

Supplementary Information for

An integrated approach unravels a crucial structural property for the function of the insect steroidogenic Halloween protein Noppera-bo

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This PDF file includes:

Figs. S1 to S12
Tables S1 to S5
Legends of Movie 1 and 2

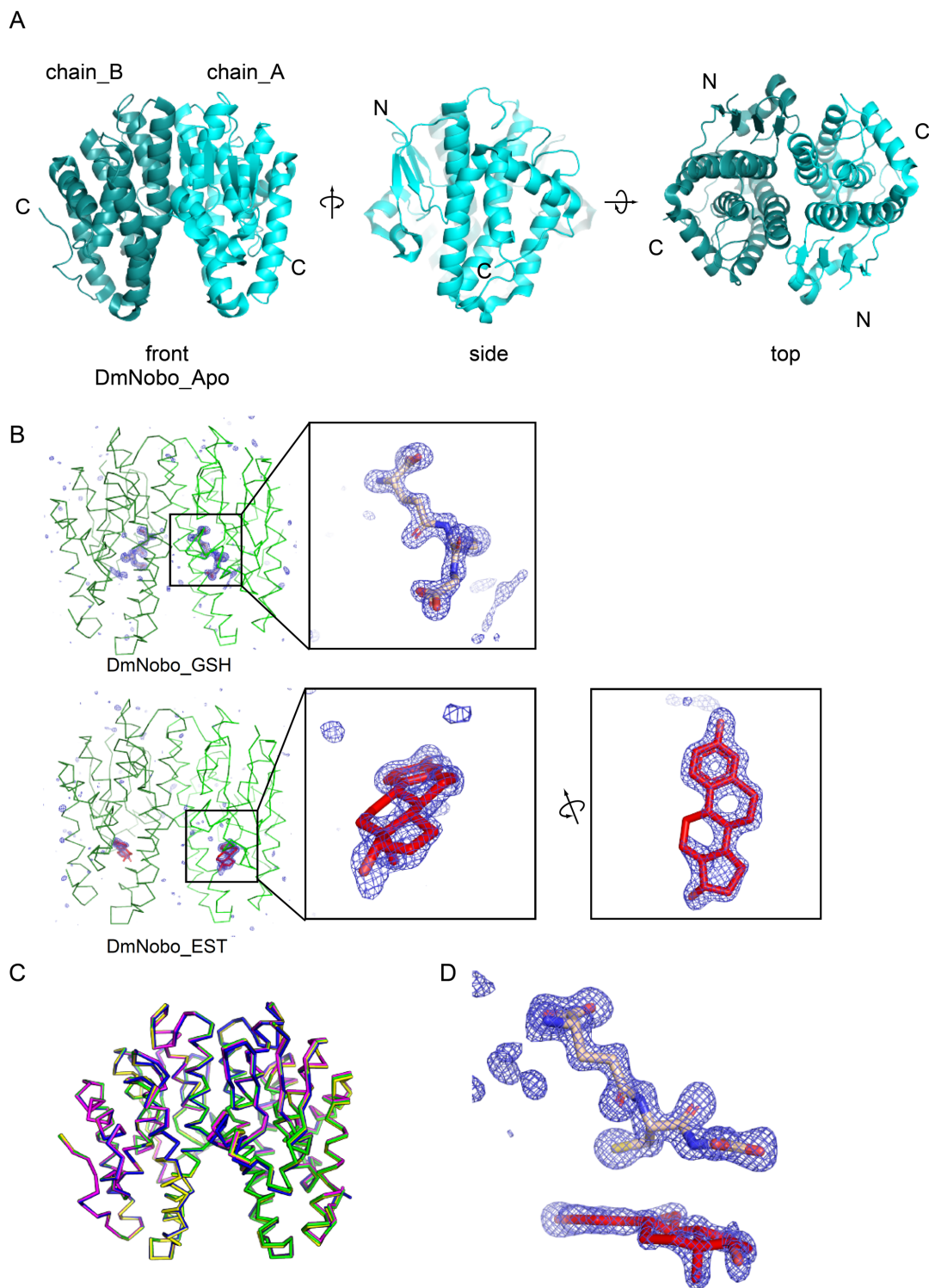


Fig. S1. Overall structures of DmNobo.

(A) The overall structure of DmNobo_Apo is represented as a ribbon diagram. Chains A and B are colored in cyan and turquoise, respectively. (B) Simulated annealing-omit maps of GSH and EST in DmNobo_GSH and DmNobo_EST, respectively. *mFo-DFc* maps (blue) are contoured at the 4.0σ level and shown with a blue mesh. A ribbon model of the DmNobo protein (green) and stick models of GSH and EST molecules are shown. Carbon atoms in GSH and EST are colored wheat and red, respectively. Oxygen atoms and nitrogen atoms are colored in green and blue, respectively. (C) Superimposed crystal structures of DmNobo_Apo

(blue), DmNobo_GSH (yellow), DmNobo_EST (magenta), and DmNobo_EST-GSH (green). Least square (LSQ) fittings were performed with the $C\alpha$ atoms of chain A. RMSD values from the LSQ fittings are summarized in Table S1. (D) Simulated annealing-omit maps of GSH and EST in the DmNobo_EST-GSH structure. $mF_o - DFc$ maps (blue) are contoured at 4.0σ and shown with a blue mesh. GSH and EST molecules are shown as stick models.

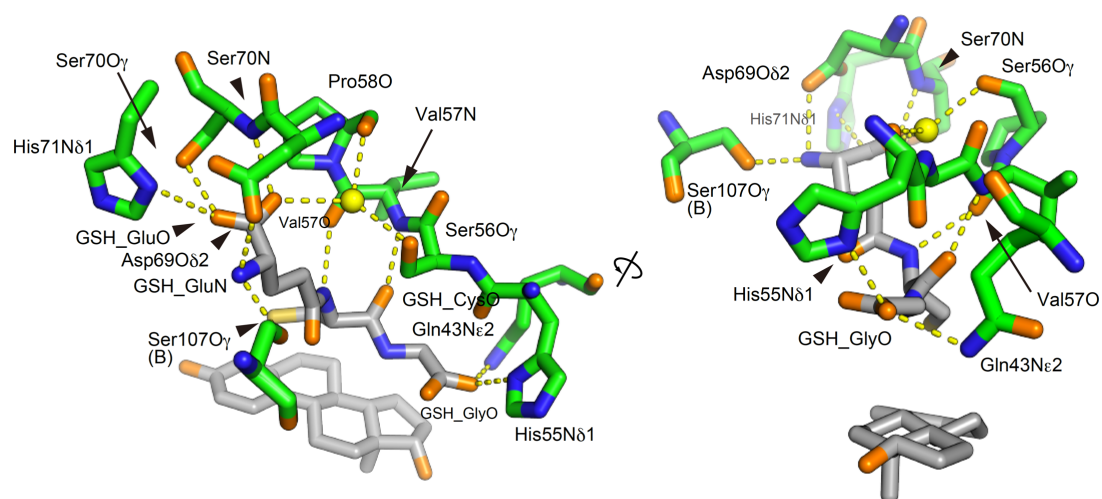
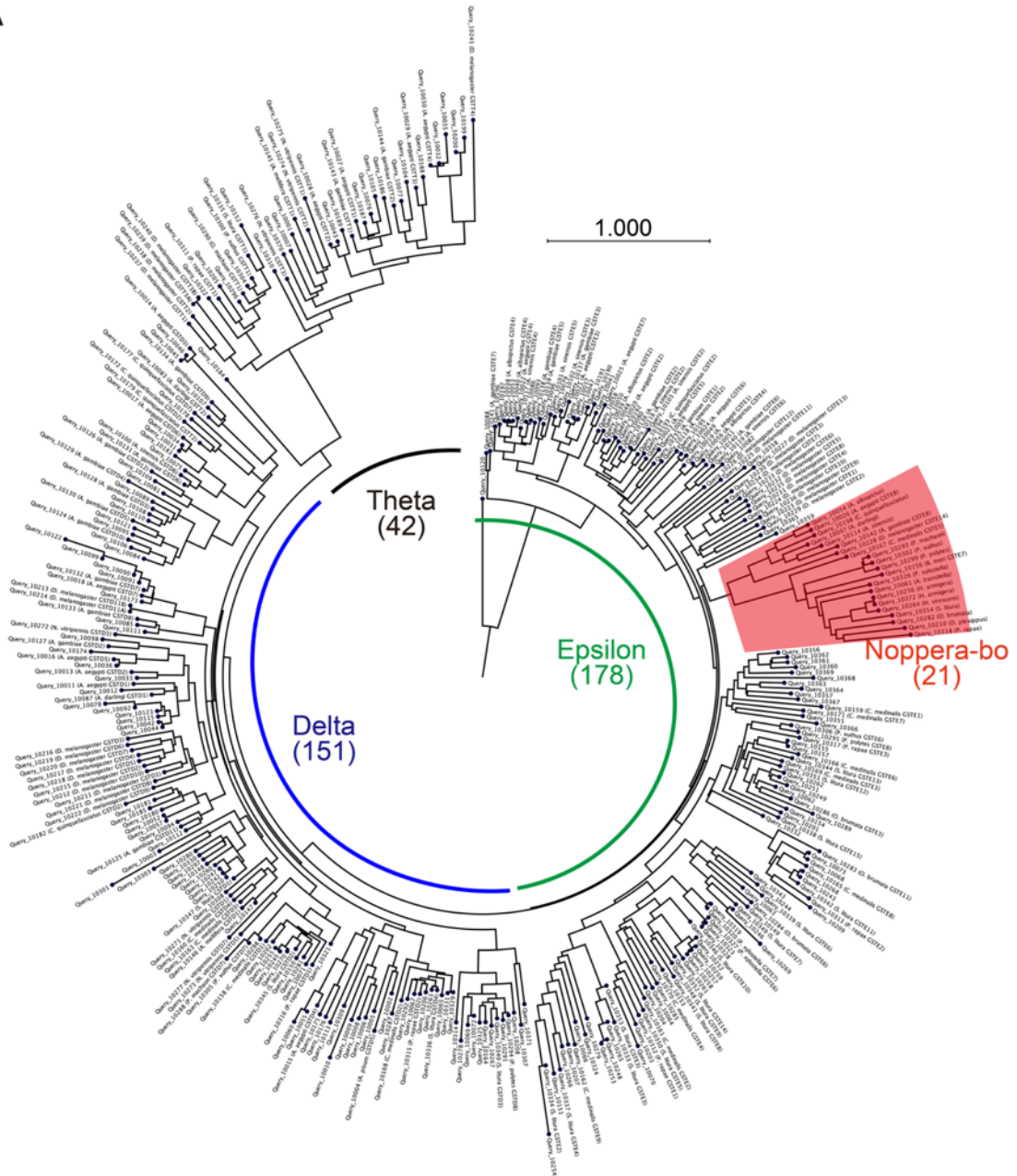


Fig. S2. A hydrogen-bond network between DmNobo and GSH.

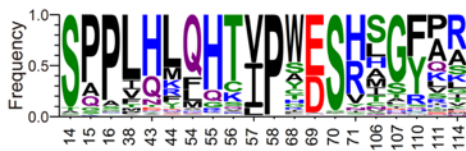
Hydrogen bonds are indicated with yellow dashed lines. Carbon atoms of the protein and ligands (GSH, EST) are shown in green and gray, respectively. One of the two conformations of Ser107, in which the O γ atom is directed towards GSH, is shown.

A



B

G-site: 350 GSTD/E/T



G-site: 21 Noppera-bo

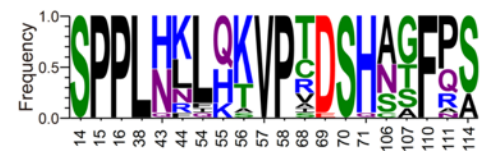


Fig. S3. Phylogenetic analysis of the delta, epsilon, and theta classes of GST.

