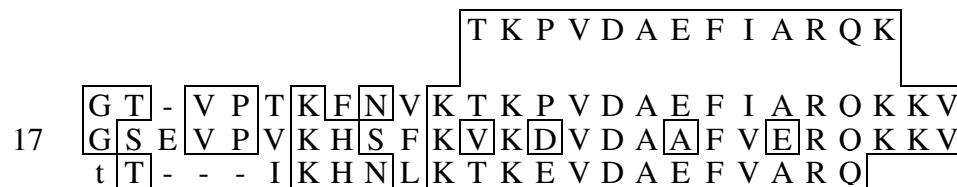


**Table 2. Peptide sequences identified by Edman sequence analysis or mass spectrometry and their alignment to the most similar database entry.**

Entry names und Datenbank accession numbers: <sup>1</sup>Arylphorin  $\beta$ ; ARYB\_MANSE, P14297 (*Manduca sexta*), <sup>2</sup>Arylphorin, Q9U5K4 (*Spodoptera litura*), <sup>3</sup>Q9VTW1, *Drosophila melanogaster* genomic sequence (SAM-methyltransferase); <sup>4</sup>Arylphorin  $\alpha$ , ARYA\_MANSE, P14296; <sup>5</sup>ABC transporter, Q8U6S8, *Agrobacterium tumefaciens*; <sup>6</sup>Arylphorin, ARY\_ANTPE, Q72Z1F8, *Antheraea pernyi*, <sup>7</sup>Arylphorin, O17478, *Hyalophora cecropia*; <sup>8</sup>Arylphorin, SSP2\_BOMMO, P20613, *Bombyx mori*; <sup>9</sup>Arylphorin, Q86QQ8, *Heliorithis virescens*; <sup>10</sup>Arylphorin, ARY\_AHTPE, Q7Z1F8, *Antheraea pernyi*. Small letters denote amino acids, which were not identified unequivocally. X, no clear signal detected. #, this peptide showed heterogeneities at certain positions indicating that it was a mixture of two very similar peptides. Modified N-glycosylation sequons are shown as black boxes. K, CB, T (ESI-MS/MS only!) or E (ESI-MS/MS only!) denotes peptides (or partial peptide sequences) derived from cleavage with lysyl endopeptidase, CNBr, trypsin or endoproteinase Glu-C, respectively. Numbers and other letters in peptide designations for K and CB peptides denote chromatographic pools. \*, sequences from Edman sequence analysis; +, peptides identified by mass spectrometry (MS/MS). In MS-derived sequences, the amino acid L stands for either L or I.

K6, K6-6\*

N-Term-1 (CB4B-1)\*  
**Arylphorin**<sup>1</sup>  
 N-Term-2\*



K7, K6-5c\*

e v d a e f v a r q k

K6-8b\*

i a t t y s v e e n i n n y t n k

**Arylphorin**<sup>7</sup>

61 I G K D Y D I E A N I D N Y T N K

**Arylphorin**<sup>1</sup>

63 E Y N I E A N I D N Y S N K

K7-4\*

E Y S I E A N I E N Y T N K

T4<sup>+</sup>

A V E D F L Q L Y R

**Arylphorin**<sup>1</sup>

78 A V E E F L Q L Y R

T6<sup>+</sup>

Y F F L P T A L D F Y Q

**Arylphorin**<sup>9</sup>

98 Y A F M P T A L D F Y Q

CB3,4A-3\*

g I V L P A P Y E V F P Q Y F V N X X L

**Arylphorin**<sup>4</sup>

156 G L V L P A P Y E V Y P Q Y F T N M E V

T11<sup>+</sup>

V F Y T N Y S N S L T Y P N D E Q R

**Arylphorin**<sup>4</sup>

210 V F Y A N Y S N S L S Y P N E E E R

T13<sup>+</sup>

Y A N Y S D S L T Y P N E E S R

CB7A-1\*

D E L V K Q

CB5A\*

D E L V K Q t G N K Y L Y K I

Q9VTW1<sup>3</sup>

226 D E L V M Q T C N K Y L N V I

---

T2 <sup>+</sup>		T G Y N P L L T T Y A Y P Y A Q R	
K2,3-1*		T G Y N P L L T T Y A Y P Y A Q R S N N Y D I H N E Q N Y e	
Arylphorin <sup>7</sup>	300	T G Y Y P L M T S Y Y Y P F A Q R P E N Y N L H S V K N Y E	
Arylphorin <sup>2</sup>	316	S N D Y N L H N E K N Y E Y I R	
T1 <sup>+</sup>		S N N Y E L H N E q n y e - - R	
T7 <sup>+</sup>		S N N Y D L H N E Q N Y E N L R	

