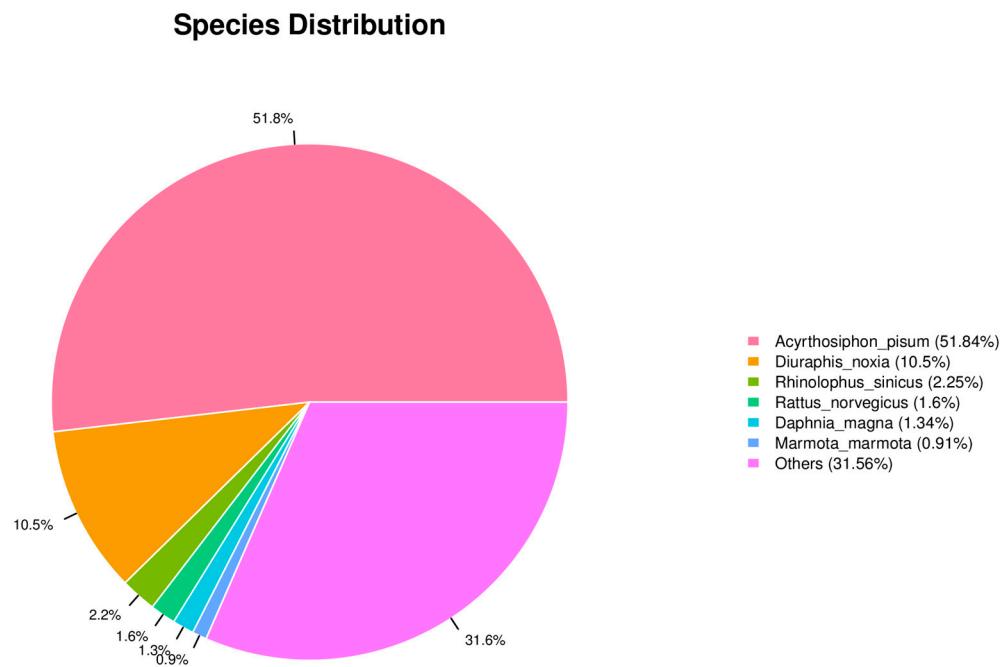
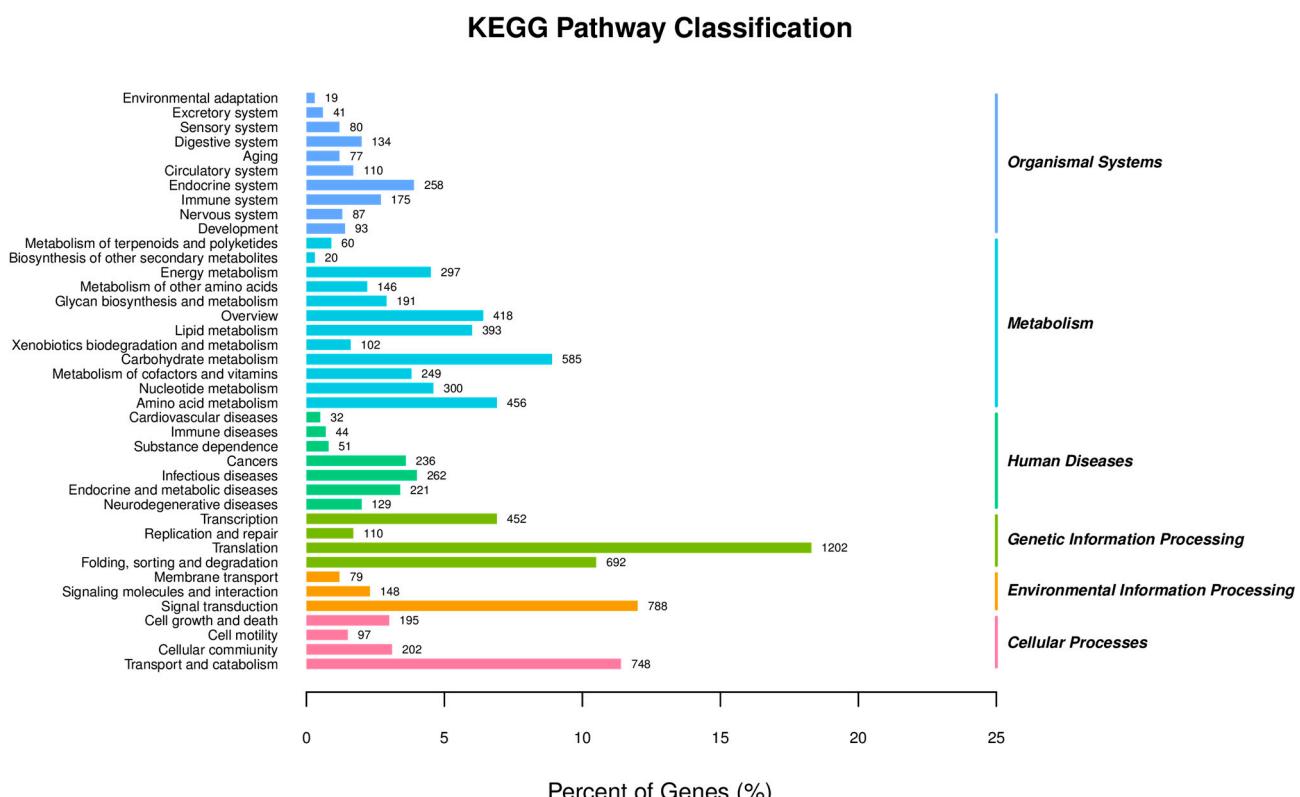


## Supplementary Materials:



**Figure S1.** Species distribution in the *M. sanborni* antennal transcriptome assembly.



**Figure S2.** KEGG classification of *M. sanborni* unigenes.

MsanOBP9	.....	0
MsanOBP2	MKVSAATAVLVALVATVQSSDPCNISTCYKSGTTKPIAV	40
MsanOBP4	.....MR	2
MsanOBP10	.....	0
Consensus		
MsanOBP9	.....MIKKTLLVSVFVI <sub>FGCLFSFNK</sub>	23
MsanOBP2	TPTHL <sub>PVQSSTPTNHPQT</sub> TYAKDHVGSTTKSGANATVT	80
MsanOBP4	GNYSL <sub>LMV</sub> FLLFTIQLQDIYCQKQELSGKCRAPDKA <sub>PLNLE</sub>	42
MsanOBP10	.....MEHLRSSNVFAIVMALLV	19
Consensus		
MsanOBP9	AADDADAADKE.....L	35
MsanOBP2	TASGASVNGTERPAVVKS <sub>S</sub> VGTGNSTTPKPTMTEGHVAL	120
MsanOBP4	IIINICQEEIKS.....AL	56
MsanOBP10	VQSSTRPQPDE.....I	31
Consensus		
MsanOBP9	ISKLFTVVFKCFKDA..DWGTCGEMLTTKYDIAQAKYKQC	73
MsanOBP2	KQKLNTIAVKCKD....ELHAPQEIMALVSNTVVPQNEQQ	156
MsanOBP4	LQEALDILNDGNLEQNTPSYSSRSRKREADEDLTNEERRVA	96
MsanOBP10	E <sub>EIKKTLYNA</sub> CSG....KFPITEEIKNDFKNSIISDDPNF	67
Consensus		
MsanOBP9	T <sub>CHLA</sub> CAGEELGLINTSGQ.PEP <sub>AKFLEYVNRI</sub> NNPGIKS	112
MsanOBP2	R <sub>CYLECVY</sub> KNLNLI <sub>KKNF</sub> SVEDGKAMAKIRFANQPEEHK	196
MsanOBP4	G <sub>CLLQCVY</sub> KKVKA <sub>DGF</sub> PVVDGLMKLYNEG <sub>VQDR</sub> NYYM	136
MsanOBP10	KCFLRCCLDEM <sub>SLIDE</sub> DGI.IDGDSLKEMAIDS <sub>SIKP</sub> ....	102
Consensus	c 1 c	
MsanOBP9	QLQLIYDKCQNVKGSE.....KCDLAEQFSIC	139
MsanOBP2	KAVTIIETCEKEAVIDPKTT.....EKCAAGR <sub>VIRNC</sub>	228
MsanOBP4	ATLSAVRHCISIAQQLKQQPSKS <sub>FDDG</sub> QTC <sub>CDL</sub> AYEMFEC	176
MsanOBP10	IIEQVSNQLK <sub>NV</sub> KQD.....GCQAAFEFISC	129
Consensus	C C C	
MsanOBP9	AFKESPAVSNNNYTSDGIII..	159
MsanOBP2	FVKNGEKINFFPKA.....	242
MsanOBP4	VSEKIEENCGVENKSNNLSQLRQ	198
MsanOBP10	GIKLNPLTMQLLPL.....	143
Consensus		

**Figure S3.** Multiple amino acid sequence alignment of candidate MsanOBPs.

MsanCSP1	.....MNLLAIFCYITVMCDTQFRRLEQPTTTPQVKRID	34
MsanCSP2	.....RYFRFDQIYFCQNIYSLK	18
MsanCSP4	.....MDSRIAVVCFVLAVFAVD	18
MsanCSP7	MARSSSSVTMKVFVIAVCVCAALARPEEAKMENKPTVVKS	40
Consensus		
MsanCSP1	QPATIATRIGQATIAPRGQVTAAPQIEQAAIASRIGQGF	74
MsanCSP2	QTKMAHLNLFVVLVASLV.....	36
MsanCSP4	QTVGAPQKDAVATGG.....	33
MsanCSP7	ETLAAPILPTTIVKRATP.....	57
Consensus		
MsanCSP1	QNVNNSVSPTTDGRKTTRQTSSYPTTRYDFIDIEAVMNNE	114
MsanCSP2	.....CFTLAEKYTTKFDNFDVDKVLNNDR	62
MsanCSP4	.....SAYTNKYDHIDIDQVLASKR	53
MsanCSP7	.....QVVSTQQDSSLNVSEDVLDKALSDRR	84
Consensus	r	
MsanCSP1	I IKILFNCVMNQGPCTREGGLELKWIVPDAIQTECAKCNER	154
MsanCSP2	ILTSYIKCLLDQGNCTNEGRELKRVILPDALKTDCSKCTGV	102
MsanCSP4	LVNSYVQCCLLDKKPCPTPEGAEELRKILPDALKTQCAKNAT	93
MsanCSP7	FVQRQLKCATGEGPCDPPIGRKIKAHAPLVLRGMCVKCSQS	124
Consensus	c c g p c kc	
MsanCSP1	QRKQAGKVLAHLLQYKPEYWNLVKKFDPPNNIYLRKYMVD	194
MsanCSP2	QKDRSEKVIKFLIKNRAADFHDHTAKYDPSGEYKKKLEKF	142
MsanCSP4	QKNAALKVVERLQRDYDKEWKQQLLDKWDPKREQFQKFQQF	133
MsanCSP7	EIKQIQRVMSHIQKNYPKEYTKMLKQYQSGF.....	155
Consensus	v	
MsanCSP1	NDDDEKLSLQKLTTNTT	211
MsanCSP2	EAERIAAAKN.....	152
MsanCSP4	LTEEEKKGGVVKF....	146
MsanCSP7	.....	155
Consensus		