(A) Phylogenetic tree of the insect GSTD/E/T proteins listed in Table S5. A clade of the *nobo* family is highlighted in red. (B) Frequencies of amino acid residues composing the G-site of 350 GSTD/E/T (left) and 21 Nobo (right) proteins displayed in A. The frequencies were calculated using LOGO, and Nobo proteins were excluded from the GSTD/E/T proteins for the frequency calculation.

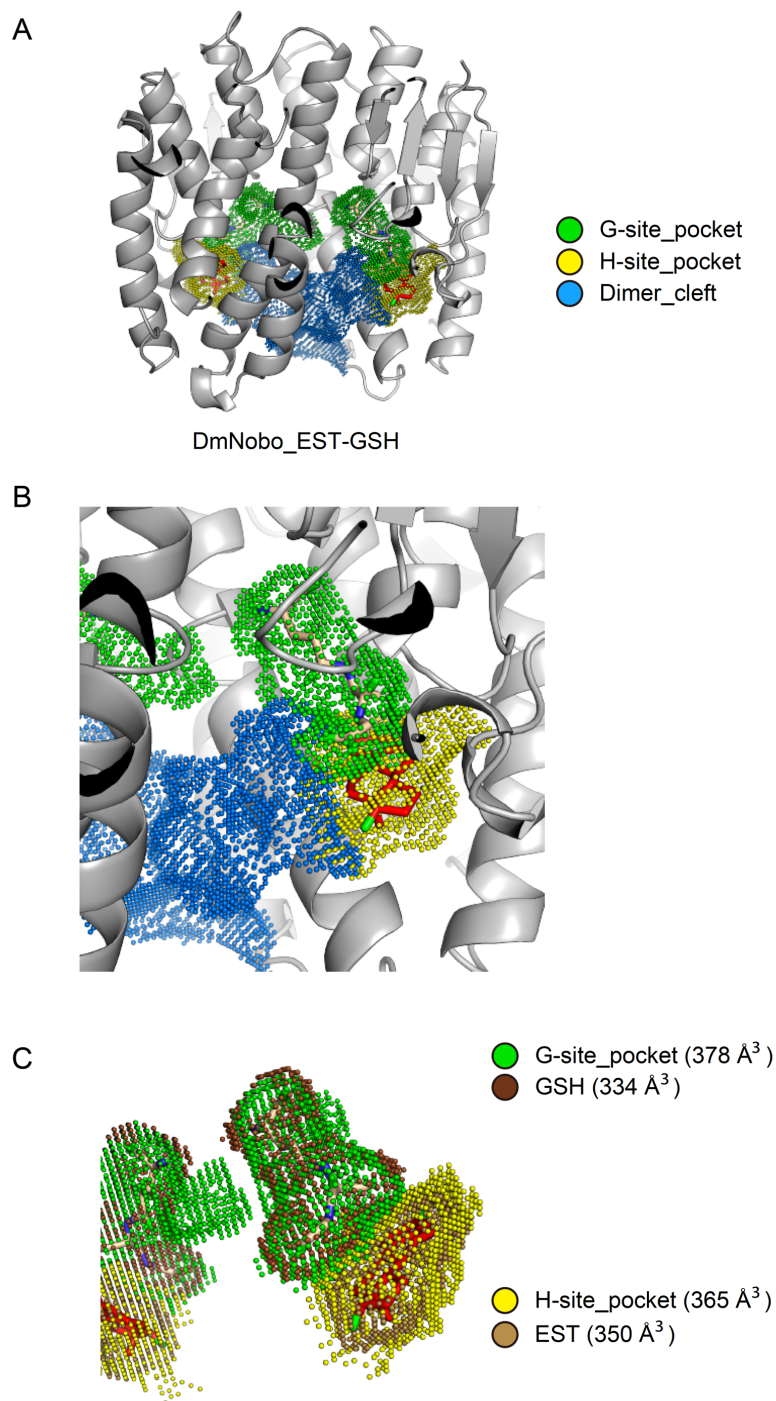


Fig. S4. Pockets in the G- and H-sites of DmNobo

(A, B) Pockets in DmNobo were calculated using 3V. The inner surfaces of the two pockets, i.e., the G- and H-sites, are represented in green and yellow dots, respectively. The cleft between the two subunits of the DmNobo_EST-GSH are shown in blue. The G-site was calculated using the crystal structure of the DmNobo_EST-GSH complex without GSH, and the H-site was calculated using the crystal structure of the DmNobo_EST-GSH complex without EST. (B) An enlarged view of the G- and H-sites. (C) The solvent-accessible surfaces of GSH and EST are represented with brown and light brown dots, respectively. The surfaces of the G- and H-sites are superimposed on GSH (green) and EST (yellow).

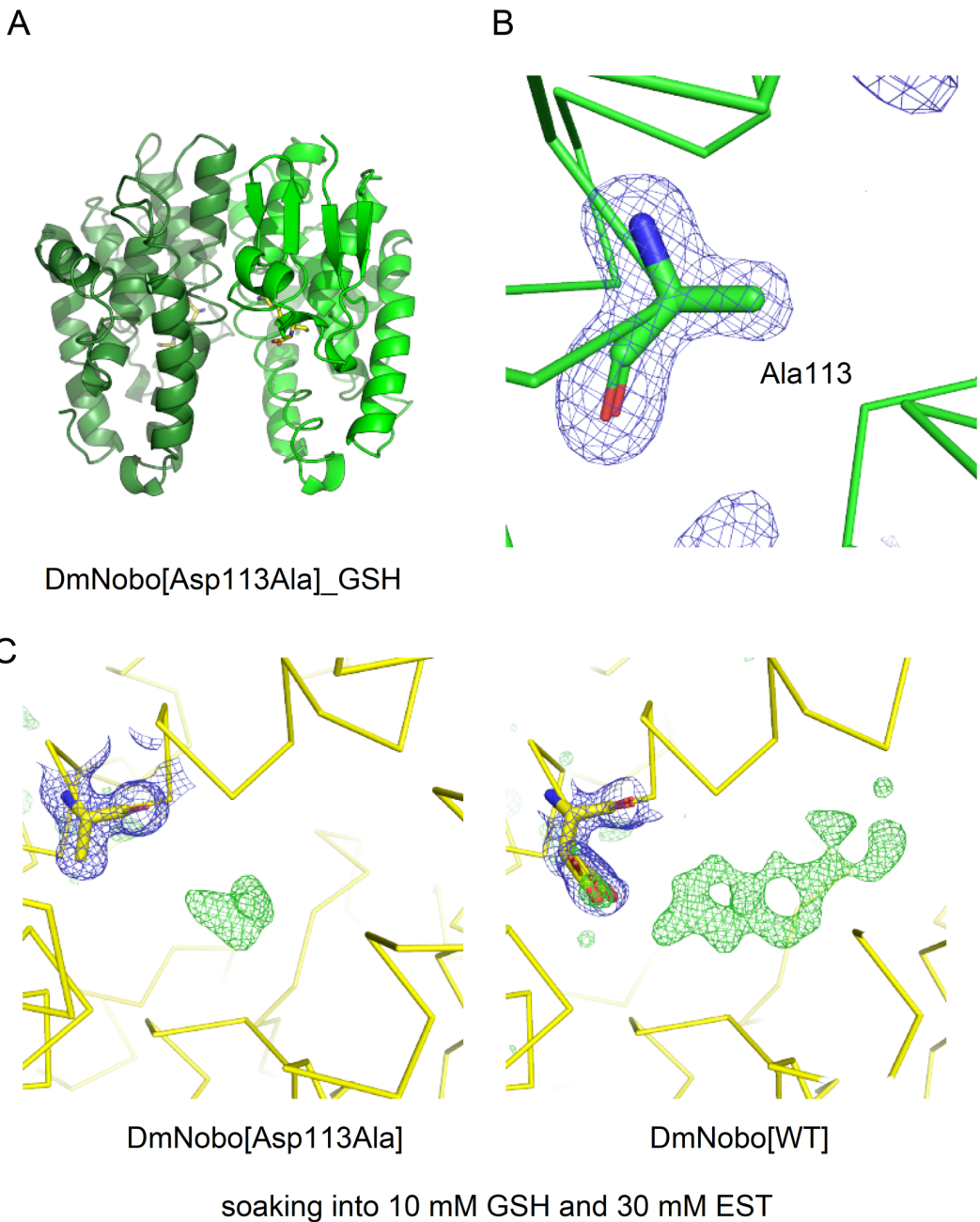


Fig. S5. Characterization of the DmNobo[Asp113Ala] protein.

(A) Overall structure of GSH in complex with DmNobo[Asp113Ala] (DmNobo[Asp113Ala]_GSH). Chains A and B are shaded green and dark green, respectively. The RMSD value from the LSQ fittings between C α atoms in chain A of DmNobo[WT]_GSH and those of DmNobo[Asp113Ala] was 0.1 Å.

(B) Simulated annealing-omit maps of Ala113 of DmNobo[Asp113Ala]_GSH. *mFo*-*DFc* map (blue) contoured at 4.0 σ was overlaid with sticks of Ala113 and a ribbon model of DmNobo[Asp113Ala]_GSH (green). (C) *mFo*-*DFc* map around the H-sites of DmNobo[Asp113Ala] and DmNobo[WT]. EST did not bind to DmNobo[Asp113Ala]. Crystals of DmNobo[Asp113Ala] and DmNobo[WT] were soaked into an artificial mother liquor (42.5% [w/v] PPG 400 in 100 mM Bis-Tris [pH 6.4]) containing 10 mM GSH and 30 mM EST.

The mF_o-DFc maps contoured at 4.0σ (green mesh) and the $2mF_o-DFc$ map contoured at 1.5σ around residue 113 (within 5 Å from residue 113, blue mesh) are shown.

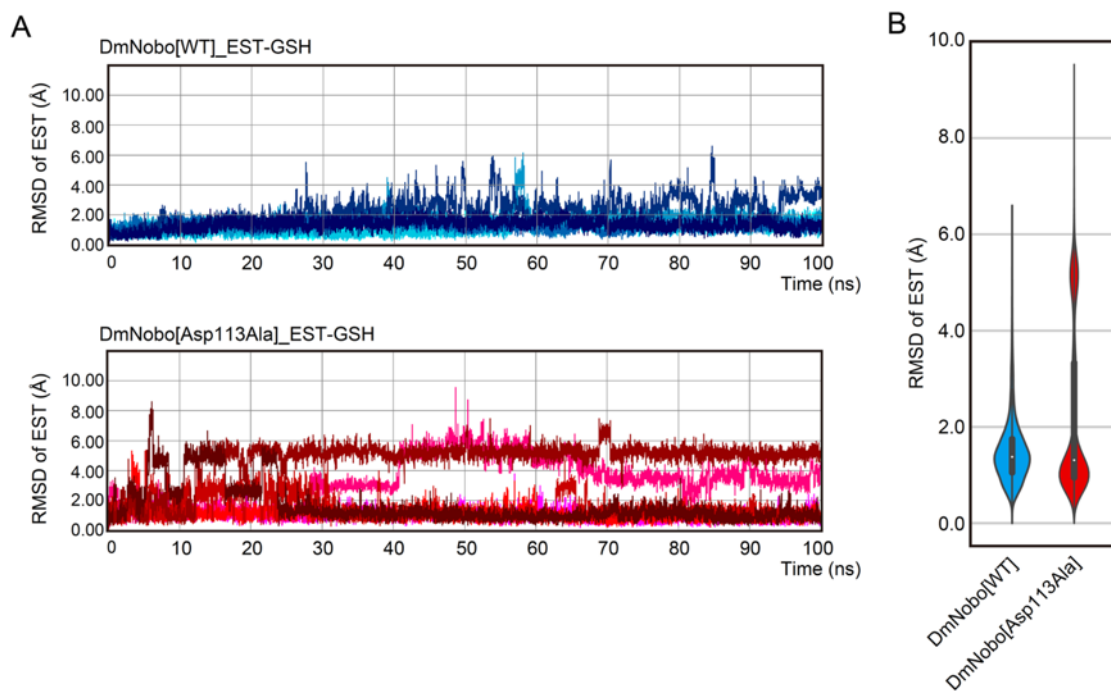


Fig. S6. *In silico* evaluation of the contribution of Asp113 to the interaction between DmNobo and EST.