K8-3*		T F F Q Y L Q K	
Arylphorin <sup>2</sup>	339	T F F Q F L Q K	
Arylphorin <sup>4</sup>	342	T F L Q Y L Q K G H F K	
K7-5*		T F F Q Y L Q S G H F K	

T3 <sup>+</sup>		A L N F V G N Y W Q N N A D L Y S E E V T K D Y Q
Arylphorin <sup>8</sup>	363	A I N F V G N Y W Q D N A D L Y G E E V T K D Y Q



T5<sup>+</sup>

Arylphorin<sup>4</sup>

411

Y	S	Y	L	P	S	S	L	D	F	Y	L	T
Y	S	F	I	P	S	A	L	D	F	Y	Q	T

K4-2\*

Arylphorin<sup>6</sup>

469

L	V	T	Y	F	D	Y	Y	D	F	<b>X</b>	<b>A</b>	<b>T</b>	N	K
L	V	T	F	F	E	Y	Y	D	F	D	A	T	N	T
L	V	T	Y	F	D	Y	F	D	F	<b>X</b>	<b>I</b>	<b>T</b>	N	K
L	V	T	Y	F	D	Y	F	D	F	<b>N</b>	<b>I</b>	<b>T</b>	N	K

K4-5\*

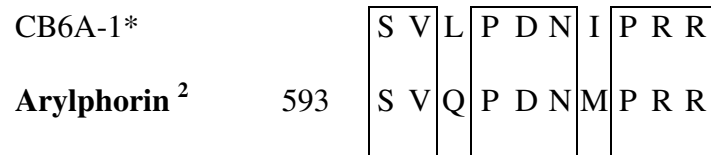
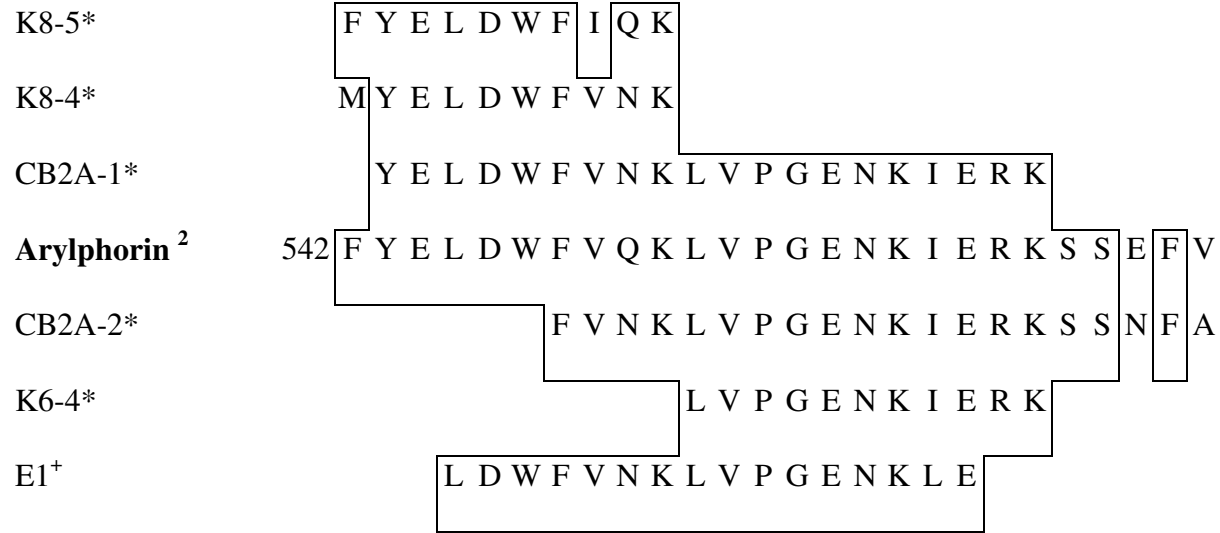
T14<sup>+</sup>

K8-2\*

Arylphorin<sup>2</sup>

510

S	E	V	S	T	D	A	V	F	K
S	D	V	A	S	D	A	V	F	K



— ————— — —————

CB1A-1\*

L P K G T K G G Y P F Q L F V F I Y P Y N G V T K

Arylphorin<sup>4</sup>

615

L P R G T K D G Y P F Q L F V F V Y P Y Q A V P K

K6-1\*

G T N G G Y P F Q L F V F V Y P Y K

K4-6\*

D V T I Y H E G E P F A W E Y N V P A Y F S K

Arylphorin<sup>6</sup>

675

D V S V Y H E G E Y H A Y E Y N V P A Y F S H