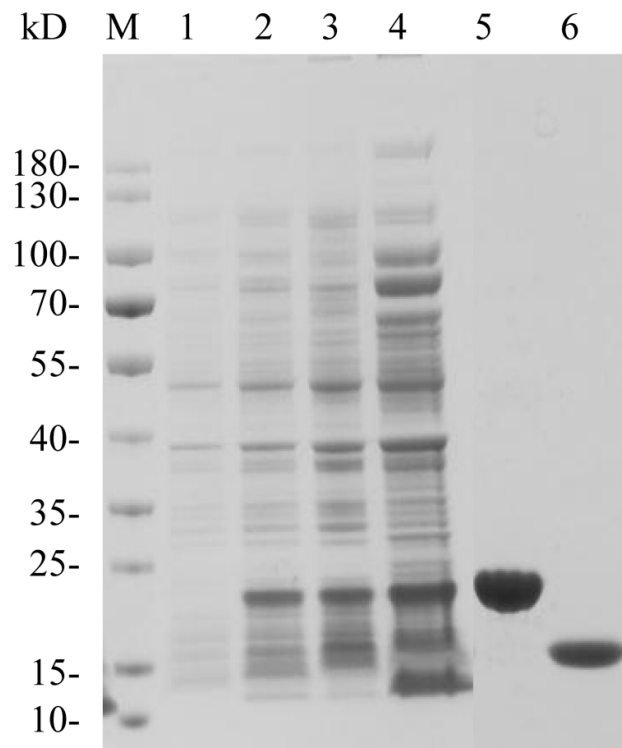
**The female-biased general odorant binding protein 2 of *Semiothisa cinerearia* displays binding affinity to biologically active host plant volatiles**

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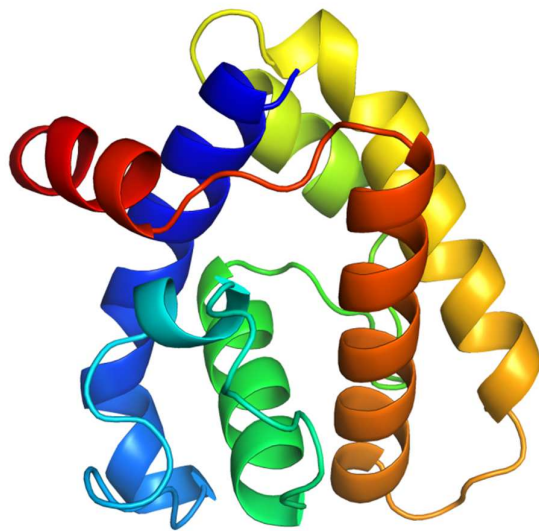
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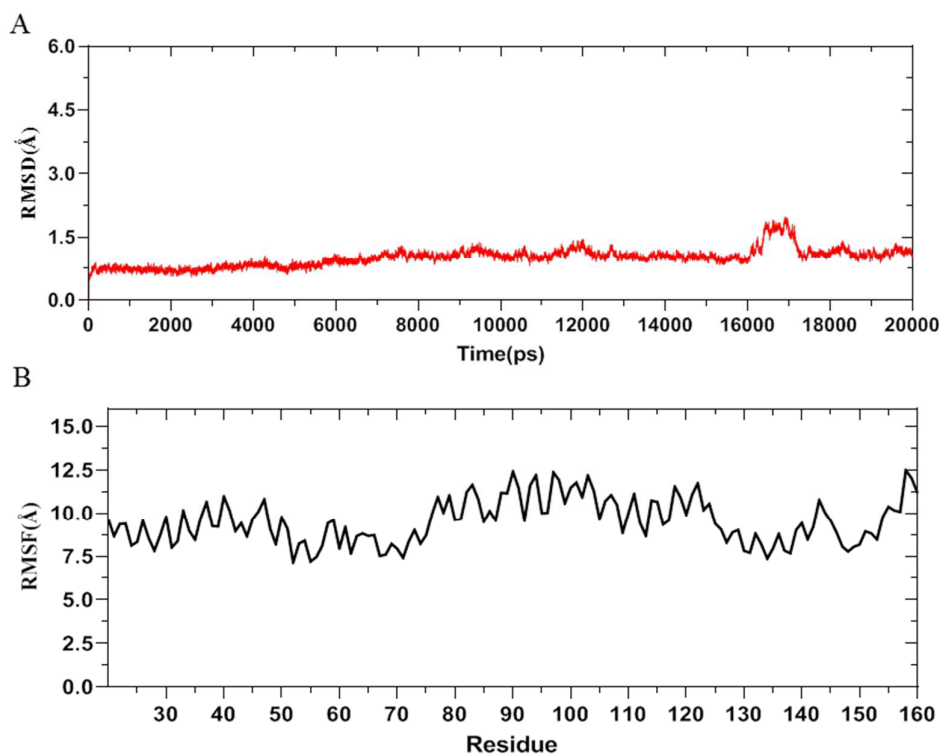
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**Figure S1.** SDS-PAGE analysis of the recombinant ScinGOBP2. M: molecular weight markers, 1: cell pellet before induction with IPTG, 2: cell pellet after induction, 3: pellet after sonication, 4: supernatant after sonication, 5: protein purified by affinity chromatography, and 6: purified protein after digestion with enterokinase.