(A) The RMSD values of EST in DmNobo[WT] (top) or DmNobo[Asp113Ala] (bottom) in triplicate independent calculations. All protein frames were aligned based on the protein backbone of the initial structure. The RMSD (Å) of EST between EST at the initial frame and each subsequent frame is plotted. (B) Violin-plot of the RMSD of EST in DmNobo[WT] or DmNobo[Asp113Ala]. The median, interquartile range, and 95% confidence interval are shown with a white dot, a bold line, and a narrow line, respectively. The width of the plot indicates the frequency of the frames.

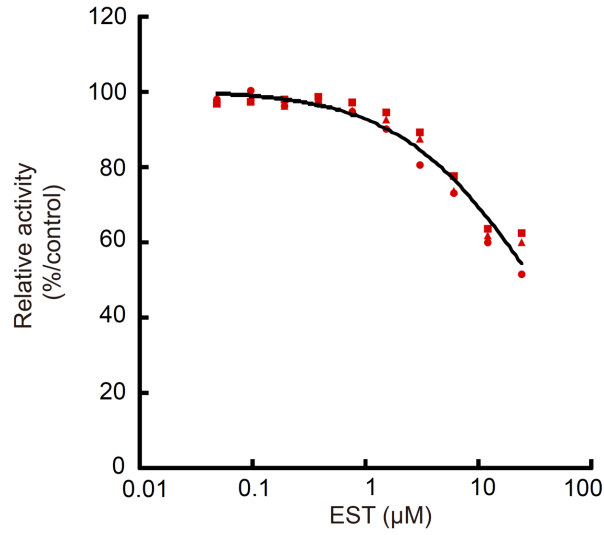


Fig. S7. EST-dependent inhibition of the GSH-conjugation activities of AgNobo[Asp111Ala].

3,4-DNADCF was used as an artificial fluorescent substrate. Relative activity is defined as the ratio of activity when compared to the protein without EST. All of the data points in triplicate assays are indicated. The value of IC_{50} was $>25 \mu M$.

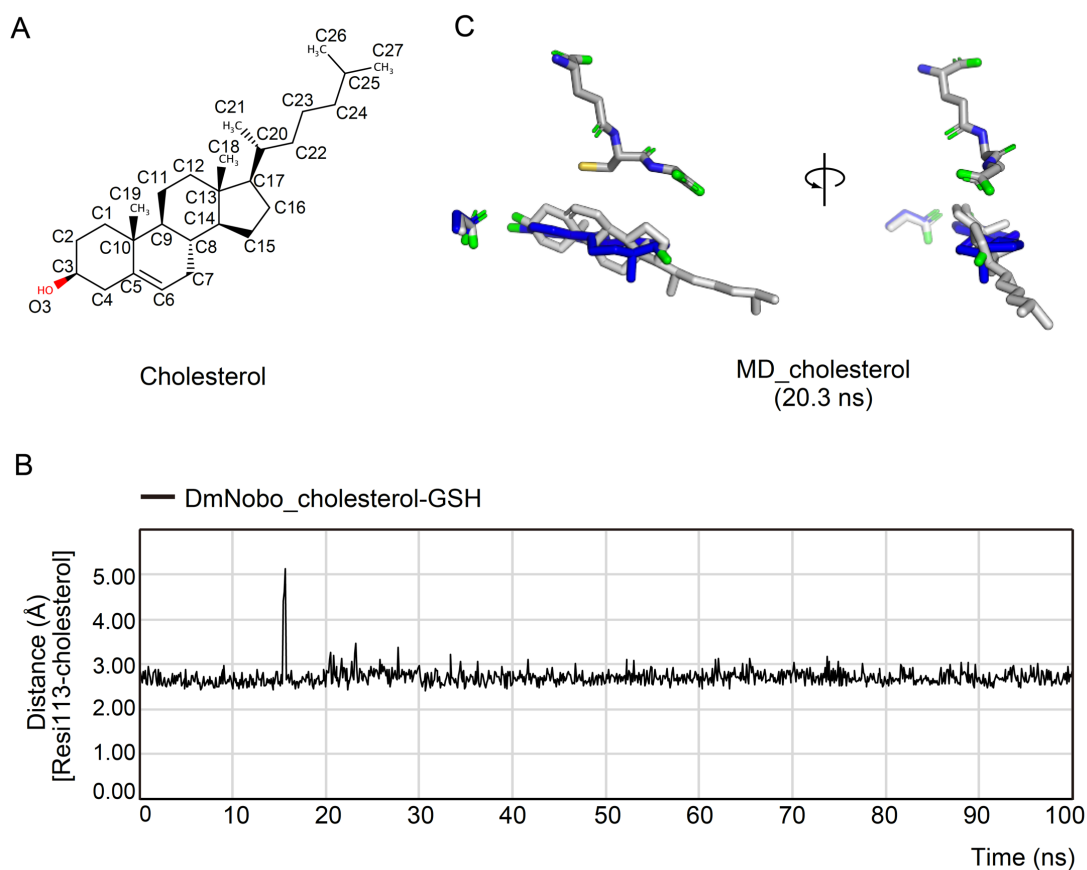


Fig. S8. *In silico* evaluation of interaction between DmNobo and cholesterol

(A) Chemical structure of cholesterol. (B) MD-simulation results for DmNobo in complex with cholesterol and GSH. The distance between O δ of Asp113 of DmNobo and O3 of cholesterol was plotted against time. (C) MD models of DmNobo_cholesterol-GSH and DmNobo_EST-GSH at 20.3 ns.

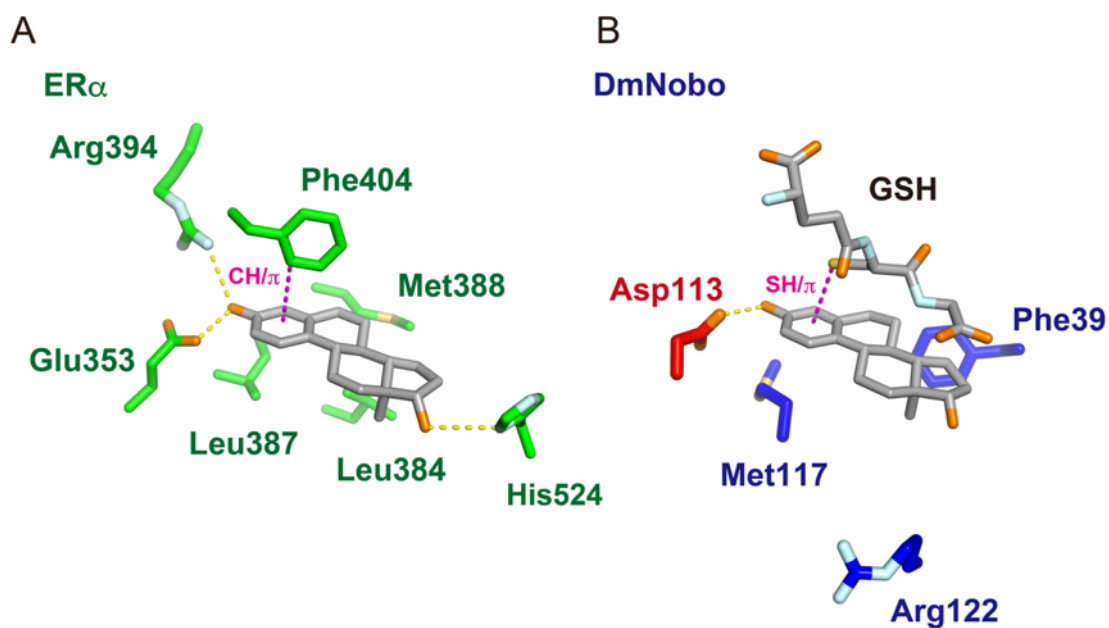


Fig. S9. Comparison of the DmNobo_EST and ER α _EST interactions.

Side chains of representative residues of ER α (A) or DmNobo (B) that interact with EST are represented with sticks (PDB ID for ER α structure = 1QKT). A hydrogen bond between the protein and EST is indicated with a yellow dashed line. A CH/ π interaction between Phe404 and EST or an SH/ π interaction between GSH and EST is indicated with a pink dashed line.

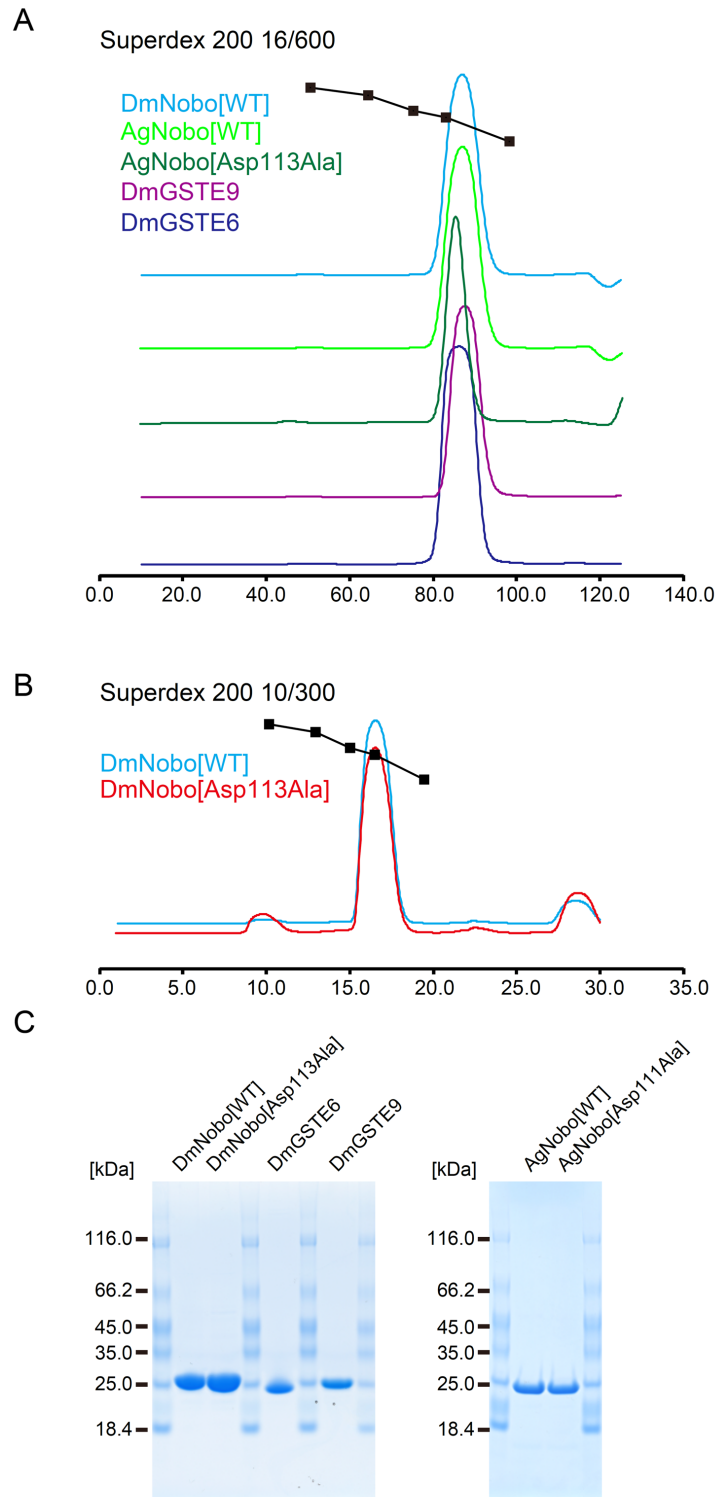


Fig. S10. Purified proteins in this study

(A) DmNobo[WT], DmGSTE6, DmGSTE9, AgNobo[WT] and AgNobo[Asp111Ala] were purified by size exclusion column chromatography with HiLoad Superdex 200 16/600 (GEhealthcare). UV charts of DmNobo[WT] (cyan), AgNobo[WT] (light green), AgNobo[Asp111Ala] (dark green), DmGSTE6 (blue), and DmGSTE9 (purple) are shown together with peak points of marker proteins. The marker proteins used were β -amylase from sweet potato (223.8 kDa), alcohol dehydrogenase from *Saccharomyces cerevisiae* (146.8

kDa), bovine serum albumin (66.5 kDa), human GSTP1-1 (46.7 kDa in solution), and RNase A (13.7 kDa).