**Figure S4.** Multiple amino acid sequence alignment of candidate MsanCSPs.

MperSNMP1.1	MGAPTTIIVIGIPLLFGVIVGVFAFPKMIKKRILESKAI	40	MperSNMP1.1	IPTDTNLASFSGGIVCRSLAFDIVEETRYNGLVVFETYSQIL	320
MperSNMP1.X2	.....	0	MperSNMP1.X2	IPTDTNLASFSGGIVCRSLAFDIVEETRYNGLVVFETYSQIL	275
SflaSNMP1-like.X1	MGAPTTIIVIGIPLLFGVIVGVFAFPKMIKKRILESKAI	40	SflaSNMP1-like.X1	IPTDTNLASFSGGIVCRSLAFDIVEETRYNGLVVFETYSQIL	219
SflaSNMP1-like.X2	.....MNVPCSVCVVNPNFVVLASKAI	21	SflaSNMP1-like.X2	IPTDTNLASFSGGIVCRSLAFDIVEETRYNGLVVFETYSQIL	300
SflaSNMP1-like.X3	.....	0	SflaSNMP1-like.X3	IPTDTNLASFSGGIVCRSLAFDIVEETRYNGLVVFETYSQIL	274
ApisSNMP1	MGAPTTIIVIGIPLLFGVIVGVFAFPKMIKKRILESKSL	40	ApisSNMP1	IPTDTNLASFSGGIVCRSLAFDIVEETRYNGLVVFETYSQIL	220
DnoxSNMP1	MGAPTTIIVIGIPLLFGVIVGVFAFPKMIKKRILESKSI	40	DnoxSNMP1	IPTDTNLASFSGGIVCRSLAFDIVEETRYNGLVVFETYSQIL	320
AcrasSNMP1	.....	6	AcrasSNMP1	IPTDTNLASFSGGIVCRSLAFDIVEETRYNGLVVFETYSQIL	286
AgosSNMP1	MGAPTTIIVIGIPLLFGVIVGVFAFPKMIKKRILESKL	40	AgosSNMP1	IPTDTNLASFSGGIVCRSLAFDIVEETRYNGLVVFETYSQIL	320
RmaiSNMP1-like	MGAPTTIIVIGIPLLFGVIVGVFAFPKMIKKRILESKL	40	RmaiSNMP1-like	IPTDTNLASFSGGIVCRSLAFDIVEETRYNGLVVFETYSQIL	320
MsanSNMP1	.....	0	MsanSNMP1	IPTDTNLASFSGGIVCRSLAFDIVEETRYNGLVVFETYSQIL	77
Consensus	.....	.....	Consensus	i dt lasfsgd crsl d et yngl vfev a l	
MperSNMP1.1	NPRSNMRQMWSHPFYIADFKIYLNVNTPEEAQKGELVII	80	MperSNMP1.1	VKEPEEKCGCLNNKKCLKGALDLTNCSGPIIATLPHFYK	360
MperSNMP1.X2	.....MRQMWSHPFYIADFKIYLNVNTPEEAQKGELVII	25	MperSNMP1.X2	VKEPEEKCGCLNNKKCLKGALDLTNCSGPIIATLPHFYK	315
SflaSNMP1-like.X1	NPRSNMRQMWSHPFYIADFKIYLNVNTPEEAQKGELVII	80	SflaSNMP1-like.X1	VKEPEEKCGCLNNKKCLKGALDLTNCSGPIIATLPHFYK	359
SflaSNMP1-like.X2	NPRSNMRQMWSHPFYIADFKIYLNVNTPEEAQKGELVII	61	SflaSNMP1-like.X2	VKEPEEKCGCLNNKKCLKGALDLTNCSGPIIATLPHFYK	240
SflaSNMP1-like.X3	.....MRQMWSHPFYIADFKIYLNVNTPEEAQKGELVII	25	SflaSNMP1-like.X3	VKEPEEKCGCLNNKKCLKGALDLTNCSGPIIATLPHFYK	314
ApisSNMP1	NPRSNMRQMWSHPFYIADFKIYLNVNTPEEAQKGELVII	80	ApisSNMP1	VKEPEEKCGCLNNKKCLKGALDLTNCSGPIIATLPHFYK	360
DnoxSNMP1	NPRSNMRQMWSHPFYIADFKIYLNVNTPEEAQKGELVII	80	DnoxSNMP1	VKEPEEKCGCLNNKKCLKGALDLTNCSGPIIATLPHFYK	360
AcrasSNMP1	NPRSNMRQMWSHPFYIADFKIYLNVNTPEEAQKGELVII	46	AcrasSNMP1	VKEPEEKCGCLNNKKCLKGALDLTNCSGPIIATLPHFYK	326
AgosSNMP1	NPRSNMRQMWSHPFYIADFKIYLNVNTPEEAQKGELVII	80	AgosSNMP1	VKEPEEKCGCLNNKKCLKGALDLTNCSGPIIATLPHFYK	360
RmaiSNMP1-like	NPRSNMRQMWSHPFYIADFKIYLNVNTPEEAQKGELVII	80	RmaiSNMP1-like	VKEPEEKCGCLNNKKCLKGALDLTNCSGPIIATLPHFYK	360
MsanSNMP1	.....	0	MsanSNMP1	VKEPEEKCGCLNNKKCLKGALDLTNCSGPIIATLPHFYK	117
Consensus	.....	.....	Consensus	vkpeekc cln kkclkgaldltncsg piiatlpfyk	
MperSNMP1.1	KEVGPIVYQEWKEKENLIDDIADATIVEFSKNTIEVDENMS	120	MperSNMP1.1	SEPYLNNDGGLSDAEKHEIICQMYFEPMTGSPLLGTRQF	400
MperSNMP1.X2	KEVGPIVYQEWKEKENLIDDIADATIVEFSKNTIEVDENMS	75	MperSNMP1.X2	SEPYLNNDGGLSDAEKHEIICQMYFEPMTGSPLLGTRQF	355
SflaSNMP1-like.X1	KEVGPIVYHEWKFKREDLEDDSKSDIVEFSKNTIEVDENMS	120	SflaSNMP1-like.X1	SEPYLNNDGGLSDENHINMIFEPMTGSPLLGTRQF	399
SflaSNMP1-like.X2	REVGPYVYHEWKFKREDLEDDSKSDIVEFSKNTIEVDENMS	101	SflaSNMP1-like.X2	SEPYLNNDGGLSDENHINMIFEPMTGSPLLGTRQF	380
SflaSNMP1-like.X3	KEVGPIVYHEWKFKREDLEDDSKSDIVEFSKNTIEVDENMS	75	SflaSNMP1-like.X3	SEPYLNNDGGLSDENHIMMIFEPMTGSPLLGTRQF	254
ApisSNMP1	KEIGGPVYHEWKKEKENLIDDIADATIVEFSKNTIEVDENMS	120	ApisSNMP1	SEPYLNNDGGLSDENHIMMIFEPMTGSPLLGTRQF	400
DnoxSNMP1	KEVGPIVYHEWKKEKENLIDDDMADIVEFSKNTIEVDENMS	120	DnoxSNMP1	SEPYLNNDGGLSDENHIMMIFEPMTGSPLLGTRQF	400
AcrasSNMP1	KEVGPIVYHEWKKEKENLIDDDINEDIVEFSKNTIEVDENMS	86	AcrasSNMP1	SEPYLNNDGGLSDENHIMMIFEPMTGSPLLGTRQF	400
AgosSNMP1	KEVGPIVYHEWKKEKENLIDDDINEDIVEFSKNTIEVDENMS	120	AgosSNMP1	SEPYLNNDGGLSDENHIMMIFEPMTGSPLLGTRQF	400
RmaiSNMP1-like	KEVGPIVYHEWKKEKENLIDDDINEDIVEFSKNTIEVDENMS	120	RmaiSNMP1-like	SEPYLNNDGGLSDENHIMMIFEPMTGSPLLGTRQF	400
MsanSNMP1	.....	0	MsanSNMP1	SEPYLNNDGGLSDENHIMMIFEPMTGSPLLGTRQF	157
Consensus	.....	.....	Consensus	se yl d glp p h myfepmtg pllyg r qf	
MperSNMP1.1	TPLPLTGDEIIVMPHLMAMIGVNTMTHIKMKPAALGIVNNKAIP	160	MperSNMP1.1	NIFLKRPSKISVNMKTIDPEEKLPLFWEEGALKNTWNS	440
MperSNMP1.X2	TPLPLTGDEIIVMPHLMAMIGVNTMTHIKMKPAALGIVNNKAIP	115	MperSNMP1.X2	NIFLKRPSKISVNMKTIDPEEKLPLFWEEGALKNTWNS	395
SflaSNMP1-like.X1	TPLPLTGDEIITMPHLMALGMGVNTMTHIKMKPAALGIVNNKAIP	160	SflaSNMP1-like.X1	NIFLKRPSKISVNMKTIDPEEKLPLFWEEGALKNTWNS	439
SflaSNMP1-like.X2	TPLPLTGDEIITMPHLMALGMGVNTMTHIKMKPAALGIVNNKAIP	141	SflaSNMP1-like.X2	NIFLKRPSKISVNMKTIDPEEKLPLFWEEGALKNTWNS	420
SflaSNMP1-like.X3	TPLPLTGDEIITMPHLMALGMGVNTMTHIKMKPAALGIVNNKAIP	115	SflaSNMP1-like.X3	NIFLKRPSKISVNMKTIDPEEKLPLFWEEGALKNTWNS	394
ApisSNMP1	TPLPLTGDEIIVMPHLMAMIGVNTMTHIKMKPAALGIVNNKAIP	160	ApisSNMP1	NIFLKRPSKISVNMKTIDPEEKLPLFWEEGALKNTWNS	440
DnoxSNMP1	TPLPLTGDEIIVMPHLMAMIGVNTMTHIKMKPAALGIVNNKAIP	160	DnoxSNMP1	NIFLKRPSKISVNMKTIDPEEKLPLFWEEGALKNTWNS	440
AcrasSNMP1	TPLPLTGDEIIVMPHLMAMIGVNTMTHIKMKPAALGIVNNKAIP	126	AcrasSNMP1	NIFLKRPSKISVNMKTIDPEEKLPLFWEEGALKNTWNS	406
AgosSNMP1	TPLPLTGDEIILMPHLMAMIGVNTMTHIKMKPAALGIVNNKAIP	160	AgosSNMP1	NIFLKRPSKISVNMKTIDPEEKLPLFWEEGALKNTWNS	440
RmaiSNMP1-like	TPLPLTGDEIILMPHLMAMIGVNTMTHIKMKPAALGIVNNKAIP	160	RmaiSNMP1-like	NIFLKRPSKISVNMKTIDPEEKLPLFWEEGALKNTWNS	440
MsanSNMP1	.....	0	MsanSNMP1	NIFLKRPSKISVNMKTIDPEEKLPLFWEEGALKNTWNS	197
Consensus	.....	.....	Consensus	n flk e ki mktl e kpl fw eeg alnkntwt	
MperSNMP1.1	LYLPDQTSAFMMGTANDIMWNGLDINCTSGEFAAVACISQ	200	MperSNMP1.1	QIKNKLNPLPITIDKHYIIVVAEGVVFIIILAVVWYNNSVK	480
MperSNMP1.X2	LYLPDQTSAFMMGTANDIMWNGLDINCTSGEFAAVACISQ	155	MperSNMP1.X2	QIKNKLNPLPITIDKHYIIVVAEGVVFIIILAVVWYNNSVK	435
SflaSNMP1-like.X1	LLYPDQNTNAFMATIANDIMWNGLDINCTSSEFFAIVACISQ	200	SflaSNMP1-like.X1	QIKNKLNPLPITIDKHYIIVVAEGVVFIIILAVVWYNNSVK	479
SflaSNMP1-like.X2	LLYPDQNTNAFMATIANDIMWNGLDINCTSSEFFAIVACISQ	181	SflaSNMP1-like.X2	QIKNKLNPLPITIDKHYIIVVAEGVVFIIILAVVWYNNSVK	460
SflaSNMP1-like.X3	LLYPDQNTNAFMATIANDIMWNGLDINCTSSEFFAIVACISQ	155	SflaSNMP1-like.X3	QIKNKLNPLPITIDKHYIIVVAEGVVFIIILAVVWYNNSVK	434
ApisSNMP1	LYLPDQTSAFMMGTANDIMWNGLDINCTSSEFFAIVACISQ	200	ApisSNMP1	QIKNKLNPLPITIDKHYIIVVAEGVVFIIILAVVWYNNSVK	480
DnoxSNMP1	FLYPDQTSVEFMMGTANDIMWNGLDINCTSREFAVACISQ	200	DnoxSNMP1	QIKNKLNPLPITIDKHYIIVVAEGVVFIIILAVVWYNNSVK	480
AcrasSNMP1	LYLPDQTSAFMMGTANDIMWNGLDINCTSGEFAAVACISQ	166	AcrasSNMP1	QIKNKLNPLPITIDKHYIIVVAEGVVFIIILAVVWYNNSVK	446
AgosSNMP1	LYLPDQTSAFMMGTANDIMWNGLDINCTSGEFAAVACISQ	200	AgosSNMP1	QIKNKLNPLPITIDKHYIIVVAEGVVFIIILAVVWYNNSVK	480
RmaiSNMP1-like	LYLPDQTSAFMMGTANDIMWNGLDINCTSGEFAAVACISQ	200	RmaiSNMP1-like	QIKNKLNPLPITIDKHYIIVVAEGVVFIIILAVVWYNNSVK	480
MsanSNMP1	.....	0	MsanSNMP1	QIKNKLNPLPITIDKHYIIVVAEGVVFIIILAVVWYNNSVK	237
Consensus	.....	.....	Consensus	qiknkl lpiti ky k v g vfiilav nynsvk	
MperSNMP1.1	IRQNSASLHKISKDHFKESSLFGVKNGTIESNSRYYIWRGKTT	240	MperSNMP1.1	TMEVTPRK	487
MperSNMP1.X2	IRQNSASLHKISKDHFKESSLFGVKNGTIESNSRYYIWRGKTT	195	MperSNMP1.X2	TMEVTPRK	442
SflaSNMP1-like.X1	IRQNSASLHKISKDHFKESSLFGVKNGTIESNSRYYIWRGKTT	240	SflaSNMP1-like.X1	TMEVTPRK	486
SflaSNMP1-like.X2	IRQNSASLHKIKNNHHFKSSLFGVKNGTIESNSRYYIWRGKTT	221	SflaSNMP1-like.X2	TMEVTPRK	467
SflaSNMP1-like.X3	IRQNSASLHKIKNNHHFKSSLFGVKNGTIESNSRYYIWRGKTT	195	SflaSNMP1-like.X3	TMEVTPRK	441
ApisSNMP1	IRQNSASLHKISKDHFKESSLFGVKNGTIESNSRYYIWRGKTT	240	ApisSNMP1	TMEVTPRK	487
DnoxSNMP1	IRQNSASLHKISKDHFKESSLFGVKNGTIESNSRYYIWRGKTT	240	DnoxSNMP1	TMEVTPRK	487
AcrasSNMP1	IRQNSASLHKISKDHFKESSLFGVKNGTIESNSRYYIWRGKTT	206	AcrasSNMP1	TMEVTPRK	453
AgosSNMP1	IRQNSASLHKISKDHFKESSLFGVKNGTIESNSRYYIWRGKTT	240	AgosSNMP1	TMEVTPRK	487
RmaiSNMP1-like	IRQNSASLHKISKDHFKESSLFGVKNGTIESNSRYYIWRGKTT	240	RmaiSNMP1-like	TMEVTPRK	487
MsanSNMP1	.....	0	MsanSNMP1	TMEVTPRK	244
Consensus	.....	.....	Consensus	t e p	
MperSNMP1.1	TFATEPVGGVIRFNKHHQCVVPGCZECNRMVYIYGTDTTIFQPF	280			
MperSNMP1.X2	TFATEPVGGVIRFNKHHQCVVPGCZECNRMVYIYGTDTTIFQPF	235			
SflaSNMP1-like.X1	MF..IVVGCVIRFNKHHQCVVPGCZECNRMVYIYGTDTTIFQPF	279			
SflaSNMP1-like.X2	MF..IVVGCVIRFNKHHQCVVPGCZECNRMVYIYGTDTTIFQPF	260			
SflaSNMP1-like.X3	MF..IVVGCVIRFNKHHQCVVPGCZECNRMVYIYGTDTTIFQPF	234			
ApisSNMP1	TFATEPVGGVIRFNKHHQCVVPGCZECNRMVYIYGTDTTIFQPF	280			
DnoxSNMP1	TFATEPVGGVIRFNKHHQCVVPGCZECNRMVYIYGTDTTIFQPF	280			
AcrasSNMP1	MFSPLEVGCVIRFNKHHQCVVPGCZECNRMVYIYGTDTTIFQPF	246			
AgosSNMP1	MFSPLEVGCVIRFNKHHQCVVPGCZECNRMVYIYGTDTTIFQPF	280			
RmaiSNMP1-like	MFSPLEVGCVIRFNKHHQCVVPGCZECNRMVYIYGTDTTIFQPF	280			
MsanSNMP1	...MFVGCVIRFNKHHQCVVPGCZECNRMVYIYGTDTTIFQPF	37			
Consensus	vggv rfn kh vwp ecn iygtdttif pf				