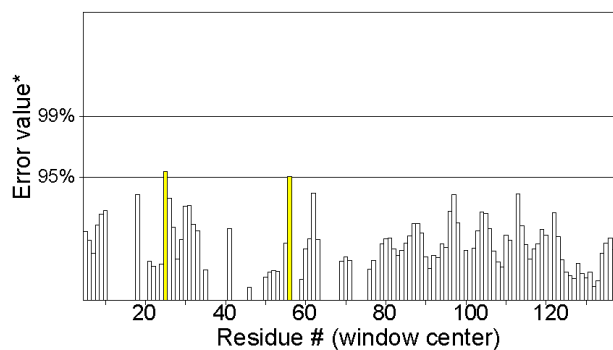


**Figure S2.** Three-dimensional (3D) structure of ScinGOBP2.



**Figure S3.** MD simulation results of ScinGOBP2. (A) RMSD plot showing the conformational changes of the protein till 20000 ps. (B) RMSF plot showing residue fluctuations for 20000 ps.

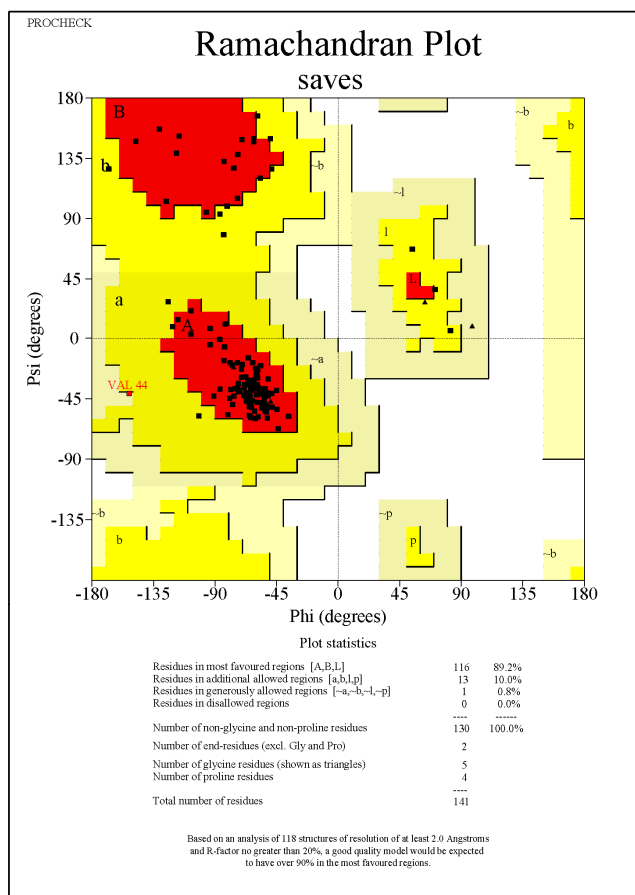
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 File: MD.pdb  
 Chain#:  
 Overall quality factor\*\*: 97.849



\*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

\*\*Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.

**Figure S4.** ERRAT results from the predicted 3D model of ScinGOBP2.



**Figure S5.** PROCHECK results from the predicted 3D model of ScinGOBP2.

**Table S1.** Primers used in this study.

Gene	Forward primer (5'-3')	Reverse primer (5'-3')
Gene cloning		
<i>GOBP2</i>	ATGTCAGAGCCGCTAGTGG	CTAATACTGTTCTAAAACAGC
RT-PCT		
<i>GOBP2</i>	TCCCCAAACATATTAGAAGAGTTCCA	TTCCAAAACAGCCTCAATCATGG
<i>β-actin</i>	CCTACAACCTCCATCATGAAGTGTGA	GTATTCCTGTTTCGAGATCCACATC
qRT-PCT		
<i>GOBP2</i>	CTGTTGATGGTAGCGGTGGT	TGAGAGCCTTCCCAAAGTGC
<i>β-actin</i>	CAGAAGGACTCGTACGTGGG	GTAGAACGTGTGGTGCCAGA
<i>TBP</i>	CCACTACCTGCAGAACGTGT	GTTTGAGAGCGGGCAGTTTG