(B) DmNobo[Asp113Ala] was purified by size exclusion column chromatography with Superdex 200 increase 10/300 (GEhealthcare). UV charts of DmNobo[Asp113Ala] (red) and DmNobo[WT] (cyan) as a control are shown together with peak points of the marker proteins. (C) SDS-PAGE analyses for DmNobo[WT], DmNobo[Asp113Ala], DmGSTE6, DmGSTE9, AgNobo[WT] and AgNobo[Asp111Ala]. Purified proteins were fractionated by SDS-PAGE in reduced condition, and stained by Coomassie Brilliant Blue G-250.

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Fig. S11.

DNA sequence of pDonor[KI]-{CG4688_LA};{3×FLAG/HA/nobo};{CG4688_RA}

Gray highlighting: 5' homology arm; blue highlighting: ATG + 3× FLAG tag; yellow highlighting: HA tag; magenta highlighting: exons of Nobo (CG4688); green highlighting: introns of Nobo (CG4688); underlined text: pUC19 ori

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TCGTC

Fig. S12.

DNA sequence of pDonor[KI]-

{CG4688_LA};{3×FLAG/HA/nobo*D113A};{CG4688_RA}

Gray highlighting: 5' homology arm; blue highlighting: ATG + 3× FLAG tag; yellow highlighting: HA tag; magenta highlighting: exons of Nobo (CG4688); green highlighting: introns of Nobo (CG4688); boxed and bold text: substitution with Ala (GAC → GCC); underlined text: pUC19 ori

Table S1. Crystallographic Summary of DmNobo crystal structures

	DmNobo_Apo	DmNobo_GSH	DmNobo_EST	DmNobo_ES T-GSH
Data Collection				
Space group	<i>P2₁2₁2₁</i>	<i>P2₁2₁2₁</i>	<i>P2₁2₁2₁</i>	<i>P2₁2₁2₁</i>
Cell Dimensions				
<i>a</i> , <i>b</i> , <i>c</i> (Å)	59.12, 76.56 106.36	58.75, 75.67, 107.84	58.40, 75.08, 109.02	58.38, 75.06, 108.52
α , β , γ (°)	90.00, 90.00, 90.00	90.00, 90.00, 90.00	90.00, 90.00, 90.00	90.00, 90.00, 90.00
Resolution* (Å)	42.83 - 1.50 (1.55 - 1.50)	46.42 - 1.75 (1.81 - 1.75)	46.12 - 1.58 (1.64 - 1.58)	46.11 - 1.55 (1.61 - 1.55)
<i>R</i> _{merge}	0.045 (0.38)	0.082 (1.05)	0.048 (0.84)	0.038 (0.36)
<i>I</i> / σ <i>I</i>	33.8 (6.53)	27.3 (2.3)	37.6 (2.6)	42.7 (3.3)
Completeness	1.00 (1.00)	1.00 (0.97)	0.87 (0.47)	0.95 (0.69)
Redundancy	13.1 (12.7)	14.3 (12.2)	14.1 (10.6)	12.3 (3.8)
CC1/2	1.00 (0.97)	1.00 (0.75)	1.00 (0.76)	1.00 (0.84)
Refinement				
Resolution (Å)	42.83 - 1.50	35.70 - 1.75	35.49 - 1.70	32.59 - 1.55
No. of reflections	77,842	49,095	51,170	65,906
<i>R</i> _{work}	0.164	0.173	0.176	0.161
<i>R</i> _{free}	0.195	0.207	0.211	0.182
No. of Atoms				
Protein	3,880	3,609	3,687	3,817
GSH	0	40	0	40
EST	0	0	40	40
Water	643	408	403	499
<i>B</i> factors				
Protein	22.0	22.0	23.5	20.1
GSH	-	17.7	-	15.5
EST	-	-	31.5	20.8
Waters	39.5	33.7	34.5	34.7
RMSD				
Bond length (Å)	0.008	0.007	0.008	0.010
Bond angles (°)	0.98	0.89	0.96	1.19
Ramachandran plot (%)				
favored	99.1	99.3	98.9	99.3
allowed	0.90	0.68	1.14	0.68
outliers	0.00	0.00	0.00	0.00
PDB ID	6KEM	6KEN	6KEO	6KEP

Each structure was determined from diffraction data from one crystal. PDB, Protein Data Bank; RMSD, root-mean-square deviation. *Highest resolution shells are shown in parentheses.

Table S1. Crystallographic Summary of DmNobo crystal structures *Continued*

	DmNobo[Asp113Ala] Apo	DmNobo[Asp113Ala] GSH
Data Collection		
Space group	<i>P2₁2₁2₁</i>	<i>P2₁2₁2₁</i>
Cell Dimensions		
<i>a</i> , <i>b</i> , <i>c</i> (Å)	58.72, 75.48, 107.11	58.37, 74.83, 107.42
α , β , γ (°)	90.00, 90.00, 90.00	90.00, 90.00, 90.00
	46.34 - 1.84	46.03 - 1.84
Resolution* (Å)	(1.90 - 1.84)	(1.90 - 1.84)
<i>R</i> _{merge}	0.072 (1.10)	0.113 (1.12)
<i>I</i> / σ <i>I</i>	21.3 (2.1)	15.2 (2.12)
Completeness	1.00 (0.99)	99.9 (99.5)
Redundancy	13.3 (13.8)	13.5 (13.9)
CC1/2	1.00 (0.83)	1.00 (0.78)
Refinement		
Resolution (Å)	46.34 - 1.84	46.03 - 1.84
No. reflections	42,099	41,768
<i>R</i> _{work}	0.208	0.189
<i>R</i> _{free}	0.240	0.221
No. of Atoms		
Protein	3,495	3,529
GSH	0	40
EST	0	0
Water	174	146
<i>B</i> factors		
Protein	33.51	21.9
GSH	-	18.1
EST	-	-
Waters	36.85	26.5
RMSD		
Bond length (Å)	0.005	0.004
Bond angles (°)	0.73	0.66
Ramachandran plot (%)		
favored	99.0	99.1
allowed	0.91	0.91
outliers	0.00	0.00
PDB		
ID	6KEQ	6KER

Table S2. root-mean-square deviation (RMSD) among DmNobo crystal structures

		RMSD (Å) of C α atoms of chain A [†] / RMSD (Å) of C α atoms of chains A and B [‡]		
	Coordinate error (Å) [*]	DmNobo_GSH	DmNobo_EST	DmNobo_EST- GSH
DmNobo_Apo	0.13	0.20 / 0.35	0.26 / 0.42	0.48 / 0.55
DmNobo_GSH	0.20		0.16 / 0.24	0.42 / 0.36
DmNobo_EST	0.21			0.40 / 0.32
DmNobo_EST-GSH	0.15			

^{*} Coordinate errors are estimated by a maximum-likelihood method.

[†] Number of aligned C α atoms in chain A: 199 atoms

[‡] Number of aligned C α atoms in chain A and B: 391 atoms

Table S3. Summary of H-site-composing, or EST-interacting atoms in DmNobo

* Atoms of DmNobo within 4.0 Å from EST.

† Atoms of EST within 4.0 Å from each EST-interacting atom.

Residue	H-site-composing atoms	EST-interacting atoms*	DmNobo-interacting atoms†	Distance ‡ (Å)	Identity among DmGST D/E/T	Identity among Nobo	Total IFIE to EST (kcal/mol)
Arg13	C, Cβ	-	-	-	0.07	0.05	-0.31
Ser14	Cα, N, Cβ	-	-	-	0.85	1.00	-1.78
Pro15	Cδ, Cγ	Cδ	O3	3.2	0.62	1.00	-3.93
		Cδ	C3	3.6			
		Cδ	C4	3.7			
		Cγ	O3	3.1			
Leu38	C, O, Cβ, Cδ	Cβ	C15	4.0	0.61	1.00	-1.86
		Cδ	C7	4.0			
Phe39	Cα, Cδ, Cγ, Cε, Cζ	Cε1	C6	3.9	0.07	1.00	-6.77
			C7	3.7			
		π	C15	3.9			
Gln43	Nε	-	-	-	0.21	0.05	-0.51
Phe110	Cε, Cζ	Cε	C2	4.0	0.42	1.00	-2.79
Asp113	Oδ	Oδ	O3	2.6	0.01	0.95	-41.4
Ser114	Cα, Cβ	Cα	C1	3.8	0.10	0.76	-2.17
		Cα	C2	3.8			
		Cβ	C1	3.9			
Met117	Cβ, Cγ, Cε	Cβ	C1	3.9	0.04	0.40	-3.52
		Cβ	C2	3.9			
		Cγ	C2	3.8			
		Cγ	C3	3.9			
Ser118	Cα, N, Cβ, Cγ	-	-	-	0.06	0.33	-3.25
Val121	Cβ, Cγ1, Cγ2	Cβ	C18	3.9	0.11	0.05	-1.63
		Cγ1	C18	3.9			
		Cγ2	C18	3.8			
Arg122	Cβ	-	-	-	0.07	0.14	-1.49
Thr172	Cγ	Cγ	O3	3.3	0.31	0.52	0.026
Leu208	Cδ1, Cδ2	Cδ1	C4	3.9	0.31	0.95	-2.17
		Cδ1	C6	3.8			
		Cδ2	O3	4.0			
		Cδ2	C4	3.9			
Met212	Sδ	-	-	-	0.05	0.95	-0.65
GSH	Cys_Cβ, Cys_Sγ	Cys_Sγ	π	3.7	-	-	-3.48

‡ Average of chains A and B in the asymmetric unit.

Table S4. FMO analysis between fragments in DmNobo and EST

Residue	Total	ES	EX	CT	DI
	[kcal/mol]	[kcal/mol]	[kcal/mol]	[kcal/mol]	[kcal/mol]
Arg13	-0.31	0.36	0.03	-0.10	-0.59
Ser14	-1.78	0.49	0.20	-1.01	-1.47
Pro15	-3.93	-1.52	2.53	-1.25	-3.69
Arg18	-1.85	-1.66	0.00	-0.02	-0.17
Leu38	-1.86	-0.67	2.75	-0.79	-3.15
Phe39	-6.77	-1.77	4.34	-1.97	-7.37
Lys40	0.13	0.28	0.00	0.00	-0.15
Gln43	-0.51	0.25	0.12	-0.18	-0.69
Phe110	-2.79	-1.08	0.31	-0.51	-1.51
Asp113	-41.38	-49.71	26.87	-12.63	-5.91
Ser114	-2.17	-0.03	3.72	-2.76	-3.11
Asp115	3.31	1.66	0.07	2.18	-0.59
Met117	-3.52	0.12	2.12	-1.36	-4.39
Ser118	-3.25	-0.41	0.87	-1.05	-2.65
Ala119	-0.36	-0.24	0.03	0.24	-0.39
Val121	-1.63	-0.74	2.35	-0.47	-2.77
Arg122	-1.49	-1.10	0.00	-0.03	-0.36
Leu208	-2.17	-0.74	2.23	-0.70	-2.97
GSH_Gly	-2.49	0.64	0.32	-0.89	-2.56
GSH_Cys	-3.48	-1.00	5.12	-1.68	-5.92
PIEDA	-82.4	-59.2	55.8	-25.8	-53.1