**Figure S5.** Multiple amino acid sequence alignment of aphids' SNMPs. Mper: *Myzus persicae*; Afla: *Siphha flava*; Apis: *Acyrtosiphon pisum*; Dnox: *Diuraphis noxia*; Acras: *Aphis craccivora*; Agos: *Aphis gossypii*; Rmai: *Rhopalosiphum maidis*; Msan: *Macrosiphoniella sanborni*.

**Table S1** Primers of *M. sanborni* chemosensory genes used for qRT-PCR

Gene Name	Forward Primer (5'-3')	Reverse Primer (5'-3')
MsanOBP2	GCTCGGACCCATGTAACATATC	CTGTCGTGACCGTAGCATTAG
MsanOBP4	CGTAGAGTTGCAGGGTCTTG	GAGGGCTGCTGTTGCTTAG
MsanOBP9	CAGATGCAGCGATAAGGAA	GTTCTGGTTGCCCTGAAGTA
MsanOBP10	CACGACCACAACCAGATGAA	GACATCTCGTCCAAGCAACA
MsanORCO	CAATGGGTCTACGTGAATGAG	TGCTTGGTATGCGAGAATGG
MsanOR2	GTGGCCCGGTATGAGTTAC	CATTCGTCACCTGGAGGTATTG
MsanOR4	CACTGTCACATCGGAGAAGT	GAAATCAACGCTCTGGATGC
MsanOR43b-1	CGCTGGTTATAGTCCCCTG	GACGCCGTGAAATAGATGA
MsanOR43b-2	GGGATGGAGTGACGACCATA	GTGGACTACGATGAACAACCAC
MsanOR46a-1	AATCGCGACGGTTCAATCAG	TTGCCACTGACAGCGTATTG
MsanOR46a-2	CACGACGGTTGATTGGATA	GACCTGCATCTGACAGCATA
MsanOR64	GGTAACCGACACAGACACATAC	CTGGCGGTAATACCCGATTG
MsanCSP1	CGACTTGAGCAACCGACTAC	CTGGAAACCTTGTCCGATCC
MsanCSP2	CGAAGGCCGAGAATTGAAGAG	CACCTGATGGGTCGTATTGG
MsanCSP4	CACCAGAAGGAGCTGAACCTAG	GTTCACGTTAGGGTCCCCT
MsanCSP7	CTACTCCTCAGGTCGTCTCTAC	ACTTGACGCACATTCCCTCTC
MsanIR25a	GACCGTACTGAAACCCGAAG	CTCCTCCTGGCGGAGTAATG
MsanIR40a	GGGTGGACGAGACGATAAAC	CACCAAATTGCGCTCGTATG
MsanSNMP1	ACGGGACAGATACCACGATA	AGGAGCACCTGAACAGTTG
Msanβ-actin (Ref.)	GGATCGGTGGTTCCATTCTC	TCACAGCCTGCATCGTAATC

**Table S2** Sequencing quality overview of antennal transcriptome of *M. sanborni*

Sample	Raw_Reads	Raw_Bases	Valid_Reads	Valid_Bases	Valid%	Q20%
AL1	51497638	7.72G	50069524	7.37G	97.23	98.71
AL2	49167846	7.38G	47948188	7.04G	97.52	98.59
AL3	57552466	8.63G	55919454	8.22G	97.16	98.69
AP1	55464352	8.32G	53863906	7.93G	97.11	98.76
AP2	57571092	8.64G	55611788	8.19G	96.60	98.71
AP3	57311562	8.60G	55917338	8.24G	97.57	98.80

**Table S3** Assembly summary of *M. sanborni* antennal transcriptome

Index	All	GC%	Min	Median	Max	Total	N50
			Length	Length	Length	Assembled	Bases
Transcript	52249	42.14	201	449	15647	47335333	1656
Gene	28323	41.22	201	314	15647	21319147	1538

**Table S4** DIAMOND annotation result statistics

Database	Annotated Gene Numbers	Ratio (%)
GO	11983	42.31
KEGG	6577	23.22
Pfam	11844	41.82
swissprot	9836	34.73
eggNOG	15144	53.47
NR	12042	42.52

**Table S5** Sequence information and best blasts match information of candidate chemosensory genes

Unigene Reference	Gene Name	Length (nt)	ORF (aa)	Blastx (Reference/Name/Species)	Best Hit	Evalue	Identity	TMD (No.)	Signal Peptide	Full Length
TRINITY_DN31343_c0_g1	MsanOBP2	1076	243	CAR85629.1/odorant-binding protein 2, partial [ <i>Acyrthosiphon pisum</i> ]	1.00E-154	96.43	0	19	Yes	
TRINITY_DN7859_c0_g1	MsanOBP4	782	200	APB03427.1/odorant-binding protein 4 [ <i>Sitobion avenae</i> ]	4.00E-141	98.00	0	22	Yes	
TRINITY_DN34070_c1_g8	MsanOBP9	763	160	AXE72026.1/OBP9 [ <i>Megoura viciae</i> ]	6.00E-89	88.89	0	24	Yes	
TRINITY_DN35164_c1_g2	MsanOBP10	641	144	APB03433.1/odorant-binding protein 10 [ <i>Sitobion avenae</i> ]	6.30E-64	83.20	0	24	Yes	
TRINITY_DN36123_c1_g6	MsanCSP1	1011	213	ULF48242.1/chemosensory protein 1 [ <i>Acyrthosiphon pisum</i> ]	1.00E-132	82.61	0	16	Yes	
TRINITY_DN4112_c0_g1	MsanCSP7	843	156	ULF48248.1/chemosensory protein 7 [ <i>Acyrthosiphon pisum</i> ]	2.00E-107	98.06	0	24	Yes	
TRINITY_DN36430_c0_g14	MsanCSP2	579	153	ULF48243.1/chemosensory protein 2 [ <i>Acyrthosiphon pisum</i> ]	3.00E-82	92.37	0	41	No	
TRINITY_DN36313_c1_g3	MsanCSP4	535	147	AWV63292.1/chemosensory protein 4 [ <i>Myzus persicae</i> ]	6.00E-76	92.59	0	22	Yes	
TRINITY_DN34819_c0_g2	MsanORCO	2503	464	XP_022162891.1/odorant receptor coreceptor isoform X1 [ <i>Myzus persicae</i> ]	1.30E-258	98.10	7	0	Yes	
TRINITY_DN35161_c1_g4	MsanOR2	3164	434	XP_016662512.2/odorant receptor 2a-like [ <i>Acyrthosiphon pisum</i> ]	2.50E-182	82.91	6	0	Yes	
TRINITY_DN37439_c1_g9	MsanOR43b-1	2375	400	XP_016660447.1/PREDICTED: odorant receptor 43b-like isoform X2 [ <i>Acyrthosiphon pisum</i> ]	2.00E-99	54.60	6	0	No	
TRINITY_DN435_c0_g1	MsanOR4	1295	399	AQS60743.1/PREDICTED: olfactory receptor 4 protein	5.80E-117	76.20	6	0	No	

				[ <i>Acyrthosiphon pisum</i> ]					
TRINITY_DN37765_c2_g1	MsanOR64	1281	391	UMT69240.1/PREDICTED: odorant receptor 64 [ <i>Myzus persicae</i> ]	4.00E- 163	59.95	6	0	No
TRINITY_DN36837_c1_g2	MsanOR43b- 2	1409	365	XP_016657134.1/PREDICTED: odorant receptor 43b-like [ <i>Acyrthosiphon pisum</i> ]	7.00E- 100	54.70	6	0	Yes
TRINITY_DN34686_c1_g1	MsanOR46a- 1	1758	329	XP_016660259.1/PREDICTED: odorant receptor 46a-like [ <i>Acyrthosiphon pisum</i> ]	1.50E- 112	47.90	5	0	Yes
TRINITY_DN37775_c1_g4	MsanOR46a- 2	969	323	XP_016660259.1/PREDICTED: odorant receptor 46a-like [ <i>Acyrthosiphon pisum</i> ]	1.30E- 110	64.80	5	0	No
TRINITY_DN36559_c0_g1	MsanIR25a	2512	838	XP_022161260.1/ionotropic receptor 25a [ <i>Myzus persicae</i> ]	0.00E+00	93.76	3	22	No
TRINITY_DN37723_c2_g7	MsanIR40a	2403	739	XP_022182311.1/ ionotropic receptor 40a isoform X2 [ <i>Myzus persicae</i> ]	0.00E+00	96.36	3	52	No
TRINITY_DN36573_c2_g4	MsanIRDelta- 1b	2769	527	XP_029347273.1/glutamate receptor ionotropic, delta-1-like [ <i>Acyrthosiphon pisum</i> ]	2.00E- 284	93.14	3	0	Yes
TRINITY_DN37799_c1_g4	MsanIRDelta- 1a	1175	368	XP_016663076.2/glutamate receptor ionotropic, delta-1-like [ <i>Acyrthosiphon pisum</i> ]	1.60E- 190	92.10	3	0	No
TRINITY_DN35872_c3_g1	MsanSNMP1	3372	246	XP_003240759.4/sensory neuron membrane protein 1 [ <i>Acyrthosiphon pisum</i> ]	7.00E- 150	90.57	1	0	Yes

**Table S6** Amount and accession numbers of olfactory-related proteins of different aphid species

Species	OBP		CSP		OR		IR		GR		SNMP	
	No.	Accession	No.	Accession								
<i>Acyrtosiphon pisum</i>	34	NP_001153534.1	16	NP_001119652.1	32	XP_029346749.1	11	XP_008183092.2	17	XP_003244120.4	1	XP_003240759.4
		NP_001353810.1		NP_001119651.1		XP_029346718.1		XP_029345195.1		XP_016660313.2		
		NP_001155983.1		NP_001119650.1		XP_029347684.1		XP_016662281.2		XP_029344591.1		
		NP_001153535.1		NP_001119649.1		XP_029347565.1		XP_029346904.1		XP_029344589.1		
		NP_001153533.1		NP_001128404.1		XP_029347069.1		XP_029347313.1		XP_029344230.1		
		NP_001153531.1		NP_001156200.1		XP_029347068.1		XP_029347065.1		XP_029343633.1		
		NP_001153532.1		ULF48242.1		XP_016662512.2		XP_029344228.1		XP_016657079.2		
		NP_001153530.1		ULF48243.1		XP_029342650.1		XP_029343909.1		XP_016662919.1		
		NP_001153529.1		ULF48244.1		XP_016657950.2		XP_029347699.1		XP_008185853.2		
		NP_001153528.1		ULF48245.1		XP_016663583.1		XP_029347698.1		XP_016659625.1		
		NP_001153527.1		ULF48246.1		XP_016661819.1		XP_016661577.1		XP_008186707.1		
		NP_001153526.1		ULF48247.1		XP_016660447.1				XP_008178128.1		
		NP_001153525.1		ULF48248.1		XP_016657134.1				XP_003248767.1		
		CAR85635.1		ULF48249.1		XP_008188009.1				XP_001942787.2		
		XP_029344816.1		ULF48250.1		XP_003245950.2				XP_029343507.1		
		XP_016663220.1		ULF48251.1		XP_001951646.2				XP_029343505.1		
		XP_008187140.1				ARJ54248.1				XP_029348406.1		
		XP_008187139.1				AQS60755.1						
		XP_008181869.1				AQS60754.1						
		XP_008181612.1				AQS60753.1						
		XP_008178459.1				AQS60752.1						
		CAX63070.1				AQS60751.1						
		CAX63069.1				AQS60750.1						
		CAX63068.1				AQS60749.1						
		CAR85637.1				AQS60748.1						
		CAR85636.1				AQS60747.1						
		CAR85634.1				AQS60746.1						
		CAR85633.1				AQS60745.1						
		CAR85632.1				AQS60744.1						
		CAR85631.1				AQS60743.1						
		CAR85630.1				AQS60742.1						
		CAR85629.1				AQS60741.1						
		CAR85628.1										
		ACI30694.1										
<i>Aphis craccivora</i>	1	CAR85658.1	0	-	37	KAF0766177.1	11	KAF0766232.1	68	KAF0773921.1	1	KAF0772486.1
						KAF0758873.1		KAF0773254.1		KAF0773181.1		
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						KAF0737851.1		KAF0772642.1		KAF0765041.1		
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						KAF0772142.1		KAF0767625.1		KAF0762692.1		