Table S5. ID of amino acid sequences used in phylogenetic analysis

Accession	Description
Query_10001	tr C4WSG3 C4WSG3_ACYPI ACYPI009122 protein OS=Acyrtosiphon pisum OX=7029 GN=ACYPI009122 PE=2 SV=1
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Query_10003	tr C4WUF9 C4WUF9_ACYPI ACYPI005620 protein OS=Acyrtosiphon pisum OX=7029 GN=ACYPI005620 PE=2 SV=1
Query_10004	tr I6SCG3 I6SCG3_ACYPI Glutathione S-transferase D5 OS=Acyrtosiphon pisum OX=7029 GN=GstD5 PE=3 SV=1
Query_10005	tr J9JLJ3 J9JLJ3_ACYPI Uncharacterized protein OS=Acyrtosiphon pisum OX=7029 PE=4 SV=2
Query_10006	tr J9K2A8 J9K2A8_ACYPI Uncharacterized protein OS=Acyrtosiphon pisum OX=7029 PE=3 SV=1
Query_10007	tr J9K372 J9K372_ACYPI Uncharacterized protein OS=Acyrtosiphon pisum OX=7029 PE=3 SV=1
Query_10008	tr J9K6N7 J9K6N7_ACYPI Uncharacterized protein OS=Acyrtosiphon pisum OX=7029 GN=100167788 PE=4 SV=1
Query_10009	tr J9M2I6 J9M2I6_ACYPI Uncharacterized protein OS=Acyrtosiphon pisum OX=7029 PE=3 SV=2
Query_10010	tr X1WJM1 X1WJM1_ACYPI Uncharacterized protein OS=Acyrtosiphon pisum OX=7029 PE=3 SV=1
Query_10011	tr Q17MA9 Q17MA9_AEDAE AAEL001061-PA OS=Aedes aegypti OX=7159 GN=GSTD1 PE=4 SV=1
Query_10012	tr Q174V0 Q174V0_AEDAE AAEL006764-PA (Fragment) OS=Aedes aegypti OX=7159 GN=AAEL006764 PE=4 SV=1
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Query_10015	tr Q17MB8 Q17MB8_AEDAE AAEL001054-PA (Fragment) OS=Aedes aegypti OX=7159 GN=GSTD4 PE=4 SV=2
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Query_10017	tr Q16SH6 Q16SH6_AEDAE AAEL010591-PA OS=Aedes aegypti OX=7159 GN=GSTD6 PE=3 SV=1
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Query_10063 XP_013196516.1 PREDICTED: glutathione S-transferase 1-like [Amyeloid transitella]

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Query_10066 XP_013194108.1 PREDICTED: uncharacterized protein LOC106137747 [Amyeloid transitella]

Query_10067 XP_013196508.1 PREDICTED: glutathione S-transferase 1-1-like [Amyeloid transitella]

Query_10068 XP_013198047.1 PREDICTED: glutathione S-transferase 1-like [Amyeloid transitella]

Query_10069 XP_013187696.1 PREDICTED: glutathione S-transferase 1, isoform C-like [Amyeloid transitella]

Query_10070 XP_013182960.1 PREDICTED: glutathione S-transferase 1-like [Amyeloid transitella]

Query_10071 NP_001299595.1 uncharacterized protein LOC106136399 precursor [Amyeloid transitella]

Query_10072 XP_013187697.1 PREDICTED: glutathione S-transferase 1, isoform C-like [Amyeloid transitella]

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OX=43151 GN=AND_000803 PE=3 SV=1

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OS=Anopheles darlingi OX=43151 GN=AND_008208 PE=3 SV=1

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OS=Anopheles darlingi OX=43151 GN=AND_008797 PE=3 SV=1

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OX=43151 GN=AND_008798 PE=3 SV=1

Query_10085 tr|W5JJP4|W5JJP4_ANODA Glutathione transferase, delta class
OS=Anopheles darlingi OX=43151 GN=AND_004770 PE=3 SV=1

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OS=Anopheles darlingi OX=43151 GN=AND_008212 PE=3 SV=1

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darlingi OX=43151 GN=AND_000833 PE=3 SV=1

Query_10088 tr|W5J6X4|W5J6X4_ANODA Glutathione S-transferase, epsilon class
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OX=43151 GN=AND_008796 PE=4 SV=1

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OX=43151 GN=AND_008211 PE=4 SV=1

Query_10097 tr|W5J6X9|W5J6X9_ANODA Glutathione S-transferase, epsilon class
OS=Anopheles darlingi OX=43151 GN=AND_008204 PE=4 SV=1

Query_10098 tr|W5JW53|W5JW53_ANODA Glutathione transferase, delta class
OS=Anopheles darlingi OX=43151 GN=AND_000835 PE=4 SV=1

Query_10099 tr|W5JC52|W5JC52_ANODA Glutathione transferase, delta class
OS=Anopheles darlingi OX=43151 GN=AND_007981 PE=4 SV=1

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OS=Anopheles sinensis OX=74873 GN=ZHAS_00021747 PE=3 SV=1

Query_10101 tr|A0A084VMZ2|A0A084VMZ2_ANOSI Glutathione s-transferase E5
OS=Anopheles sinensis OX=74873 GN=ZHAS_00006696 PE=3 SV=1

Query_10102 tr|A0A084WQQ1|A0A084WQQ1_ANOSI Glutathione transferase epsilon3
OS=Anopheles sinensis OX=74873 GN=ZHAS_00020795 PE=3 SV=1

Query_10103 tr|A0A084WQQ3|A0A084WQQ3_ANOSI Glutathione s-transferase E2
OS=Anopheles sinensis OX=74873 GN=ZHAS_00020699 PE=3 SV=1

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OS=Anopheles sinensis OX=74873 GN=ZHAS_00007604 PE=3 SV=1

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OS=Anopheles sinensis OX=74873 GN=ZHAS_00021754 PE=3 SV=1

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Query_10113 tr|A0A084VUG1|A0A084VUG1_ANOSI AGAP003257-PA-like protein
OS=Anopheles sinensis OX=74873 GN=ZHAS_00009226 PE=3 SV=1

Query_10114 tr|A0A084VMZ0|A0A084VMZ0_ANOSI AGAP009190-PA-like protein
OS=Anopheles sinensis OX=74873 GN=ZHAS_00006694 PE=3 SV=1

Query_10115 tr|A0A084WTJ6|A0A084WTJ6_ANOSI AGAP004164-PB-like protein
OS=Anopheles sinensis OX=74873 GN=ZHAS_00021770 PE=3 SV=1

Query_10116 tr|A0A084VMZ4|A0A084VMZ4_ANOSI Glutathione s-transferase E2
OS=Anopheles sinensis OX=74873 GN=ZHAS_00006698 PE=4 SV=1

Query_10117 tr|A0A084VMZ3|A0A084VMZ3_ANOSI Glutathione s-transferase E4
OS=Anopheles sinensis OX=74873 GN=ZHAS_00006697 PE=4 SV=1

Query_10118 tr|A0A084WQQ2|A0A084WQQ2_ANOSI Glutathione s-transferase E2
OS=Anopheles sinensis OX=74873 GN=ZHAS_00020698 PE=4 SV=1

Query_10119 tr|A0A084VMZ1|A0A084VMZ1_ANOSI Glutathione s-transferase E6
OS=Anopheles sinensis OX=74873 GN=ZHAS_00006695 PE=4 SV=1

Query_10120 tr|A0A084WCJ1|A0A084WCJ1_ANOSI AGAP011334-PA-like protein
OS=Anopheles sinensis OX=74873 GN=ZHAS_00015997 PE=4 SV=1

Query_10121 tr|A0A084WTI0|A0A084WTI0_ANOSI AGAP004173-PA-like protein
OS=Anopheles sinensis OX=74873 GN=ZHAS_00021753 PE=4 SV=1

Query_10122 tr|A0A084WTJ9|A0A084WTJ9_ANOSI AGAP004163-PB-like protein
OS=Anopheles sinensis OX=74873 GN=ZHAS_00021774 PE=4 SV=1

Query_10123 sp|Q93113|GST1D_ANOGA Glutathione S-transferase 1, isoform D
OS=Anopheles gambiae OX=7165 GN=GstD1 PE=1 SV=1

Query_10124 tr|Q7QA79|Q7QA79_ANOGA AGAP004383-PA OS=Anopheles gambiae
OX=7165 GN=GSTD10 PE=4 SV=1

Query_10125 tr|Q8MUS1|Q8MUS1_ANOGA Glutathione S-transferase D11 OS=Anopheles
gambiae OX=7165 GN=GSTd11 PE=2 SV=1

Query_10126 tr|Q9GPL6|Q9GPL6_ANOGA AGAP004380-PA OS=Anopheles gambiae
OX=7165 GN=GSTD12 PE=2 SV=1

Query_10127 sp|Q94999|GSTT2_ANOGA Glutathione S-transferase 2 OS=Anopheles
gambiae OX=7165 GN=GstD2 PE=3 SV=2

Query_10128 tr|Q7PQ95|Q7PQ95_ANOGA AGAP004382-PA OS=Anopheles gambiae
OX=7165 GN=GSTD3 PE=3 SV=3

Query_10129 tr|Q5TT03|Q5TT03_ANOGA AGAP004381-PA OS=Anopheles gambiae
OX=7165 GN=GSTD4 PE=3 SV=1

Query_10130 tr|Q7QB59|Q7QB59_ANOGA AGAP004173-PA OS=Anopheles gambiae
OX=7165 GN=GSTD5 PE=4 SV=1

Query_10131 tr|Q8MUS2|Q8MUS2_ANOGA Glutathione S-transferase D6 (Fragment)
OS=Anopheles gambiae OX=7165 GN=GSTd6 PE=2 SV=1

Query_10132 sp|O76483|GSTT7_ANOGA Glutathione S-transferase D7 OS=Anopheles
gambiae OX=7165 GN=GstD7 PE=2 SV=1

Query_10133 tr|Q5TTE5|Q5TTE5_ANOGA AGAP004171-PA OS=Anopheles gambiae
OX=7165 GN=GSTD8 PE=3 SV=2

Query_10134 tr|Q86D84|Q86D84_ANOGA AGAP004172-PA OS=Anopheles gambiae
OX=7165 GN=GSTd9 PE=4 SV=1

Query_10135 tr|Q9GPL9|Q9GPL9_ANOGA AGAP009195-PA OS=Anopheles gambiae
OX=7165 GN=GSTE1 PE=2 SV=1

Query_10136 tr|Q7PVS6|Q7PVS6_ANOGA AGAP009194-PA OS=Anopheles gambiae
OX=7165 GN=GSTE2 PE=1 SV=3

Query_10137 tr|Q8WQJ9|Q8WQJ9_ANOGA AGAP009197-PA OS=Anopheles gambiae
OX=7165 GN=GSTe3 PE=3 SV=1

Query_10138 tr|Q8WQJ8|Q8WQJ8_ANOGA AGAP009193-PA OS=Anopheles gambiae
OX=7165 GN=GSTe4 PE=2 SV=1

Query_10139 tr|Q8WQJ7|Q8WQJ7_ANOGA AGAP009192-PA OS=Anopheles gambiae
OX=7165 GN=GSTe5 PE=2 SV=1

Query_10140 tr|A0NG89|A0NG89_ANOGA AGAP009191-PA OS=Anopheles gambiae
OX=7165 GN=GSTE6 PE=3 SV=1

Query_10141 tr|Q7PVS4|Q7PVS4_ANOGA AGAP009196-PA OS=Anopheles gambiae
OX=7165 GN=GSTE7 PE=4 SV=3

Query_10142 tr|Q8WQJ5|Q8WQJ5_ANOGA AGAP009190-PA OS=Anopheles gambiae
OX=7165 GN=GSTe8 PE=2 SV=1

Query_10143 tr|Q8MUQ1|Q8MUQ1_ANOGA AGAP000761-PA OS=Anopheles gambiae
OX=7165 GN=gstT1 PE=2 SV=1

Query_10144 tr|Q8MUQ2|Q8MUQ2_ANOGA AGAP000888-PA OS=Anopheles gambiae
OX=7165 GN=gstT2 PE=2 SV=1

Query_10145 tr|A0A087ZVS9|A0A087ZVS9_APIME Uncharacterized protein OS=Apis
mellifera OX=7460 GN=GstT1 PE=3 SV=1

Query_10146 tr|A0A088AFL5|A0A088AFL5_APIME Uncharacterized protein OS=Apis
mellifera OX=7460 GN=GstD1 PE=4 SV=1