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KAF0770681.1	KAF0766106.1	KAF0762198.1
KAF0766047.1	KAF0761777.1	KAF0761972.1
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KAF0765716.1	KAF0756485.1	KAF0759983.1
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KAF0744260.1		KAF0760652.1
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		KAF0747416.1
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		KAF0719564.1
		KAF0715541.1

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		ACJ64044.1	XP_027847498.1		
		ACJ64046.1	XP_027847411.1		
			AQS60756.1		
<i>Aulacorthum solani</i>	1	AHH34994.1	0	-	0
			0	-	0
<i>Brevicoryne brassicae</i>	1	AEX65667.1	0	-	0
			0	-	0
<i>Cinara cedri</i>	25	VVC24262.1	0	-	23
			23	VVC25273.1	0
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		VVC24260.1		VVC25231.1	
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		VVC25280.1		VVC25910.1	
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		VVC25306.1		VVC26167.1	
		VVC25514.1		VVC26166.1	
		VVC26092.1		VVC28590.1	
		VVC26168.1		VVC28589.1	
		VVC29378.1		VVC28588.1	
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		VVC29375.1		VVC31899.1	
		VVC30360.1		VVC33585.1	
		VVC30725.1		VVC37787.1	
		VVC32662.1		VVC39717.1	
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		VVC35805.1		VVC39900.1	
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		VVC43934.1			
<i>Diuraphis noxia</i>	0	-	0	-	6
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<i>Metopolophium</i>	7	CAR85643.1	0	-	0	-	0	-	0	-	0
<i>dirhodum</i>		CAX63256.1									
		CAR85642.1									
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		CAR85638.1									
<i>Myzus persicae</i>	21	QLI60787.1	11	AWV63290.1	54	UMT69211.1	13	XP_022161260.1	14	XP_022180784.1	6
		AWV63287.1		AWV63291.1		UMT69212.1		XP_022161203.1		XP_022180783.1	
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AER92705.1

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*Tuberolachnus salignus* 1 CAR85659.1 0 - 0 - 0 - 0 -

**File S1.** The amino acid sequences of 172 odorant binding proteins (OBPs) from 20 Hemiptera species.

>SaveOBP1

MNLKVMMFLCLSVTVVYCEIEENRLNNNTAIEICILETNIPKDEFQAMVTMPNNPDVDIL  
TTRAQKCMGLGCVMRKNHIINDGYVSTDVLRYVMNFYGAVPNTKRKLLSRTVSKVIDCT  
KKDNLPTEECVLADLIMTCVRSEALKRGLQR

>SaveOBP2

MKVSAATAVLVALVATVQSSDPCNISTCYKSGTTKPPMAVTPTRLPVQSSSTPTSHPQTTYA  
KDHVHGTTIKSGANATATTASGAVNGTERPIVVKSSAGVIGNSTTPKPTMTEGHVALKQ  
KLNTIAVKCKDELHAPQEIMALVSNTVVPQNEQQRCYLECVYKNLNLKNNKFSVEDGK  
AMARIRFANQPEEHKKAVTHIETCEKEAIIDPKITEKCAAGRIIRNCFVKNGEKINFFPKA

>SaveOBP3

MISSTFYITSVFGIALLISCGYGRFTTDQIDYYGKACNASEDDLVVKSYKVPSTETGKCL  
MKCMITKLGLLNDGSYNKTGMEAGLKKYWSEWSTEKIENINNKCYEEALLVSKEVVAT  
CNYSYTVMACLNKQLLDKST

>SaveOBP4

MRGNYSLMVFLFAIGLQDIFCQKQEPESGKCRAPDKAPLNLEIIINICQEEIKSALLQEALDI  
LNDGNLEQNTPSHSSRSKREADEDLTNEERRVAGCLLQCVYKKVKAVDETGFVVDGLM  
KLYNEGVDQRNYYMATLSAVRHICISIAQQLKQQPSKSFDGQTCDLAYEMFECVSEKIE  
ENCGVENKSNNLSQRQV

>SaveOBP5

MSVNSATIKCIAVAVVLLQISIIFADAGHHRRGKELLDTEDSDFFRCKQASRKSCCGPENAM  
KRGDKDKVAADECYAQVAEKFATVTATTPKQDLFSAEAVKITKKQFCLHECIGKKNNL  
LTEDGSLNKTIFIADYAMKSVFKEQWQKQVGKALDKCLEETYIPWPAEDKENVCNPVYV  
QFQHCLWLQYESNCPANKIKTTKCEKTRNRYRMQKSTSN

>SaveOBP6

MQKVVFCIFAIICQTVFTAGYDRTWILRQKRMTNDDECRTLIPSPEKKLPSCCQMPDILPN  
SNSTWEKCFETFKQFKDKPETKEYKEMAHGKEPPCLFQCIFMQSLTSDGKLNEAITK  
KMSEGINNDEWKSTWQNSLNKCFDDVKQEDKKQIPIMNTPAGRLMKCFLRDHYMSCP  
KNVVVESSECLNMKDLVQKCPMEMPPVFKSPPKLI

>SaveOBP7

MYNMLPKTVLFAIIAATVLKDCDAYLSEAAIKKTQQMLKTVCSKKFSVEEDVFTDIKKGIF  
PEDNNNIKYFACNFKTMQLINQKGSIDKKMFKDCKMTMAPPNVLKVLLPVIEQCTGID  
KGEELCQSSYNLIKCAHTVDPRSLEYLPL

>SaveOBP8

MFALKVACLCLSVAVVFGENNQQNGPSDRSASIFQSCIAETKLSGDALKGFRSMSIPKTQA  
EKCMMGCLMRKVNVINKGKFSVEEATKVAQKYYGTNEVMMKKAKDLIDVCAKKAQST  
TEECALAGIVTCIVEEAQKAGLAGGPGSRRTVSPKFRRDAM

>SaveOBP9

MIKKTLLSVFVLFGCLFSINKAADDADAGDKELMSKLFVVLKCFKDADWGTGEMIT  
TKYDITQAKYKQCTCHMACAGEELGMINTSGQPEPAKFLEYVNKINHPSIKSQLQLIYDK  
CHNVKGSEKCDLAEQFAICAFKESPALKERAATLMEMLVKMKPKSK

>SaveOBP10

MEHLRSTNVVFAIVMALLVVQSSTRPQPDEMEEIKKLYNACAGKFPIEEIKKNAKNAIIS  
DDPTFKCFLKCCFDEMSLIDEDGILDGDSMKAMAPDHIKPIFEQVIPSLKNVKQDGCEAS  
FEFISCGMKNPLTVELLPL

>SaveOBP13

MDACTVHCVFNQLEMLNSNSRPDKYSIVNIMTNQIKDVELKEFIQDSIDECDTLELDNN  
NKCEFSKNFAVCMENKAQRNCDDWDENLSANKINSAGLQDGTNQQDKRKGY

>AgosOBP2

MKVSAATAVLVALVATVQSSDPCNISTCYKSGTTKPPPTVTPTRLPVQSSSTPTSHQQTTYA  
KDHVHSSTATKSGVNTTATTSGASVNGTERTTVVKSSSGVAGNVTPKPTMTDGHVALK  
QKLNTIAVKCKDELHAPQEIMALVSNTVVPQNEQQRCYLECVYKNLNLIKNNKFSVDDG  
KAMAKIRFANQPEEHKKAVTIIETCEKEAIIDPKTTEKCAAGR VIRNCFVKNGEKINFFPKA  
>AgosOBP3

MISSTFYTSLMFGIAMLISCSFGRFTTEQIDHYGKACNATEDDLVIVKSYKVPTSDTGKCL  
MKCMISKLGLLNDDGSYNKTGMEAGLKLYWSEWSTDIESINNKCYEEALLVSKDIIATC  
NYAYVVMACLNKQLKLDNST

>AgosOBP4

MRGNYSLVVFLFGFGLLEIYCQKQELSGKCRAPDKAPLNLEIIINICQEEIKSALLQEALDI  
LNDGTLEQNTPSYRSKRDADEDLSNEERRVAGCLLQCVYKKVKA VDETGFVVDGLMK  
LYNEG VQDRNYYMATLSAVRH CISIAQQLKQQQPSKSFDDGQTCDLAYEMFECVSEKIEE  
NCGVENKLNNLSQRQV

>AgosOBP5

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PENAMKRGDKDKVAADECYAQVAEKFATVTATTPKQDLFSGEAVKITKKQFCLHECIG  
KKNKLLTEDGSLNKTFIADYAMKSVFKEWQKQIGQKALDKCLEETYIPWPAEETENKC  
NPVYVQFHCLWLEYESNCPDNKIKLT KCEKTRNRYRMQKSPSNQ

>AgosOBP6

MQKVVFLCIFAIICQTVFTVGFERTWILRQKRMTNDNECRALFPSPEKKLPTCCQMPNILP  
GLDNAWEVCFEKFQFKDKHATKEYKEMVHENEPPLFCQVFMQSGLTTSDGKV NEDA  
VIKKMAEGMDNDEKWKSIWRNTFNKCLNDVKQEDKEQIKVMNTPTGRLMKCFLRDLY  
MNCPKNVWVENSECSNLKDLVEKCPKLPPVFQSPPKLI

>AgosOBP7

MNMLPATVLLAVVAATILKDSDAYLSEEAIKKTQKMLKNVCSKKHSVEEVFTDIKGIFP  
ENNNNIKCYFACNFKTMQMVNQKGILDKKMFKD KMTMLAPPVLAILLPIEQCIGNDK  
DTEICQSSYNFIKCAHRVDPKSLEFLPL

>AgosOBP8

MFAFKVACLCLSVAVVFGENNQQNSNDRSASIFQSCISETKLSGDALKGFRSMSIPKTQAE  
KCMMGCLMRKVNVINKGKFSVEEATKVAQKYYGTNESMMKKAKDLIDVCAKKAQSTT  
EECALAGIVTTCIVEEAQKAGLTGGPGSRSKTVSPKFRHSIV

>AgosOBP9

MIKKTLLVSGFVLGCMFSINKAADDADTADKELMSKLITVAFKCFKDADWGTCGEMIT  
TKYDITQAKYKQCTCHMACAGEDLGLINSNGQPEPAKFLEYVKRINNSVIKSQLQHIYDK  
CQNVKGTEKCDLAEQFAICAFKESPEMKERVTCLIEMLVKMKPKSK

>AgosOBP10

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>MperOBP8

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>MperOBP10

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>ApisOBP10

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>AlinOBP12

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>AlinOBP13

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>AlinOBP14

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>AlinOBP15

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>AlinOBP16

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>AlinOBP17

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>AlinOBP19

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KVKDLLLSRVNETWQKEVLGQAVDTCATSKFDQTWKDDQDEYKCNPQALQFKHCVWK  
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>AlinOBP20

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>AlinOBP21

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>AlinOBP22

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>AlinOBP23

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>AlinOBP24

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>AlinOBP25

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NKAIEICMGRKYQTSCPSGIDGMMECFAVQMMLNCPAKHWSGGEDCKETKQLIKECGEV  
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>AlinOBP26

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>AlinOBP27

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>AlinOBP28

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>AlinOBP29

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>AlinOBP30

MQLKNTSDSLVGHLSIALPNTLLNPSQLPELAITSRQSPDIVSIACFLHAIGSNFLFASKTP  
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>AlucOBP1

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>AlucOBP2

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>AlucOBP3

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ALKARLTKCSNAMPPFPHHKH

>AlucOBP4

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>AlucOBP5

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>AlucOBP6

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>AlucOBP7

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>AlucOBP8

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>AlucOBP9

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>AlucOBP10

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>AlucOBP11

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GDWKVIANSGSNCEGFKVLAQSMEKKCPTSESDVSFNCMTLQWYMNCPKSAWTSS  
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>AlucOBP12

MTC SHFIA LL SVVAL SLS GEINE ECKDIEN LKT QLEN FYGCCDFESMIERVVRTEEEVETD  
RFC REER KKINST DGKVPLASEGHDCFMECVLKR MGAM QDFK FIREKL DFFLR GYPE  
EV KQAGKLA FDKCLS KNFSKKY CASG INGLMMCLPEELVMNC PANI WSSHE CPIA KEAI  
KKC PSYR VMIEQE