Query_10147 tr|Q6IVB7|Q6IVB7_APILI Glutathione-S-transferase 1 (Fragment) OS=Apis
mellifera ligustica OX=7469 GN=gst1 PE=2 SV=2

Query_10148 tr|Q2I0J5|Q2I0J5_BOMMO Glutathione S-transferase 3 OS=Bombyx mori
OX=7091 GN=693114 PE=2 SV=1

Query_10149 tr|H9IYE6|H9IYE6_BOMMO Uncharacterized protein OS=Bombyx mori
OX=7091 PE=3 SV=1

Query_10150 tr|O61996|O61996_BOMMO Glutathione S-transferase OS=Bombyx mori
OX=7091 GN=692678 PE=1 SV=1

Query_10151 tr|H9JAU4|H9JAU4_BOMMO Uncharacterized protein OS=Bombyx mori
OX=7091 PE=4 SV=1

Query_10152 tr|H9JK84|H9JK84_BOMMO Uncharacterized protein OS=Bombyx mori
OX=7091 PE=3 SV=1

Query_10153 tr|H9JKA0|H9JKA0_BOMMO Uncharacterized protein OS=Bombyx mori
OX=7091 PE=3 SV=1

Query_10154 tr|H9JKP2|H9JKP2_BOMMO Uncharacterized protein OS=Bombyx mori
OX=7091 PE=3 SV=1

Query_10155 tr|H9JKP3|H9JKP3_BOMMO Uncharacterized protein OS=Bombyx mori
OX=7091 PE=3 SV=1

Query_10156 BmoriGSTE7

Query_10157 tr|B0LB16|B0LB16_BOMMO Epsilon-class glutathione transferase
OS=Bombyx mori OX=7091 GN=gste PE=2 SV=1

Query_10158 tr|A0A077D6E7|A0A077D6E7_CNAME Glutathione S-transferase delta 1
OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10159 tr|A0A077D817|A0A077D817_CNAME Glutathione S-transferase epsilon 1
OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10160 tr|A0A0A7KNK1|A0A0A7KNK1_CNAME Glutathione S-transferase delta 4
OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10161 tr|A0A077D9Y8|A0A077D9Y8_CNAME Glutathione S-transferase epsilon 2 OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10162 tr|A0A0A7KL70|A0A0A7KL70_CNAME Glutathione S-transferase epsilon 9 OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10163 tr|A0A0A7KQB0|A0A0A7KQB0_CNAME Glutathione S-transferase delta 3 OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10164 tr|A0A077D602|A0A077D602_CNAME Glutathione S-transferase OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10165 tr|A0A0A7KLA5|A0A0A7KLA5_CNAME Glutathione S-transferase epsilon 8 OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10166 tr|A0A077D820|A0A077D820_CNAME Glutathione S-transferase epsilon 6 (Fragment) OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10167 tr|A0A077D5Z1|A0A077D5Z1_CNAME Glutathione S-transferase epsilon 5 (Fragment) OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10168 tr|A0A077D5Y7|A0A077D5Y7_CNAME Glutathione S-transferase delta 2 OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10169 tr|A0A077DB43|A0A077DB43_CNAME Glutathione S-transferase epsilon 3 OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10170 tr|A0A077D6F2|A0A077D6F2_CNAME Glutathione S-transferase epsilon 4 OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10171 tr|A0A0A7KLF5|A0A0A7KLF5_CNAME Glutathione S-transferase epsilon 7 OS=Cnaphalocrocis medinalis OX=437488 PE=2 SV=1

Query_10172 tr|B0VZJ3|B0VZJ3_CULQU Glutathione S-transferase D2 OS=Culex quinquefasciatus OX=7176 GN=6031025 PE=3 SV=1

Query_10173 tr|B0W6A9|B0W6A9_CULQU Glutathione-s-transferase theta, gst OS=Culex quinquefasciatus OX=7176 GN=6033850 PE=4 SV=1

Query_10174 tr|B0W6B2|B0W6B2_CULQU Glutathione S-transferase 1-1 OS=Culex quinquefasciatus OX=7176 GN=6033854 PE=3 SV=1

Query_10175 tr|B0W6C3|B0W6C3_CULQU Glutathione S-transferase 1 OS=Culex quinquefasciatus OX=7176 GN=6033865 PE=4 SV=1

Query_10176 tr|B0W6C4|B0W6C4_CULQU Glutathione S-transferase 1 OS=Culex quinquefasciatus OX=7176 GN=6033866 PE=4 SV=1

Query_10177 tr|B0W6C5|B0W6C5_CULQU Glutathione S-transferase D7 OS=Culex quinquefasciatus OX=7176 GN=6033867 PE=3 SV=1

Query_10178 tr|B0W6C7|B0W6C7_CULQU Glutathione transferase I OS=Culex quinquefasciatus OX=7176 GN=6033869 PE=3 SV=1

Query_10179 tr|B0W6C8|B0W6C8_CULQU Glutathione S-transferase theta-2 OS=Culex quinquefasciatus OX=7176 GN=6033870 PE=3 SV=1

Query_10180 tr|B0W6C9|B0W6C9_CULQU Glutathione S-transferase OS=Culex quinquefasciatus OX=7176 GN=6033871 PE=4 SV=1

Query_10181 tr|B0W6D0|B0W6D0_CULQU Glutathione S-transferase OS=Culex quinquefasciatus OX=7176 GN=6033872 PE=3 SV=1

Query_10182 tr|A0A1S4J718|A0A1S4J718_CULQU GSTD2 protein OS=Culex quinquefasciatus OX=7176 PE=3 SV=1

Query_10183 tr|B0W6D2|B0W6D2_CULQU Glutathione S-transferase 1-1 OS=Culex quinquefasciatus OX=7176 GN=6033874 PE=3 SV=1

Query_10184 tr|B0WQW9|B0WQW9_CULQU Glutathione S-transferase 1 OS=Culex quinquefasciatus OX=7176 GN=6041912 PE=3 SV=1

Query_10185 tr|B0WUG8|B0WUG8_CULQU Glutathione S-transferase 1-5 OS=Culex quinquefasciatus OX=7176 GN=6043364 PE=3 SV=1

Query_10186 tr|B0X3C7|B0X3C7_CULQU Glutathione-s-transferase theta, gst OS=Culex quinquefasciatus OX=7176 GN=6047041 PE=3 SV=1

Query_10187 tr|B0X3C8|B0X3C8_CULQU Glutathione-s-transferase theta, gst OS=Culex quinquefasciatus OX=7176 GN=6047042 PE=3 SV=1

Query_10188 tr|B0X3C9|B0X3C9_CULQU Glutathione-s-transferase theta, gst OS=Culex quinquefasciatus OX=7176 GN=6047043 PE=3 SV=1
 Query_10189 tr|B0X3D0|B0X3D0_CULQU Glutathione S-transferase theta-1 OS=Culex quinquefasciatus OX=7176 GN=6047044 PE=3 SV=1
 Query_10190 tr|B0XGJ6|B0XGJ6_CULQU Glutathione-s-transferase theta, gst OS=Culex quinquefasciatus OX=7176 GN=6052508 PE=3 SV=1
 Query_10191 tr|B0XGJ7|B0XGJ7_CULQU Glutathione-s-transferase theta, gst OS=Culex quinquefasciatus OX=7176 GN=6052509 PE=4 SV=1
 Query_10192 tr|B0XGJ8|B0XGJ8_CULQU Glutathione S-transferase 1-1 OS=Culex quinquefasciatus OX=7176 GN=6052510 PE=3 SV=1
 Query_10193 tr|B0XGJ9|B0XGJ9_CULQU Glutathione S-transferase E2 OS=Culex quinquefasciatus OX=7176 GN=6052511 PE=4 SV=1
 Query_10194 tr|B0XGK0|B0XGK0_CULQU Glutathione-s-transferase theta, gst OS=Culex quinquefasciatus OX=7176 GN=6052512 PE=3 SV=1
 Query_10195 tr|B0XGK1|B0XGK1_CULQU Glutathione S-transferase 1-1 OS=Culex quinquefasciatus OX=7176 GN=6052513 PE=4 SV=1
 Query_10196 tr|B0XGK2|B0XGK2_CULQU Glutathione-s-transferase theta, gst OS=Culex quinquefasciatus OX=7176 GN=6052515 PE=4 SV=1
 Query_10197 tr|B0XGK3|B0XGK3_CULQU Glutathione-s-transferase theta, gst OS=Culex quinquefasciatus OX=7176 GN=6052516 PE=4 SV=1
 Query_10198 tr|B0XGK4|B0XGK4_CULQU Glutathione-s-transferase theta OS=Culex quinquefasciatus OX=7176 GN=6052517 PE=4 SV=1
 Query_10199 tr|B0XJU4|B0XJU4_CULQU Glutathione transferase AtGST OS=Culex quinquefasciatus OX=7176 GN=6053908 PE=4 SV=1
 Query_10200 tr|B0XLC5|B0XLC5_CULQU Glutathione transferase AtGST OS=Culex quinquefasciatus OX=7176 GN=6054553 PE=3 SV=1
 Query_10201 DPOGS200212-PA
 Query_10202 DPOGS202622-PA
 Query_10203 DPOGS204831-PA
 Query_10204 DPOGS207576-PA
 Query_10205 DPOGS207703-PA
 Query_10206 DPOGS208312-PA
 Query_10207 DPOGS209578-PA
 Query_10208 DPOGS210477-PA
 Query_10209 DPOGS210488-PA
 Query_10210 DPOGS210526-PA
 Query_10211 sp|P20432|GSTD1_DROME Glutathione S-transferase D1 OS=Drosophila melanogaster GN=GstD1 PE=1 SV=1
 Query_10212 tr|Q9VGA1|Q9VGA1_DROME Glutathione S transferase D10, isoform A OS=Drosophila melanogaster GN=GstD10 PE=1 SV=1
 Query_10213 tr|B7Z0S9|B7Z0S9_DROME Glutathione S transferase D11, isoform B OS=Drosophila melanogaster GN=GstD11 PE=4 SV=1
 Query_10214 tr|Q8SXQ9|Q8SXQ9_DROME Glutathione S transferase D11, isoform A OS=Drosophila melanogaster GN=GstD11 PE=2 SV=1
 Query_10215 sp|Q9VG98|GSTD2_DROME Glutathione S-transferase D2 OS=Drosophila melanogaster GN=GstD2 PE=1 SV=1
 Query_10216 sp|Q9VG97|GSTD3_DROME Inactive glutathione S-transferase D3 OS=Drosophila melanogaster GN=GstD3 PE=2 SV=1

Query_10217 sp|Q9VG96|GSTD4_DROME Glutathione S-transferase D4 OS=Drosophila melanogaster GN=GstD4 PE=1 SV=1

Query_10218 sp|Q9VG95|GSTD5_DROME Glutathione S-transferase D5 OS=Drosophila melanogaster GN=GstD5 PE=1 SV=2

Query_10219 sp|Q9VG94|GSTD6_DROME Glutathione S-transferase D6 OS=Drosophila melanogaster GN=GstD6 PE=1 SV=1

Query_10220 sp|Q9VG93|GSTD7_DROME Glutathione S-transferase D7 OS=Drosophila melanogaster GN=GstD7 PE=1 SV=1

Query_10221 tr|Q9VG92|Q9VG92_DROME Glutathione S transferase D8 OS=Drosophila melanogaster GN=GstD8 PE=2 SV=1

Query_10222 tr|Q9VGA0|Q9VGA0_DROME Glutathione S transferase D9, isoform A OS=Drosophila melanogaster GN=GstD9 PE=1 SV=1

Query_10223 tr|Q7KK90|Q7KK90_DROME GH14654p OS=Drosophila melanogaster GN=GstE1 PE=1 SV=1

Query_10224 tr|Q4V6J1|Q4V6J1_DROME Glutathione S transferase E10, isoform A OS=Drosophila melanogaster GN=GstE10 PE=2 SV=1

Query_10225 tr|Q7JVZ8|Q7JVZ8_DROME Glutathione S transferase E11, isoform A OS=Drosophila melanogaster GN=GstE11 PE=1 SV=1

Query_10226 tr|Q9XYZ9|Q9XYZ9_DROME Glutathione S transferase E12, isoform A OS=Drosophila melanogaster GN=GstE12 PE=1 SV=1

Query_10227 tr|Q7JVI6|Q7JVI6_DROME Glutathione S transferase E13, isoform A OS=Drosophila melanogaster GN=GstE13 PE=1 SV=1

Query_10228 sp|Q7JYX0|GSTEE_DROME Glutathione S-transferase E14 OS=Drosophila melanogaster GN=GstE14 PE=1 SV=1

Query_10229 tr|Q7JYZ9|Q7JYZ9_DROME Glutathione S transferase E2 OS=Drosophila melanogaster GN=GstE2 PE=2 SV=1

Query_10230 tr|A1ZB68|A1ZB68_DROME FI01423p OS=Drosophila melanogaster GN=GstE3 PE=1 SV=1

Query_10231 tr|A1ZB69|A1ZB69_DROME Glutathione S transferase E4 OS=Drosophila melanogaster GN=GstE4 PE=3 SV=1

Query_10232 tr|A1ZB70|A1ZB70_DROME Glutathione S transferase E5 OS=Drosophila melanogaster GN=GstE5 PE=3 SV=1

Query_10233 tr|A1ZB71|A1ZB71_DROME Glutathione S transferase E6 OS=Drosophila melanogaster GN=GstE6 PE=1 SV=1

Query_10234 tr|A1ZB72|A1ZB72_DROME Glutathione S transferase E7 OS=Drosophila melanogaster GN=GstE7 PE=1 SV=1

Query_10235 tr|A1ZB73|A1ZB73_DROME Glutathione S transferase E8, isoform A OS=Drosophila melanogaster GN=GstE8 PE=3 SV=1

Query_10236 tr|Q7K8X7|Q7K8X7_DROME Glutathione S transferase E9 OS=Drosophila melanogaster GN=GstE9 PE=1 SV=1

Query_10237 tr|Q7K0B6|Q7K0B6_DROME Glutathione S transferase T1 OS=Drosophila melanogaster OX=7227 GN=GstT1 PE=1 SV=1

Query_10238 tr|A1Z7X7|A1Z7X7_DROME Glutathione S transferase T2 OS=Drosophila melanogaster OX=7227 GN=GstT2 PE=1 SV=2

Query_10239 tr|Q9VRA4|Q9VRA4_DROME Glutathione S transferase T3, isoform A OS=Drosophila melanogaster OX=7227 GN=GstT3 PE=3 SV=2

Query_10240 tr|E1JJS1|E1JJS1_DROME Glutathione S transferase T3, isoform B OS=Drosophila melanogaster OX=7227 GN=GstT3 PE=3 SV=1

Query_10241 tr|Q8MRM0|Q8MRM0_DROME GH16740p OS=Drosophila melanogaster OX=7227 GN=GstT4 PE=1 SV=1

Query_10242 tr|A0A291ARU4|A0A291ARU4_HELAM Glutathione S-transferase OS=Helicoverpa armigera OX=29058 GN=GST8 PE=2 SV=1

Query_10243 tr|A0A2W1BRB0|A0A2W1BRB0_HELAM Uncharacterized protein OS=Helicoverpa armigera OX=29058 GN=HaOG200226 PE=3 SV=1

Query_10244 tr|A0A2W1BSA5|A0A2W1BSA5_HELAM Uncharacterized protein OS=Helicoverpa armigera OX=29058 GN=HaOG200219 PE=3 SV=1

Query_10245 tr|A0A2W1BUA9|A0A2W1BUA9_HELAM Uncharacterized protein OS=Helicoverpa armigera OX=29058 GN=HaOG200217 PE=3 SV=1

Query_10246 tr|A0A2W1BZ02|A0A2W1BZ02_HELAM Uncharacterized protein OS=Helicoverpa armigera OX=29058 GN=HaOG200220 PE=3 SV=1

Query_10247 tr|A0MSN0|A0MSN0_HELAM Glutathione S-transferase OS=Helicoverpa armigera OX=29058 PE=2 SV=1

Query_10248 tr|B6A8L4|B6A8L4_HELAM Glutathione S-transferase (Fragment) OS=Helicoverpa armigera OX=29058 PE=2 SV=1

Query_10249 tr|C8YL89|C8YL89_HELAM Glutathione S-transferase 16 OS=Helicoverpa armigera OX=29058 GN=GST16 PE=2 SV=1

Query_10250 tr|D7NI45|D7NI45_HELAM Glutathione S-transferase OS=Helicoverpa armigera OX=29058 GN=GST6 PE=2 SV=1

Query_10251 AIB07715.1 glutathione S-transferase GSTD1 [Helicoverpa armigera]

Query_10252 AIB07714.1 glutathione S-transferase GSTD3 [Helicoverpa armigera]

Query_10253 AIB07716.1 glutathione S-transferase GSTD4 [Helicoverpa armigera]

Query_10254 AIB07717.1 glutathione S-transferase GSTD5, partial [Helicoverpa armigera]

Query_10255 XP_021189521.1 glutathione S-transferase D7-like isoform X1 [Helicoverpa armigera]

Query_10256 Helicoverpa_armigera_GSTE14-like_isoform_X2

Query_10257 tr|Q7Z0Q7|Q7Z0Q7_HELAM Glutathione S-transferase (Fragment) OS=Helicoverpa armigera OX=29058 PE=2 SV=1

Query_10258 tr|Q7Z0Q8|Q7Z0Q8_HELAM Glutathione S-transferase (Fragment) OS=Helicoverpa armigera OX=29058 PE=2 SV=1

Query_10259 tr|Q7Z0Q9|Q7Z0Q9_HELAM Glutathione S-transferase (Fragment) OS=Helicoverpa armigera OX=29058 PE=2 SV=1

Query_10260 tr|A0A2A4JDE9|A0A2A4JDE9_HELVI Uncharacterized protein OS=Heliothis virescens OX=7102 GN=B5V51_3669 PE=3 SV=1

Query_10261 tr|A0A2A4IXQ2|A0A2A4IXQ2_HELVI Uncharacterized protein OS=Heliothis virescens OX=7102 GN=B5V51_11472 PE=3 SV=1

Query_10262 tr|A0A2A4JI76|A0A2A4JI76_HELVI Uncharacterized protein OS=Heliothis virescens OX=7102 GN=B5V51_1534 PE=3 SV=1

Query_10263 tr|A0A2A4JDN1|A0A2A4JDN1_HELVI Uncharacterized protein OS=Heliothis virescens OX=7102 GN=B5V51_3670 PE=3 SV=1

Query_10264 tr|A0A2A4JU40|A0A2A4JU40_HELVI Uncharacterized protein OS=Heliothis virescens OX=7102 GN=B5V51_11931 PE=3 SV=1

Query_10265 tr|A0A2A4IV17|A0A2A4IV17_HELVI Uncharacterized protein OS=Heliothis virescens OX=7102 GN=B5V51_12180 PE=3 SV=1

Query_10266 tr|A0A2A4IXK8|A0A2A4IXK8_HELVI Uncharacterized protein OS=Heliothis virescens OX=7102 GN=B5V51_10494 PE=3 SV=1

Query_10267 tr|A0A2A4JCV1|A0A2A4JCV1_HELVI Uncharacterized protein OS=Heliothis virescens OX=7102 GN=B5V51_3945 PE=3 SV=1

Query_10268 tr|A0A2A4JV70|A0A2A4JV70_HELVI Uncharacterized protein OS=Heliothis virescens OX=7102 GN=B5V51_11943 PE=3 SV=1

Query_10269 tr|A0A2A4IY34|A0A2A4IY34_HELVI Uncharacterized protein (Fragment) OS=Heliothis virescens OX=7102 GN=B5V51_11290 PE=4 SV=1

Query_10270 tr|A0A2A4JKT9|A0A2A4JKT9_HELVI Uncharacterized protein OS=Heliothis virescens OX=7102 GN=B5V51_845 PE=4 SV=1

Query_10271 NP_001165913.1 glutathione S-transferase D1 [Nasonia vitripennis]

Query_10272 NP_001165914.1 glutathione S-transferase D3 [Nasonia vitripennis]
 Query_10273 NP_001165915.1 glutathione S-transferase D5 [Nasonia vitripennis]
 Query_10274 NP_001165925.1 glutathione S-transferase T2 [Nasonia vitripennis]
 Query_10275 NP_001165926.1 glutathione S-transferase T1 [Nasonia vitripennis]
 Query_10276 NP_001165927.1 glutathione S-transferase T3 [Nasonia vitripennis]
 Query_10277 XP_001600187.1 PREDICTED: glutathione S-transferase D7 [Nasonia vitripennis]
 Query_10278 tr|A0A0L7KM86|A0A0L7KM86_9NEOP Glutathione S-transferase OS=Operophtera brumata OX=104452 GN=OBRU01_24524 PE=3 SV=1
 Query_10279 tr|A0A0L7LFQ3|A0A0L7LFQ3_9NEOP Glutathione S-transferase epsilon (Fragment) OS=Operophtera brumata OX=104452 GN=OBRU01_09353 PE=4 SV=1
 Query_10280 tr|A0A0L7LME0|A0A0L7LME0_9NEOP Glutathione S-transferase 1-6 (Fragment) OS=Operophtera brumata OX=104452 GN=OBRU01_05580 PE=3 SV=1
 Query_10281 tr|A0A0L7LPT4|A0A0L7LPT4_9NEOP Glutathione S-transferase OS=Operophtera brumata OX=104452 GN=OBRU01_04185 PE=3 SV=1
 Query_10282 tr|A0A0L7LTB4|A0A0L7LTB4_9NEOP Glutathione S-transferase OS=Operophtera brumata OX=104452 GN=OBRU01_01600 PE=3 SV=1
 Query_10283 tr|A0A0L7LTL7|A0A0L7LTL7_9NEOP Glutathione S-transferase epsilon 11 OS=Operophtera brumata OX=104452 GN=OBRU01_01599 PE=3 SV=1
 Query_10284 tr|A0A0L7LI53|A0A0L7LI53_9NEOP Glutathione S-transferase epsilon 6 (Fragment) OS=Operophtera brumata OX=104452 GN=OBRU01_07826 PE=4 SV=1
 Query_10285 tr|A0A0L7KLM3|A0A0L7KLM3_9NEOP Glutathione S-transferase 10 OS=Operophtera brumata OX=104452 GN=OBRU01_24503 PE=4 SV=1
 Query_10286 tr|A0A0L7L1M8|A0A0L7L1M8_9NEOP Glutathione S-transferase epsilon 3 OS=Operophtera brumata OX=104452 GN=OBRU01_16992 PE=4 SV=1
 Query_10287 tr|A0A0L7LM54|A0A0L7LM54_9NEOP Glutathione S-transferase 1 OS=Operophtera brumata OX=104452 GN=OBRU01_05579 PE=4 SV=1
 Query_10288 tr|A0A194QXR6|A0A194QXR6_PAPMA Glutathione S-transferase D7 OS=Papilio machaon OX=76193 GN=RR48_13110 PE=4 SV=1
 Query_10289 tr|A0A194R5D8|A0A194R5D8_PAPMA Glutathione S-transferase 1 OS=Papilio machaon OX=76193 GN=RR48_10522 PE=4 SV=1
 Query_10290 tr|A0A0N1PJW2|A0A0N1PJW2_PAPMA Glutathione S-transferase theta-1 OS=Papilio machaon OX=76193 GN=RR48_04090 PE=3 SV=1
 Query_10291 tr|A0A194QX62|A0A194QX62_PAPMA Glutathione S-transferase 1, isoform D OS=Papilio machaon OX=76193 GN=RR48_13184 PE=3 SV=1
 Query_10292 tr|A0A194REA6|A0A194REA6_PAPMA Glutathione S-transferase 1-1 OS=Papilio machaon OX=76193 GN=RR48_07011 PE=3 SV=1
 Query_10293 XP_014368559.1 PREDICTED: glutathione S-transferase E14-like [Papilio machaon]
 Query_10294 tr|I4DRD9|I4DRD9_PAPPL Glutathione S transferase D8 OS=Papilio polytes OX=76194 PE=2 SV=1
 Query_10295 tr|I4DRZ4|I4DRZ4_PAPPL Glutathione S transferase E8 (Fragment) OS=Papilio polytes OX=76194 PE=2 SV=1
 Query_10296 XP_013145092.1 PREDICTED: glutathione S-transferase theta-1-like [Papilio polytes]
 Query_10297 XP_013142369.1 PREDICTED: glutathione S-transferase 1, isoform D-like [Papilio polytes]
 Query_10298 XP_013142272.1 PREDICTED: glutathione S-transferase D7-like isoform X2 [Papilio polytes]