>AlucOBP13

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>AlucOBP14

M ALNAKA VLLLGVCGLVYV SAYQ EVLKATLKDCKGKE ITQEEVDEF MKPLIPK NEEER  
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DLAGEV MSCRNK YIDHGYDQDP

>AlucOBP15

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IGYE FSTCKK ELVKKV GLPPPTPLKE

>AlucOBP16

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>AlucOBP17

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LQKADPV NFMVI

>AlucOBP18

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SLGRAVREC FNHGKQVNFFPSA

>AlucOBP19

M NSRGIVFAS LALL HITNAG NIKEGYVAKIAEIKDKCLKEHNVDH SVVEDLLKKSIKPEV  
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>AlucOBP20

M YTFK TFFV LT ASYVIA APPADEPAECKPMKEKEEEISK CCKLE PVTKEQAAFVDCMK  
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VEKCLAQVAENKD KTV CSTSGADV YT KCIFRESYINCPEKSWNSDACKANKER VI KCPK  
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>AlucOBP21

M KFFV VSA ALVLLV AAAV KANE KKANE KVTE IFN KCKETWP VTDEEIEQVKQKQSIPDSK  
NVK CILACMLKEAKILRDGEYNKDN AELM ADVLYKDEPEHA EKS KQII EMCSSEL GTKTE  
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>AlucOBP22

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>AlucOBP23

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>AlucOBP24

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>AlucOBP25

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>AlucOBP26

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>AlucOBP27

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>AlucOBP28

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>AlucOBP29

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AVKSCHETITKRETPQEGTCKDSAHEFTHCVMRQLFLSCPASEWNNNDECNLVKSRMQA  
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>AlucOBP30

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>AlucOBP31

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>AlucOBP32

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>AlucOBP33

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>AlucOBP34

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>AlucOBP35

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>AlucOBP36

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CEWGLALTCKALKHGKEAGIPPPDMEHPKRR

>AlucOBP37

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>AlucOBP38

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>AsutOBP1

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>AsutOBP2

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>AsutOBP3

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>AsutOBP4

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>AsutOBP5

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>AsutOBP6

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>AsutOBP7

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>AsutOBP8

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>AsutOBP9

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>AsutOBP10

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>AsutOBP11

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>AsutOBP12

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>AsutOBP13

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DSSESYDRVESYGGIPSGTPRGIPYNGYHNNANIRWPDSNSQGNARKNGSSLEDVEPCTIL  
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>AsutOBP23

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>AsutOBP31

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>AsutOBP32

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>MsanOBP9

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>MsanOBP2

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>MsanOBP4

MRGNYSLMVFLFTIGLQDIYCQKQELSGKCRAPDKAPLNLEIINICQEEIKSALLQEALDI  
LNDGNLEQNTPSYSSRSKREADEDLTNEERRVAGCLLQCVYKKVKADETGFVVDGLM  
KLYNEGVDQRNYYMATLSAVRHICISIAQQLQQQPSKSFDDGQTCDLAYEMFECVSEKIE  
ENCGVENKSNNLSQRQV\*

>MsanOBP10b

MEHLRSSNVVFAIVMALLVVQSSTRQPQDEIEEIKKLYNACSGKFITEEIKNDFKNSIISD  
DPNFCKFLRCCLDEMMSLIDEDGIIDGDSLKEMAIDS IKPIIEQVNSNCLNVKQDG CQA AFE  
FISCGIKLNPLTMQLLPL\*

**File S2.** The amino acid sequences of 77 chemosensory proteins (CSPs) from 10 Hemiptera species.

>AgosCSP1

MNILTIFCYVTVMCDTQVKPAVSAQRQLQSVNQNVTPTNDGRKTIRETSSYPTRYDYIDIEA  
VMNNERIIKILFNCVMSRGPCCTREGLELKRVIPDAIQTECAKCNERQRKQAGKVALHLLQ  
YKPEYWVMLVQKFDPNNVYLKYMADNDDDEKLSQLKLSNDTTKKKRNI\*

>AgosCSP2

MAHLNLVFVVLIASLIYFTSAAEELYTTKFDNFVDVKVLNNNRILTSYIKCLLDEGNCTNEG  
RELKRVLPDALKTDCSKCTDVQKDRSEKVIKFLIKNRSTDFFDLTAKYDPTGEYKKNLEK  
FEKERASAKPLKA\*

>AgosCSP4

MDSRIAVVCVVLAAFADVDTVGAPQKDAVAASGPAYTTKYDHIDVDQVLASKRLVNSYV  
QCLLDKKPCTPEGAELRKILPDALKTQCAKCNATQKNAALKVVDRQLQDYDAEWKQLL  
DKWDPKREHFQKFQQFLAEEKKKGFTKF\*

>AgosCSP5

MHCKVLIALCCVAVYAVQASPAGTATAAAVSADDEIKDFPAYMKRFDKLNVEQVLNNDRV  
LASHLKCFNLNEGPCVQQSRDLKRVIPVIANGCNGCTERQMTTIKKSLNFLRTKKPTEWA  
RLVKIYDPSGTKLNKFLDA\*

>AgosCSP6

MIKLILAIACVSITMTVVQTAPAKYTTKYDNVNIDEILNNDRLVASYFKCLMETGKCTPE  
GEEIKRWLPEAIENKCEDCSEKQKLGSEKIKFLFEKKNDMWKQLEAKYDPQGTYRQRYA  
EEAKKLNINV\*

>AgosCSP7

MSRSSSSVTMKVFVIAICVCAALARPEDVKVENKPAVIKSETLAAPLPTNIVKRATDTIQLD  
SSLNVSEDVLDKALSDRRFVQRQLKCATGEGPCDPIGRKIKAHAPLVLRGMCVKCSQSEI  
KQIQRVMMSHIQKNYPKEYTKMLKQYQSGF\*

>AgosCSP8

MNNIIMNNSRGRYGFISLLAVTIAAIMLVHQPATVRCADGGIITPQQQQQTMMFTAPTGY  
YVSTYDHIDVGRLRNKVVSGYVKCFVNEGPCPDGKLVKAYLLPEIIRTVC GKCTPRQ  
KDMARMVLKHIYTYRQADFEKIMQIYDTDGKRNEILAFMNH\*

>AgosCSP9

MSAFCLNSFILMTMITVIVTHATFTRSTKFDDRTGIDIHLVKRDTDVNDENSVESDEGFF  
YRFTHFFQDSSDKEDDDDEKKPDFITTFDIFKLLDEEYAMQQFYCVINEDPCDEVGMRL  
KATIPEEINRNCERCTSTERNNIRRLNYVKKHYPFWKRVEPIYKKKI\*

>AgosCSP10

MINTRPRKLVR CIRGV SISVAKGDDAVNAENKDDDSHLVNREEIQRYSMSMMEKINIDQML  
NNTRLMSNNVKCFLNEGPCTAHLREMKKMVPMLVKDSCSSCTKEQKIMMKKAMDAVK  
ARRPNDYEKLSKFFDPEGKYEKKFLENLNESK\*

>MperCSP1

MNLLAVFCYITMMCDSQLFKRLEQPAAISQVKRIEQPAMIANRIGQPTVAPRFGQPTIAPRF  
GLPTIAPQVGQAAITPQVGQAAIASRFGLPTVAPQVGQAAITPQVGQAAIASRFGLPTVAP  
QVGQAATTPQVGQAAIASRFGLPTVAPQVGQAAITPQVGQAAIASRFGLPTVAP  
NERIIKILFNCVMNQGPCTREGLELKRVIPDAIQTECAKCNERQRKQAGKVALHLLQYKP  
EYWNMLVKKFDPNNVYLKYMADNDDDEKVSLQKLTNDTTK\*

>MperCSP2

MAHLNLVVLVASLVCFTLAEEKYTTKFDNFVDVKVLNNNRILTSYIKCLLDEGNCTNEG  
RELKRVLVDALKTDCSKCTEVQKDRSEKVIKFLIKNRSTDFFDLTAKYDPSGEYKKKIEKF  
DSEKAAAACKH\*

>MperCSP4

MDSRIAVVCVVLAVFAVDQTVGAPQKDAVAASGPAYTTKYDHIDIDQVLGSKRLVNSYVQ  
CLLDKKPCTPEGAELRKILPDALKTQCVKCNAALKVVDRQLRDYDKEWKQLLD  
KWDPKREYFQKFQQFLAEEKKKGVVKF\*

>MperCSP5

MNCKVLIALCCVAVYAAHASPAGAATAAAASADEEIKDFPAYMKRFDKLNVEQLNNDR  
VLASHLKCFLNEGPCVQQSRDLKRVIPVIANGCNGCTERQMTTIKSLNFLTCKPVEW  
ARLVKIYDPSGTKLNKFLDA\*

>MperCSP6

MNTLLAVALCIAITMTVVQTAPAKYTTKYDNVNIDDILNNDRVLASYFKCLMETGKCTP  
EGEEIKRWLPEAIENKCENCSEKQKIGSEKIIKFLIEKKNDMWKQLEQKYDPQGLYKQRYS  
EEAKKLNLDV\*

>MperCSP7

MDRSSSSVTMKVFVIAVCVCAALARPEDSKVENKPAAVKSETLAAPLPTTIVKRATPQVVS  
TQQGASLPNVSEDVLDKALSDRRFVLRQLKATGEGPCDPGRKIKAHAPLVRGMCVKC  
SQSEIKQIQRVMMSHIQKNPKEYTMMMLQYYQSGF\*

>MperCSP8

MTNNNMNSPRCRPEIFSLLAVAAIAATVLVHQPSTVHCADAGVYPPQQQQEATMFTAPSG  
YYVSTYDHMDVGRLRNKVVAGFVKCFTNEGPCPCTPEGRLAKAYLLPEIIRTVCGKCTPR  
QKDMARL VIRHIYT RRGDFDKIMQIYDTDGKKNEIIDFMNQK\*

>MperCSP9

MTSFCLNSVILMTITTIVAHAASTGMTAFNNRSGSDIHMAQRDYNENKADKAEGFFITIT  
NFFSRRKHDDDPDFITTFDIIRLLDEKYAMQFYCVINKEPCDATGLRLKATIPEEINNDC  
ERCTATETSNIIRILNYVKKHYPEFWDRVEPIYRNNMTA\*

>MperCSP10

MVSKLFVSVFVLMCSVVGVSYSVTEGDDDAAKVADKDLHPVNQEELKKFLSMMEKVDid  
QILNNNRLMSNNVKCFLNEGPCGTQLREMKKMVPMLVKDSCSSCNKEQKNMMKKAMD  
AMKARRPNEYEQISKFFDPEGKYEKKFLENLNESK\*

>ApisCSP1

MNLLAIFCYITMMCDSQFRRLEQMTAMPQVKQPATIATRIGQATIAPRFGQPTIAPRFGQAT  
VAPQVGQAATPQIGQAAIGSRIGQSFQS VNGSVTPPTDGRKTTRTASYPTRYDFIDIEAV  
MNNDRIIKILFNCVMNQGPCTREGLELKRIVPDAIQTECAKCNERQRKQAGKVL AHL LQY  
KPEYWNMLVKKFD PNNIYL RKY MADN DD DEKL SLQ KLT NNTTK\*

>ApisCSP2

MAHLNLVVLVASLVCFTLAEEKYTTKFDNFVDVEKVLNNDRILTSYIKCLLDEGNCTNEG  
RELKRVLVDALKTDCSKCTDVQKDRSERVIKFLIKNRSAEFDKLTAKYDPSGEYKKKIEKF  
DAERA AAAACKH\*

>ApisCSP3

MVHLNLFVVLVASLVCFTLAEEKYTTKFDNFDVEKVLNNDRILTSYIECLLDQGNCTNEG  
RELKRVLPDALKTDCSKCTDVQKDRSERVIKFLIKNRSAEFDKLTAKYDPSGEYKKLEKF  
SA\*

>ApisCSP4

MDSRIALCVVLAFFAVDQTVGAPQKDAASGPVYTTKYDNIDIDQILASKRLVNYYVQCL  
LDKKPCTPEGAE LRKILPDALKTQCSKCNPQKNAALKVVDR LQKD YDKEWKL LD KW  
DPKREQFQK FQQFLVEEKKGVVKF\*

>ApisCSP5

MNCKLIALCCVAVYAAQANPAGVATATAADEEIKDLPAYMKRFEKLNV EQVLNNDRVLA  
SHLK CFLNEGPCVQQSRDLKRVIPVIANNSCNGCTERQITTIKSLNFLRTKPVEWARLV  
KIYDPSGVKL NKF LDA\*

>ApisCSP6

MNKLFLAFAFCIVTMMTVVQTAPAKYTTKYDNVNIDDLNNDR LVNSYFKCLMETGKCT  
PEGEEIKRWLPEAIENKCEDCSEKQKL GSEKIIKFLIEKNDMWKQLEE KYDSKGLYRQRY  
SEDAKLDIHI\*

>ApisCSP7

MARSSS VTMKV FVIA CVCA ALAR PEEAKMENKPAVVKSETLAAPLPTTIVKRATPYVV  
STQQDSSL PVSEDVLDKALSDRRFVQRQLKCATGEGPCDPIGRK IKAHAPLVMRGMCV  
KCSQSEIKQIQRVM SHIQKNYPKEYTKMLKQYQSGF\*

>ApisCSP8

MTNNNMNC PRSRPEIFSLLTVTAIAAVLVHQPTTVYC ADGGTYPQQQLQQQQQQQQQQ  
QQQQFTAPSGYYVSTYDHIDVG RLLRNQKVSGYV KCFVN EGPCTPDGKL V KAYLLPEII  
RTVC GKCTPRQKEMARMVLRHIYT YRRADFD KIMQIYDTDGKNEIINF MNQK\*

>ApisCSP9

MSSFCLNSVILMTVITVVVARVAFAESTTSNDRPGSDIRLVKKDVDYNE DADDREEGFFF  
RISHFFGFTSYDDD KPDFITT FDLIR LLDE KYAM QFYCVINE EPCDAVGL RLKATIPEEINR  
DCERCTATE SNIRRI NYVKKHYPKF WERVEPIYRNNTTA\*

>ApisCSP10

MVSKRFISVFMFMAVVGVSFSVPEDDATKVVNKEVDHSVIQEEIKKFLSMMEKINIDQI  
LNNDRLMSNNVKCFLNEG SCTAQLREM KKMLPV LIKDSCSSCTKEQRNMIKKAMDAIKA  
RRPNEYERVTKFFDPEKKYEKKLSEKLNES\*

>SaveCSP2

FVVLVASLVCFTLAEEKY STKYENFDV DKVLNDDSLTSYINCLLDEENCTEEGQALKRVL  
PDALKTNCGKCTDTQKM KIEKILKFLMKNRSTD FDR LTAKYDPSGEYKKLEKF SA

>SaveCSP4

MDSRIAVV C VVLAFFAVDQTVGAPQKDALAAGSPTTYTNKYDHIDIDQVLASKRLV NSY  
VQCLLDKKPCTPEGAE LRKILPDALKTQCAKCSATQKNAALKVVDR LQKD YDKEWKL QL  
LDKWDPKREQFQK FQQFLTEEKKGVVKF\*

>SaveCSP5

MNCKV LIALCCVAVYAAQANPAGAATATAADDEIKDFPAYMKRFDKLNV EQVLNNDRV L  
ASHLK CFLNEGPCVQQSRDLKRVIPVIANNSCNGCTERQMTTIKSLNFLRTKPVEWAR  
LVKIYDPSGTKL NKF LDA\*

>SaveCSP7

MARSSSTSVMKVFVMAVCVCAALARPEEAKMENKPTAVKSETLAAPLPTTIVKRATPQV  
VSIQKDASLPNVSEDVLDKALSDRRFVQRQLKCATGEGPCDPIGRKIAHAPLVLRGMCV  
KCSQSEIKQIQRVMSHIQKNYPKEYTKMLQYQSGF\*

>SaveCSP1

MNLLAIFCYITMMCDSQFRRLEQPTAIPQVKRIEQPATIATRIGQATIAPRFGQPTVAPRFGQ  
PTIAPRFGQATAAPQTGEAAIGPRIGQTFQNVDNSPPTDGRKTRETSSYTRYDFIDIEA  
VMNNDRIIKILFNCVMNQGPCTREGLELKRVPAIQTECAKCNERQRKQAGKVLAHLLQ  
YKPEYWNMLVKKFDPPNNIYLRKYMADNDDEKLSLQKLSNNTTK\*

>AgylyCSP1

MNILTIFCYVTVMCDTQVKPAVSAQRLQSVNQNVTPTNDGRKTIRETSSYTRYDYIDIEA  
VMNNERIIKILFNCVMSRGPCREGLELKRVPAIQTECAKCNERQRKQAGKVLAHLLQ  
YKPEYWKMLVQKFDPNNVYLRKYMADNDDEKLSLQKLSNDTTKKKRNI\*

>AgylyCSP2

MGINIYKLKRIKMAHLNLFFVVLIASLIYFTSAAEEKYTTKFDNFVDVKVLNNNRILTSYIKC  
LLDEGNCNEGRELKRVLPDAKTDCKCTDVQKDRSEKVIKFLIKNRSTDFFDLTAKYD  
PTGEYKKNLEKFETERATAKPLKA\*

>AgylyCSP4

MDSRIAVVCVLAFAFDQTVGAPQKDAVAASGPAYTTKYDHIDVDQVLASKRLVNSYV  
QCCLDKKPCTPEGAEKLKILPDALKTQCAKCNTTQKNAALKVVDRQLQKDYDAEWKQLL  
DKWDPKREHFQKFQQFLAEEKKKGFTKF\*

>AgylyCSP5

MHCKVLIALCCVAVYAVQASPAGTATAAAVSADDEIKDFPAYMKRFDKLNVEQVLNNDRV  
LASHLKCFLNEGPCVQQSRDLKRVPIVPIANNGCNGCTERQMTTIKKSLNFLRTKKPTEWA  
RLVKIYDPSGTKLNKFLDA\*

>AgylyCSP6

MIKLILAIACVTITMTVVQTAPAKYTTKYDNVNIDEILNNDRLVASYFKCLMETGKCTPE  
GEEIKRWLPEAVENKCEDCSEKQKLGSEKIJKFLFEKNDMWKQLEAKYDPQGIYRQRYA  
EEAKKLNINV\*

>AgylyCSP7

MYMGNPSPSIDRIWSHYCHHLNTRSMSRSSSVTMKVFVIAICVCAALARPEDVKVENKP  
AVIKSETLAVPLPTNIVKRATDTIQLDSSLNVSEDVLDKALSDRRFVQRQLKCATGEGPCD  
PIGRKIKDILGADPSSRTASVERNVRQVFTVGNQTDSTCHVPYSEELSQGVHQDAETVPER  
ILITMRRPCTIFLFMTSGFWHNL\*

>AgylyCSP8

MNNSRGRYEIFSLLAVTIAAIMLVHQPATVRCADDGIITPQQQQQTMMFTAPTGYVSTY  
DHIDVGRLLRNNKVVSGYVKCFVNEGPCTPDGKLVKAYLLPEIIRTVCVGKCTPRQKDMAR  
MVLKHIYTYRQADFEKIMQIYDTDGKRNEILAFMNH\*

>AgylyCSP9

MSAFLCLNSFILMTMITVIVTHATFIRSIKFDDRTGIDILVKRDITDVKDDENSVESDEGFF  
YKITHFFQHHDKEDDDDEEKPDFITTFDILKLLDEEYAMEQFYCVINEDPCDEVGMRLK  
ATIPEEINRNCERCTSTERNNIRRILNYVKKHYPFWKRVEPIYKKKI\*

>AgylyCSP10

MNSKIFISVFMFITIVSISVAERDDAVKAENKDDDSHPINREEIQRYMSMMEKINIDQML  
NNTRLMSNNVKCFLNEGPCATAHLREMKKMVPMLVKDSCSSCTKEQKIMMKKAMDAVK  
ARRPNDYEKLSKFFDPEGKYEKKFLENLNESK\*

>LeryCSP

MDSRIAVVCVVLTVFAVDQTVGAPQKD TAVVNGPAYTTKYDNIDIDQVLASKRLVNSYVQ  
CLLDKKPCTPEGAE LRKILPDALKTQCTKNATQKNAALKVVDR LQRDYDKEWKQLLD  
KWDPKREYFQKFQQYLAEEKKGVVKF

>AsutCSP1

MLPFYVFSLCAVFVACQETYTSKYDNVNVEDALKNDRLYKAYFNCLADRGPC TREGNML  
KEALPDGLRNNCSLCTDPQRRGTHQVIRFLFKYRPEDMLKLEEIYDPEGIYKT KYAEERK  
KLME

>AsutCSP2

MGHFPPVFSLSPVLLVASLHTMNTSTLLKIAFLLGCVAA CLAAETRSSVSDEALEAALKDK  
RYLTRQLKCALGEGACDPVGRRLKTYAPLVRGACP KCTPSEVRQIQQVLSHIQRHYPKE  
WAKILKQYAGQ

>AsutCSP3

MKFVAALLVASVAVLAVEAANQYTTKYDNIDLDDILKNQR LYKKYFECLTGKGKCTPDGK  
ELKEHLPDALKTGCSK CSEKQRAGSEKVIKHLLKNKPQDYAVLEKIYDPSGIYKKYEA  
AKKLGINV

>AsutCSP4

MRIILSAFLVAMACSLATEMTEEEFYTKVFEVDPDFILDNERILTSYLKCFYSEIECNAHA  
EVVKKSIPDVLATVCGRCSDKQKSIFKYSLNKFIPAHPKDWEKILSIYDPSGEAWPKVKAFI  
ES

>AsutCSP5

MDYKFFVVMQIGVISSVCAAGTYTDKYDNVNLD EVLNNERLYRNYFNCLQGKGKCTLD  
GAILKEVIPSALKTDCALCSV RQKKGAEKVLIFLITKPDDFKILEDKFDPEGVYRKKYE  
QRKLVEEGKPIH

>AsutCSP6

MVCKLF AVVLMGILAGVWAADKYTDKYDNIDIDEILTNERLYKKYFDCI QGIGKCTPDGIE  
LKEK IPEALKTECAKCNEKQKAGVEKVMRYLITKKPEDFKILEDKFDPEGVYRKKYE  
KLVEEGKPVEY

>AsutCSP7

MVSKLSMVLLIGALADVWASELYTDKYDSIDIDEILNNDRMYKNYFNCVMGN GKGKCTPDG  
TELKAKIPEALQTECAKCS DKQKKGV EKVLRF LIKEKKDDYKLLEEKFDPEGVYRKKYE  
AQKKLVEEGKPIEY

>AsutCSP8

MDYKLSVMLVMGV LACAWAADMYTDQYDNIDIEEILTNERLYKKYFDCIIGNGKGKCTPDG  
TELKETIPDALKTACAKCNDKQKAGVEKVLHLLTKKAEDYKILEAKFDPEGVYRKKYE  
AQKKLAE EGKPIVL

>AlucCSP1

MLKVLVLLAAVVCCV SAAATYTSKYDNIDLDEILSNTR LYKKYFDCLANKGKGKCTPDGKEL  
KESLPDALKTNCAKCTKKQQEGTDKVLHV LKNKPNDYKVLESIYDPTGIYRKKYEIEAE  
KRGIKLPGSH

>AlucCSP2

MVGKLSVLLIGAVGMVLAADKYTDKYDNIDVDEILGNQRLYQKYFDCIQGKGKCTPDG  
AELKKNIPEALQTCAKCSEKQKAGVEKVLRHLINEKPEDYKVLEEQFDPEGVYRKYE  
HLKKKVEEGKPVEY

>AlucCSP3

MLKVLVLLAAVVCCVSAAATYTTKYDNIDLDEILSNQRLYKKYYDCLANGKCTPDGKE  
LKEALPDALKTNCSKCSKKQQEGTDKVLRYVLKNKPNDYKVLENIYDPSGNYRKRYEDE  
ASKRGIKLPGSH

>AlucCSP4

MVKLSIVLLIGALADVWASELYTDKYDNIDVDEILGNQRLYQKYFDCIQGKGKCTPDGA  
ELKKNIPEALQTCAKCSEKQKAGVEKVLRHLINEKPEDYKVLEEQFDPEGVYRKYEH  
LKKKVEEGKPIEY

>AlucCSP5

MVGKLSVLLIGAVGMVLAELYTDKYDNIDVDEILGNQRLYQKYFDCIQGKGKCTPDG  
AELKKNIPEALQTCAKCSEKQKAGVEKVLRHLINEKPEDYKVLEEQFDPEGVYRKYE  
HLKKKVEEGKPV

>AlucCSP6

MVKLSIVLLIGALADVWASELYTDKYDNIDVDEILGNQRLYQKYFDCIQGKGKCTPDGA  
ELKKNIPEALQTCAKCSEKQKAGVEKVLRHLINEKPEDYKVLEEQFDPEGVYRKYEH  
LKKKVEEGKPIEY

>AlucCSP7

MVKLSIVLLL GALADVWAAELYTDKYDNIDIDEILNNDRMYKNFNCVMGNGKCTPDG  
LELKAKIPEALQTECAKCSDKQKKGAEKVLRFIINQKKDDYKLLEEKFDPEGVYRKYE  
QKKLAEEGKPIEY

>AlucCSP8

MLKVLVLLANAASTYTTKYDNIDLDEILSNQRLYKKYYDCLANGKCTPDGKELKEALP  
DALKTNCSKCSKKQQEGTDKVLRYVLKNKPNDYKVLENIYDPSGNYRKRYEDEASKRG  
I KLPGSH

>AlinCSP1

MLKVLVLLAAVVCCVSAAATYTSKYDNIDLDEILSNTRLYKKYFDCLANGKCTPDGKEL  
KESLPDALKTNCAKCTKKQQEGTDKVRHVLKNKPNDYKVLESIYDPPGIYRKYEAEA  
EKRGIKLPGSH

>AlinCSP2

MKAVLVLLCVGAALSAEVYTSKYDNIDVDKILSNDRILTRYIKCLMEEGNCTNEGKELK  
KTLPDALASGCTKSEKQKAQTEKVLRHL SKNPRDWALLKTYDPKGEYSKKYEKEA  
KALTA