Query_10299 Papilio_polytes_GST1-1-like_isoform_X1

Query_10300 tr|A0A194PX26|A0A194PX26_PAPXU Glutathione S-transferase theta-1 OS=Papilio xuthus OX=66420 GN=RR46_11408 PE=3 SV=1

Query_10301 tr|Q4R1I6|Q4R1I6_PAPXU Glutathione-S-transferase OS=Papilio xuthus OX=66420 GN=GST-pxcs1 PE=3 SV=1

Query_10302 tr|I4DKS5|I4DKS5_PAPXU Glutathionetransferase OS=Papilio xuthus OX=66420 PE=2 SV=1

Query_10303 tr|A0A194QHF9|A0A194QHF9_PAPXU Glutathione S-transferase 1-1 OS=Papilio xuthus OX=66420 GN=RR46_01739 PE=3 SV=1

Query_10304 tr|I4DNY4|I4DNY4_PAPXU Glutathionetransferase OS=Papilio xuthus OX=66420 PE=2 SV=1

Query_10305 tr|A0A194QG68|A0A194QG68_PAPXU Glutathione S-transferase D7 OS=Papilio xuthus OX=66420 GN=RR46_08238 PE=3 SV=1

Query_10306 tr|I4DQ12|I4DQ12_PAPXU Glutathione S transferase E6 (Fragment) OS=Papilio xuthus OX=66420 PE=2 SV=1

Query_10307 tr|E0VVCV3|E0VVCV3_PEDHC GSTD1-5 protein, putative OS=Pediculus humanus subsp. corporis OX=121224 GN=8238066 PE=4 SV=1

Query_10308 tr|E0VGM2|E0VGM2_PEDHC GSTD1-5 protein, putative OS=Pediculus humanus subsp. corporis OX=121224 GN=8240051 PE=3 SV=1

Query_10309 tr|E0VGM3|E0VGM3_PEDHC GSTD1-5 protein, putative OS=Pediculus humanus subsp. corporis OX=121224 GN=8240052 PE=3 SV=1

Query_10310 tr|E0VUR9|E0VUR9_PEDHC GSTD1-5 protein, putative OS=Pediculus humanus subsp. corporis OX=121224 GN=8230516 PE=3 SV=1

Query_10311 tr|A0A1P8L0T5|A0A1P8L0T5_PIERA Glutathione S-transferase theta 1 OS=Pieris rapae OX=64459 PE=2 SV=1

Query_10312 tr|A0A1P8L0U3|A0A1P8L0U3_PIERA Glutathione S-transferase epsilon 1 OS=Pieris rapae OX=64459 PE=2 SV=1

Query_10313 tr|A0A1P8L0T0|A0A1P8L0T0_PIERA Glutathione S-transferase epsilon 2 OS=Pieris rapae OX=64459 PE=2 SV=1

Query_10314 tr|A0A1P8L0T7|A0A1P8L0T7_PIERA Glutathione S-transferase OS=Pieris rapae OX=64459 PE=2 SV=1

Query_10315 tr|A0A1P8L0S7|A0A1P8L0S7_PIERA Glutathione S-transferase delta 2 OS=Pieris rapae OX=64459 PE=2 SV=1

Query_10316 tr|A0A1P8L0S9|A0A1P8L0S9_PIERA Glutathione S-transferase delta 1 OS=Pieris rapae OX=64459 PE=2 SV=1

Query_10317 tr|A0A1P8L0S2|A0A1P8L0S2_PIERA Glutathione S-transferase epsilon 3 OS=Pieris rapae OX=64459 PE=2 SV=1

Query_10318 XP_022126447.1 glutathione S-transferase E14-like [Pieris rapae]

Query_10319 tr|O77409|O77409_PLUXY Glutathione S-transferase isozyme 3 OS=Plutella xylostella OX=51655 GN=GST3 PE=2 SV=1

Query_10320 tr|Q2ABX5|Q2ABX5_PLUXY Glutathione S-Transferase-Epsilon7 OS=Plutella xylostella OX=51655 GN=GST3 PE=2 SV=1

Query_10321 tr|X5D044|X5D044_PLUXY Glutathione S-transferase (Fragment) OS=Plutella xylostella OX=51655 PE=2 SV=1

Query_10322 tr|X5CJS2|X5CJS2_PLUXY Glutathione S-transferase OS=Plutella xylostella OX=51655 PE=2 SV=1

Query_10323 tr|X5CYF6|X5CYF6_PLUXY Glutathione S-transferase OS=Plutella xylostella OX=51655 PE=2 SV=1

Query_10324 tr|X5CCB3|X5CCB3_PLUXY Glutathione S-transferase OS=Plutella xylostella OX=51655 PE=2 SV=1

Query_10325 tr|X5CYG4|X5CYG4_PLUXY Glutathione S-transferase OS=Plutella xylostella OX=51655 PE=2 SV=1

Query_10326 tr|X5CJR9|X5CJR9_PLUXY Glutathione S-transferase OS=Plutella xylostella OX=51655 PE=2 SV=1

Query_10327 tr|A0A1L8D6F5|A0A1L8D6F5_PLUXY Glutathione S-Transferase-Epsilon6 OS=Plutella xylostella OX=51655 PE=2 SV=1

Query_10328 tr|X5CHJ9|X5CHJ9_PLUXY Glutathione S-transferase OS=Plutella xylostella OX=51655 PE=2 SV=1

Query_10329 tr|D7URW9|D7URW9_PLUXY Glutathione S-transferase delta OS=Plutella xylostella OX=51655 GN=PxGSTd PE=2 SV=1

Query_10330 tr|X5CCB0|X5CCB0_PLUXY Glutathione S-transferase OS=Plutella xylostella OX=51655 PE=2 SV=1

Query_10331 tr|X5CJR6|X5CJR6_PLUXY Glutathione S-transferase OS=Plutella xylostella OX=51655 PE=2 SV=1

Query_10332 tr|X5D048|X5D048_PLUXY Glutathione S-transferase OS=Plutella xylostella OX=51655 PE=2 SV=1

Query_10333 tr|D2I931|D2I931_SPOLT Glutathione S-transferase epsilon 3 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10334 tr|D2I930|D2I930_SPOLT Glutathione S-transferase epsilon 2 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10335 tr|A0A075X2X0|A0A075X2X0_SPOLT Glutathione S-transferase theta 1 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10336 tr|A0A075X3S8|A0A075X3S8_SPOLT Glutathione S-transferase delta 4 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10337 tr|A0A075X2I2|A0A075X2I2_SPOLT Glutathione S-transferase epsilon 4 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10338 tr|A0A075X2W2|A0A075X2W2_SPOLT Glutathione S-transferase epsilon 15 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10339 tr|A0A075X8X2|A0A075X8X2_SPOLT Glutathione S-transferase epsilon 6 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10340 tr|A0A075X8Y6|A0A075X8Y6_SPOLT Glutathione S-transferase delta 3 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10341 tr|A0A075X244|A0A075X244_SPOLT Glutathione S-transferase epsilon 8 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10342 tr|A0A075X8X7|A0A075X8X7_SPOLT Glutathione S-transferase epsilon 11 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10343 tr|Q1EGY7|Q1EGY7_SPOLT Gst1 OS=Spodoptera litura OX=69820 GN=gst1 PE=2 SV=1

Query_10344 tr|A0A075X250|A0A075X250_SPOLT Glutathione S-transferase epsilon 13 (Fragment) OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10345 tr|A0A075X2W6|A0A075X2W6_SPOLT Glutathione S-transferase delta 2 (Fragment) OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10346 tr|A0A075X2V8|A0A075X2V8_SPOLT Glutathione S-transferase epsilon 10 (Fragment) OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10347 tr|A0A075X2J6|A0A075X2J6_SPOLT Glutathione S-transferase delta 1 (Fragment) OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10348 tr|A0A075X2I7|A0A075X2I7_SPOLT Glutathione S-transferase epsilon 9 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10349 tr|A0A075X3R3|A0A075X3R3_SPOLT Glutathione S-transferase epsilon 7 (Fragment) OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10350 tr|A0A075X2V3|A0A075X2V3_SPOLT Glutathione S-transferase epsilon 5 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10351 tr|A0A075X3R8|A0A075X3R8_SPOLT Glutathione S-transferase epsilon 12 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10352 tr|A0A075X2J2|A0A075X2J2_SPOLT Glutathione S-transferase epsilon 14 OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10353 tr|A0A077D0A2|A0A077D0A2_SPOLT Glutathione S-transferase epsilon 3 (Fragment) OS=Spodoptera litura OX=69820 PE=2 SV=1

Query_10354 XP_022837684.1 glutathione S-transferase E14-like isoform X1 [Spodoptera litura]
Query_10355 TC003103_001 peptide: TC003103_001 pep:protein_coding
Query_10356 TC003104_001 peptide: TC003104_001 pep:protein_coding
Query_10357 TC003345_001 peptide: TC003345_001 pep:protein_coding
Query_10358 TC003347_001 peptide: TC003347_001 pep:protein_coding
Query_10359 TC003348_001 peptide: TC003348_001 pep:protein_coding
Query_10360 TC004442_001 peptide: TC004442_001 pep:protein_coding
Query_10361 TC004443_001 peptide: TC004443_001 pep:protein_coding
Query_10362 TC004444_001 peptide: TC004444_001 pep:protein_coding
Query_10363 TC004447_001 peptide: TC004447_001 pep:protein_coding
Query_10364 TC004448_001 peptide: TC004448_001 pep:protein_coding
Query_10365 TC004449_001 peptide: TC004449_001 pep:protein_coding
Query_10366 TC004450_001 peptide: TC004450_001 pep:protein_coding
Query_10367 TC004940_001 peptide: TC004940_001 pep:protein_coding
Query_10368 TC004941_001 peptide: TC004941_001 pep:protein_coding
Query_10369 TC004942_001 peptide: TC004942_001 pep:protein_coding
Query_10370 TC006215_001 peptide: TC006215_001 pep:protein_coding
Query_10371 TC009482_001 peptide: TC009482_001 pep:protein_coding
Query_10372 tr|A0A2W1BRE1|A0A2W1BRE1_HELAM Uncharacterized protein
OS=Helicoverpa armigera OX=29058 GN=HaOG200227 PE=3 SV=1

Movie Legends

Movie 1. Trajectory of MD simulations of DmNobo[WT]_EST-GSH or DmNobo[Asp113Ala]_EST-GSH.

The C α atoms of chain A of DmNobo[WT]_EST-GSH (blue) or DmNobo[Asp113Ala]_EST-GSH (white) in each frame were superimposed for 100 ns with those of DmNobo_EST-GSH at the initial state. The main chain of chain A of the protein is shown by a ribbon. Asp113 in DmNobo[WT]_EST-GSH, Ala113 in DmNobo[Asp113Ala]_EST-GSH, GSH, and EST are represented by sticks. Carbon atoms of EST in DmNobo[WT]_EST-GSH and those in DmNobo[Asp113Ala]_EST-GSH are colored in blue and magenta, respectively. The colors are the same as indicated in Fig. 4D.

Movie 2. An enlarged view of the trajectory of EST in MD simulations for DmNobo[WT]_EST-GSH or DmNobo[Asp113Ala]_EST-GSH.

An enlarged view of the trajectory of EST in MD simulations of DmNobo[WT]_EST-GSH or DmNobo[Asp113Ala]_EST-GSH (Movie 1)