>AlinCSP3

MISKLSMVLLIGAFADVWAAEQYTDKYDNIDIDEILNNDRMYKNFHCMGNGKCTPDG  
LELKAKIPEALQTECAKCTDKQKKEVEKVLRFIINQKKDDYKLLEEKFDPEGVYRKYE  
QKKLVEEGKPIEY

>AlinCSP4

MRIILSAFLVAMACSLATEMTEEFYTKVFEEVDPDFILDNERILTSYLKFYNEIECNAH  
AEVVKK SIPDV LATVCGRCS DKQKSIFK YSLNK FIPAHPKDWEKILSIYDPSGEAWPKVKA  
FIES

>AlinCSP5

MGHLTIVLLAAAFEVLTGSRAYTTHYIDVDQVLNNTRLYTKYVECLLGQGKCTPEARE  
LRDKLPEALQTNCARCSERQASESHRVIRFLIQNRQEDFKLEAKYDPSGLYFKRFEETK  
RNVSLS

>AlinCSP6

MFYKLSVVVLMGILAGVWAADKYTDKYDNIDIDEILTNERLYKKYFDCIQGTGKCTPDGI  
ELKEKIPEALKTECAKCNEKQKAGVEKVMRYLITKKPEDFKILEDKFDPEGVYRKKYEAQ  
RKLVEEGKPVEY

>AlinCSP7

MNYKLSVILLIGVLASVWAASYTDKYDNIDLDEILTNERLYKKYFDCIQGKGKCTPDGTE  
LKEAIPDALKTECAKCNAKQKAGVEKVLRHLLTKKAEDYKILEDKFDPEGVYRKKYEAQ  
KKLADEGKPIVL

>AlinCSP8

MDYKLSVMLMGVLACAWAADKYTDKYDNIDIDEILNNERLYKKYFDCILGNGKCTPDG  
TELKETIPDALKTACAKCNDKQKAGVEKVLRHLLTKKAEDYKILEAKFDPEGVYRKKYEAQ  
AQKKLAEEGKPIAL

>AlinCSP11

MKVFFSGLLLVCMASVSLCADEYTDKYDSVLDEILNNQRLYQKYIDCMGKGKCTPDG  
ALLKEKIPEALQNECAKCSAKQKKGAEKVLRFLINEKADDYKALEEKYDPEGFRSKYEE  
QKKNLKEGKPLSV

>AlinCSP12

MMIIIVFGISALLVVVEGAPLQYSDDTRYDDVELTILSNDELYIKLFQCLIGRGKCTPDWEIL  
KDALPGALLDNCSECSNKQKFGTKTLLAHLVHERPSDMRLLEGEFDPDGSRKELEKEEK  
ESNDINRKRSANLEEVEILDKIKRIIK

>AlinCSP13

MKFVAALLVASAVLAVEAANQYTTKYDNIDLDDILKNQRLYKKYFECLTGNGKCTPDGK  
ELKEHLPDALKTGCSKCSEKQRAGSEKVIKHLLKNKPQDYAVLEKIYDPSGIYKKKYEAE  
AKKLGINV

>AlinCSP14

MNSAIVLCVVALAGMVLARPDDTYTTKYDNVDLDEILGNDRLLVPYIKCTLDEGKCAPD  
AKELKEHIREALENGCAKCTDKQKEGTRRVIAHLIKHKNADWQKLAKYDPEGKYTHK  
YEKELEEVQH

>AlinCSP15

MKLIVAVALLCVVAESWAASYTDKWDNINVDEILESQRLLKAYVDCLLDRGRCTPDGKA  
LKETLPDALENECSKCTDKQKSGSDKVIRHLVNKRPEMWKELSAKYDPNNIYQDRYKDK  
IEAVKGQ

>AlinCSP16

MLPFYVFSLCAVFVACQETYTSKYDNVNVEDALKNDRLYKAYFNCLADRGPCREGNML  
KEALPDGLRNNSLCTDPQRRGTHQVIRFLFKYRPEDMKLLEEIYDPEGIYKTKYAEERK  
KLME

>MsanCSP2

RYFRFDQIYFCQNIYSLKQTMAHLNLFVVLVASLVCFTLAEEKYTTKFDNFVDVKVLNN  
DRILTSYIKCLLDQGNCTNEGRELKRVLPDALKTDCSKCTGVQKDRSEKVIKFLIKNRAAD  
FDHLTAKYDPSGEYKKLEKFEAERIAAAKN\*

>MsanCSP7

MARSSSSVTMKVFVIAVCVCAALARPEEAKMENKPTVVKSETLAAPLPTTIVKRATPQVV  
STQQDSSLNVSEDVLDKALSDRRFVQRQLKCATGEGPCDPIGRKIKAHAPLVLRGMCVK  
CSQSEIKQIQRVMMSHIQKNYPKEYTKMLKQYQSGF\*

>MsanCSP4

MDSRIAVVCFVLAVFAVDQTVGAPQKDAVATGGSAYTNKYDHIDIDQVLASKRLVNSYVQ  
CLLDKKPCTPEGAE LRKILPDALKTQCAKC NATQKNAALKVVERLQRDYDKEWKQLLD  
KWDPKREQFQKFQQFLTEEKKGVVKF\*

>MsanCSP1

MNLLAIFCYITVMCDTQFRRLEQPTTPQVKRIDQPATIATRIGQATIAPRGQVTAAPQIEQ  
AAIASRIGQGFQNVNNSVSPTTDGRKTTRQTSSYTRYDFIDIEAVMNNERIIKILFNCVMN  
QGPCTREGLELKWIVPDAIQTECAKCNERQRKQAGKVL AHLQYKPEYWNMLVKKFDP  
NNIYLRKYMVDNDDDEKLQLKLTNTTK\*

**File S3.** The amino acid sequences of 85 odorant receptors (ORs) from 11 Hemiptera species.

>ApisOR2

MDVMQKPERFILTPFQKFCIRWSVFFDSSSDRLSRIETVLRTIQFSTIMITSGMTMTSVLIAD  
NKKALESFTYFVICVFMLAIITFAIRTKRFNRAMLLMVVDEFPGYNRPMVDLKRKMAAI  
RTSYGDFTMKVIVSYLTLVLFIEPATAMVPLAAASLTDVKLGSQSTMVVLWFPADTSQVG  
MYAVSYVIQFLIVVTVKFIITGIMCSFSFFVSQMISEFQILSAYVEHAVEIVEYDQSADKTTE  
QKLLDHVKNCVMLHDRLIYFKDQLNESGYIILLELMFSTLYFCLSAFMIFVGNRFVMV  
KGLLTLSNYLAELFIFCMYGSMVEDAHMGLRASYSVAWYAQPVRFRQSLTMVMSRTQT  
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>ApisOR2a-like

MTTTPRVTELTAPASEDLTIVDNRLFKAICLHQILDPTKGGNRYYRLAFMVVMWVSLSVQI  
IQLVGLYFAVNDLQRFAFTTVIFNALLCLSKGYVLVNVNADRLRASLEVARYEFTSCGARN  
QRLVRRSRAVLSTILRTFAVLSWVTCIFIWALTPLFAMDEYLQVTNADGTVSRYRTIYNVW  
LPVPATVYNETTVWSLVYAVEVIACFVNFSWLLFDSDYVVTMCFTFNAQFRTVSASCTTIG  
HHSDSFRSPPPHAPEGTNDDNNNTFNCYDELINRIKDNQSIKIYDDFFEILQPAILFQIIGGSY  
SVITLIFLTSITYLMGFSIISIPV ррлквffglsvtfelflycyvfnhiетекcnmnglyssnw  
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>ApisOR4

MTSIGKKNQRKFYQTLMTLAFFLDTSQYRYISRFVKQFYIFDWMLVSVAAFTILEGNY  
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KTVKSLSIPLAISLSIALGPLISTINDIGKLPLDNRAHFVLFWPTIVDTNKLMSMYGIYTLQV  
IFTIILYISVLSFNLCGYMVFLNELITQFEMLLNGINDAFKYKMDKQFQTLFIDCIRHHQIIK  
LDDLKSYFKWMILIEIIVVQVILALIYNLTKVNASLGYKVKIAGSILFNLLPICFHCHVGEV  
VSLSHTRLSNHIYNMPWYDMPNKNKQLIVIMLQRTQRDLTSSALFSSERASRSLISKVIK  
QVYTILNVLLKT

>ApisOR5

MQRIDTINMFLQMTGCTDSKAMILTYFEFLITFYLIATYASIVHFEQSUTIQLFALLCMLI  
ECVILLNITFRLYHKNHIREMHQYSRRLGIPDSYRSVINVTKYHLIASNIFVVFPVTAIFCD  
SVRVGDPFTPFLDVLPMHTDNLAIYACKYLVYASVYIAHVELCFINTTFIYYVGVLKHRL  
ETIVQTIGEAFADNDEQKFKYAIHQKLLSYFNTMKIVFSKPILLSMSFNAIYFGLTSFVI  
QAIRGYINQAILSICIASSAAVINITIYTFYGSELMDLHDKILHVLFDNAFFYVSKSFKSSILI  
MMTRVTIPLKFTVGYIFTINLNLLKILKMSYTVLNVLLSSETIKPHKLS

>ApisOR10

MAHIVDIFFQNMGCSDHGYGMVFFNCCELAITLFFTSTYPTIADPTQNLISRLYGVCL  
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LDWVRIGDPFTPFLDVLPIKTTNVTVYVCKYIVYALPVYFAHLETCLNVTMFSGIVKR  
HFQILNDQVEEAIVNEDEQKLKIAIKHHQQVLKYFEDMKTVYEKPILMTIEFCGLYVGLTS  
CFVIQVIQGFIHQIILGLCIVSSIACLMTIIIYCIYASNMYALHNGILNALFEHRSCYSRNKSFK  
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>ApisOR17

MTTTPRVTELTAPASEDLTIVDNRLFKAICLHQILDPTKGGNRYYRLAFMVVMWVSLSVQI  
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QRLVRRSRAVLSTILRTFAVLSWVTCIFIWALTPLFAMDEYLQVTNADGTVSRYRTIYNVW  
LPVPATVYNETTVWSLVYAVEVIACFVNFSWLLFDSDYVVTMCFTFNAQFRTVSASTTIGH

HSDSFRSPPPHAPEGTSDDNNTFNCYDELINRIKDNQSIKIYDDFFEILQPAILFQIIGGSYSV  
ITLIFLTSLTYLMGFSIISIPVLKVFFGFLSVTFELFLYCYVFNHIETEKCNMNGLYSSNWT  
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>ApisOR20

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LNDLQRFAVMAAVIYGMMCSFKGYVLTNAADYGYTGCGRDPSRLRR  
CRATLSALLRTFVALSYGTLIVWIVLPFFDEYTGITNSDGTTRYRTTIHNMQYPIPLAYV  
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PDTTFAGVRRIKFDEIESNHYSDLISHIQDNQNLIKFDVFEVVRPVVLVQIANGSYSV  
IFLTALMYLMGVPVLSAFLKFICGLISLTIELFIFCYGFNHIETAKSVLNFGIYSSNWTEMD  
LTFKKTMLLTMKMNSSHKRAMKVSPNSAVGLEMFARVMNMSYSTVSVLLNSRS

>ApisOR23

MNLNDEQNYIVNLKLMKITGFYHLISSRAPKYFGFNVYKVTAIAEVMTGIFSIIMLFLSSYY  
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RAKSISTTILFVILWSSVTVAWSISPFFVKDVYLNFKDETTRFRYNSLNVYPISSEFYNE  
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LEAMFNLKLLIQDQQNMFKKIKEIYKIFEPVTVQLAAQSMILILQAYMIFINHYNGFSLLS  
VPIIKLIVTVAPNIIHLFITCYLYTNINHQQDSMNFALYSSDWTAMSINYKKMLLFTMRMND  
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>ApisOR25

MATGIKTVSKNEDNFMINMRLMKKTGFYQLLDSRSLKVFHNVFKCMSVVQMSILSSVA  
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RRILEEGRSKSTSILIMFMWLNLIVWSLGPLFVTNYFLIVEQNDEIYRYRFNIMNFAFP  
TDRFYNDNFMIYYGIEFITLVLWCHCTMNFVLLSMNITFKYQLKTISNSFSAFNFTRYN  
DFKNNRTKVNHHKESESMDFKSLIYDQQRVIENMKNIYRVFRPVVLQLASESLIIMLL  
SCIIMNYFNGISLLSALNLRIFAASTFLFHIYVICYLFDVNEQKDSMNLALYSSDWTTSD  
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>ApisOR31

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FIALTVITQCLIGFGNCGLFELEDTTDNIDLFLIIFSNSYFCLTEWKVVLIIINRKKFLELLDV  
TDLIFLKSQCRKNIKILCKHRIRALQLTNLYFKFCIFVIEWIIFPIMINSFIAHKTENRRLEN  
VVNRYPDVNTYNKYYILFYVFEIIIGVKTIVLVMVDILLSIGWAIVIQCYEVLAEAFKN  
IGYNENLQKDHDHDVDDYKYFKSILFDQQQLDSKVKLYFPIVKPIVLMHVAINSVLFIMLS  
NSFLMVLSTESTYKIVNLFKIGTGILYICLQLFLYCHLFDNINLKRKSVNLGIYSCNWTK  
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>ApisOR37

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KYRDRSITITNLYQNYSTMVFIWMITPLVLNTFVVVGGPNQRYHNIFNMQYPVSANIYNQ  
YYYLFLYMEIAMGIFVLYSMIVDNFLISLCWVIIAQYEVITTAFEKIGNDCELTTLQNEKN  
NNSEAYEDELSILMDQNKLYIKLKSFYRVVIIIVFLIIIDSVLLIILTYSFVMICSSAESFSIF  
NILKISTAFFVFVLIQLYLYCYLFDVLNDKESVNFGLYCCDWTKMDLRFKKLLLATKFNN  
ANTLKIKSTPNKIVNLQLFSSVMTTAFNIVTVMLKTMNGKN

>ApisOR38

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LGYFTEMEDVIDSIFHIQIMFCYLAYSLSLLKIITFLYKANNIWDLRVTRINFLTSTQCQAHI  
GILHKHRNKSIKITNLISGFAIVTLEWILPVLRLLSKTDASHSNKRFENIFNFRFPVTVC  
YNNYYFIFYIMESFIAIFMLYAYVVTDVFFISVCYVIIAQYEIIKRAYEIVNCEQTSENNEN  
KNHNNIIVNDCCDDLISIVMDQQNHYAKLRLFYSTYKLIIVSTVVINSASIILTYASVVIFTS  
PETIPILSIVKLISAFTYMFFVLFCLCYLMECINNKIESVQLGMYSCNWTAMNIKKLLLFS  
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>ApisOR39

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LRCRSRHSKLITKNFVKRCKKSTTITKWIARSFLVGLILWLMGPFIANEEHTEPNTVVRHKNI  
INIKFPVTMKTYYFVFLMEAVGFCIVYGSVLIDAYLMSFCWIISAQYQSVTKAFAT  
FGYNKQGSPKDIYKDFKSIIDHQNIYLKMKSFYAVVRPITLIHFAYSCSLIMYAYVITIFN  
SKELFIIAEIMKIVMTVSNTMEVFIFCYLFELIDNKEDVNFGLYSCNWTGMDIKFKQLL  
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>ApisOR42

MPNSSEECVMSSMAKCTGLHYIIDPEGPTVGGHNVHVTVMVIGFTVVCLSMCPFGL  
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FRKCRDASSTFTGWFAASSHFVLLVWTLLPVVVVGKGVEINNRDGSTSYYHNPYNMYF  
LVSSETYNRLHLVFLVEWAFLGLCFVLIMVAFTDFMVTLCVAITCQMRGIGNAYSKLGH  
RCATASNVCSDGGIESNKSNNYEYLRDLKLIKDHQAVLGKMNDFYKIVGPVILPQLIVASFT  
IIFVSFIIRNYFNGMLLTSQLKMCCFPIFFYQVYYTCHAFGNLSHRKNVNMFALYSSDW  
TQMEIKFKLLLLAMQMHDANKLDMKLTDKLVINLELFTRVINMCYSIFSVLVNSQLKIA  
DKQ

>ApisOR43

MDSKQEKKYIFNMKLARIMGLYQILFPNSTSFFGYNIYHVTVFFVSFTAISMLFPIGLLY  
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TRSIRITYIYIVIALFAFFCWIFSPCIMNKS VIAIRNIDGSYSKYRMNIFNLYLIASNETYNKNF  
YIFYVIEIIISICYVYFTIVFDVLLVCFAISYQLETISNTIKSLGHEIYTRDNIRSGNSIKLKE  
KHGILYNDLITIMTDHQNVLKKLNDFYNIFRSITLTQIFIASSSHVFIWFIAAMSIDEGDNAD  
SILSFKLFIVLPLINFQLFMTCSLFGTINEKKDSIIFALYSSNWTNMDLKSKKMILFNLTINNA  
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>ApisORCO X1

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PHPLFAESHSRFHAKSLSRMRQLLIVSIVTFTTISWTITFFGESVWKVPDPETFNQTMYV  
PVPRMLHSWYPWDSSHGLGYIVAFVLQFYWIFITLHSNLMELLFSSFLVHACEQLQHLK  
EILNPLIELSATLDSSVHNPAEIFRANSAKNQSINGIDHDYNGSYVNEITEYGTGENEPNR  
KGPNNLTSNQEVLRSAIKYWVERHKHVVKYVSLITECYGSALLFHMLVSTVILAYQA  
TKINGNVNFAFSTIGYLMYSFAQIFMFCIHGNELIEESSSVMEAAYGCHWYDGSEEAKTFV  
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>MperOR22b-like

MEDFRDEEVVINLKLLQYRFYHMLKFNETKILNCNVYRLILFLYGSIMTCMVVYGSIVL  
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YDYRERTIKITNYFFVFSMIVLMQWIIFPILAITFKKSDFENIRSENVMNFRFPVSTHTYNQY  
FFIFYIMEVAIVTFPIYLIIVMDTLVLSFCCVIIAQQEVLASAFRNIGHEENSQLEYYEDFKSV  
LGDQIQLNLKIKSYYSLMRNIILVQVAMSSTFFIMVAYVLIVVCFSKDSNQILTIIKGSSVIFI  
GSEIFLYCYLFGSMLKRESVNFSLYSCDWTKMDNKFKLLLLTMRMNNANNLMIKASP  
KKVVVDLQMFANVISIAYNVISVMLKSMDSN

>MperOR46a-like

MFTDTSDVTHLEKRFDALYDDLKIIIDHQTIVRLKEYCTIFRPVALFQIFITSSSHIVIWF  
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>MperOR43b-like

MPHIDTINMFLQMTGCTDNKKMLYLTYFEFLITFYYLIAAYISILHFEESVTIQLFTLLCMLI  
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SVRVGDPFTPFLDVLPQTGNLAIYACKMVY AISVYIAHIELCFINTTFIYYVGVLKQRLD  
TIVQTIQEAVVDDDEQKFKYAIKHKQLLTYFNTMKIVFAKPILLSMSFNAYFGLTTSFVIQ  
AIRGYINQAILSICIASSAAVINITYTFYGSVLLDLQDEILHVLFDNAYFYVNKSFKSSILI  
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>MperOR4-like

MSSSRPFVSVIDVMQKSERFILTPFQKFCIRWSVLFDSSSDRSLRTETVLRSVQFSTIMITSG  
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ALKRKITDIRTSYGDFTMKVIVSYLTVLFEIPATGMVPLAAATLTEVKLGSQSTQMVVWL  
FPADTSQVGMYALSYVIQFLIVVTVKFIITGIMCSFSFFVNQMISEFQILSAYIEHAVEIVEFD  
QSVDKTTEQKLLEHVKSCTMLHDRLIHFKDQLNESYGYIILLELMFSTLYFCLSAFMNIFV  
GNRFVMVKGLLTSNYLAELFIFCMYGSMVEDAHMGLLRASYSAQWYAQPVRFRQSLM  
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>MperOR67a-like

MVISYQYKLLASAFEVLEYRMDNKDDSIISDEKLLETFISIVSDSQIIHKKLKMLYDIIRPIG  
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ISSVLLINSNIN

>MperOR22c-like

MENPERVDYDSNGVTGNPAEKAEGGEMDNPPKNDTEGGTILDVELFKIIGVYQLLRPDEF  
GLNARLCRTTAIVVCLTGLQSMQVCRLYALARHDLQMFANVGVMINGLMCLLKGYMV  
AANADRMSATLNAARYAFTGCGNRDQSCLRRLCRARLSTILRTFVRLSGFTLIVVVMPW  
FMASEYDDPSIWATVYVIESIILTVNVFCWTSFDCYLVTCFVLEALFCSTMSTGYETLGR  
HRAAAKSSAGQQLAIAGTISDVSIIDVNYDDLTSHILDNQNIIEQYDEFFDVVRPMVLVQIA  
NGMYSIITLIFLTLTYLSGYSIVSAPFLKFVCGLASLTIELYIYCYGFNHIEDGKSTVNFGLY  
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>MperOR33b-like

MEHQAMMEKYEDFLILFRPMILLQIFISSFVIMLLFTFMMGFSNVEIFESSTFVQTRLFCTI  
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>MperOR2a-like

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IVRRSRNVLSTVRLTFIVLSWVTCFIWALTPLFGMDEYLQVTNADGTTRYRVTIYNVWLP  
VPATVYNATAVVALVYSAEVIVCFVNFSWLLFDSYVVTMCFTNAQFRTVSASCATIGH  
GDCSGSPSPHATGTHNIIRDDNNILNCYDELINHKDNQSIIKKCDDFFEIJKPAILFQIIGGSY  
SVTILFLTLTYLMGFSIISIPVLKVFFGFLSVTFELFMYCIVFNHIETEKCKMNFGMYSCN  
WTAMDLFKKTLFAMNNNSAHRVMKVTPKSIINLEMFSNVNMMSYSIVSVLLNSRVQ  
K

>MperOR64

MDVRNEKNYVFNIKLAKFIGLYRILDPTVKCRGRNVYHIIMACILVYMFAISMILNLNGL  
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RERSVSLTTIYAIMYSMSTITYMVITLAFSEDVSPVKNHDGSVGYYRHNMNFYLIVSDET  
YNTHFYIFYIAEALYLIFLTISFLIFDILLVLCFGMGCQLQLICCASESIGHKKLSDNSPIDY  
TDEYNKIPNEHDIIYDDLKTVIMDHQAVMEKYEKFILLFRRVMLLQIVVSSLVITLWFIFI  
MSFSNDDRFKASEVVVIKKMFCSSIPLLFQIFMVCYLFGNLHNQQDSIIFALYSSNWTEMDM  
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>MperORCO X1

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LVQLK

>RmaiOR2a-like

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KVRNKSIRLTNFIFGFATMTFIIWIYPLVNNFLIATDQNNHQRYQNIFNMRYPVSINTYNK  
YFFIFYAIEVIMGLFILYNSILIDTFLVSFCWVFIAQYKILSKAFENIELKDVDKLNKNCINA  
YNDLKLILGDQRLNSKLKLYYSIIWYMLTYVVFSSCSIITLTYSFIMVCISTTKSLPVLSII  
KIIAPFIIVSFQLFLHCYFFGLINFKESVTYGMYSCDWTSMDLKFKLLLLSMRMNDVDT  
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>RmaiOR67a

MNTTDKRYAFDLTLFKIIGYYQMIDPNSKKIFGYNIYNVINMAIVIFTSIVTVIGLLGFFYKP  
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GKLSNEEIQKEFVLIILDCQTVEQLETIYGIARPIVLIYMGDSIGMITMPFLIVMFYMQD  
KSIFNSNVIAYSWTLFVVGIQLYMCSLLQNVNEQKENINFGLYSCDWLTDIEIKKLILL  
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>RmaiOR43b-like

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VRVGDPFTFPFLDVLPPIKTDNLVIYAGKYFVYASVYIAHVELCFINTTFIYYVGVLKNRLE

AIVQTIREAVVDNDEQKMKYAVIQQHQRLLTYFNIMKKVFTKPILLSMSFNAYFGLTTSVLIA  
QAIRGYINQTLSICIASSIAAIINITIYTFYGSVLLDLHDEILHVLFDNSYFYLNKSFKSSILIM  
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>RmaiOR22b-like

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YLKQMOKISYWYLFGGIVAGIFIIVSPLLTYSKGDRSDFQYYNDPKSYPLSCWIPFTLNENY  
MFLVVVFVCHSIALFLIILVYLGIDTYFFGAIYAVGGQIELLNTSLNNENNLAQLENSCTNQ  
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VIETISVICFICMSVWHQYLNFFGEFIIQKQLSVCTALYNVPWWRCDKRVRQLLTLMILRS  
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>RmaiOR46a-like

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>RmaiOR22a-like

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YDNRERTIKITNYFFIFSMIVLMQWIIFPIMVITFTAPDIEYYRLPNIMNLRFPVSTHTYNQY  
YFIFYLMEVVISTFPIYVIMVTDTLILSFLAIISSQQEVLSRAFKNVGHKENSQSKCYEDFKSI  
LGDHIQLNLKIKSYYSVRPVILANVAMSSTFFIIVTVYVLIVVCFSKESNQILTIIKLGSSALFI  
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>RmaiOR33b-like

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>RmaiOR22c-like

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CGVTLSAMLRSFVALSYATLIVWIALPFFVDEFTAIIQLDGTVTRYRTTIHNMQFPVPLALY  
NSRPVWMLIYFTEVAVCIVNVFIWSMFDCYLVTCVLNAQFHMSAGYVTLGRRARP  
SPPETPDTSVRMKLNDVESNHYDDLIGHIQDNQKLICKVYDVFFDVVRPVVLVQIGNGSYS  
VISLIFLISLMLMGIPVLSAPFLKFIGVISLTIELFICYGFNHIETAKSVINFGLYSSNWTE  
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>AcraOR1

MNFVYPATDQFYNDNFMIIYCIEFVFLILWCHSTMNFDVLFLSMNITFKYQLKTIANSFST  
FNIAHYIKICYSHNHTKVNKHRKESELMLDFKSIYDQQRVIENMRNIYQIFQPVVLQLAI  
ESIVIILQSCIIMMNYFNGISLISAMNRLFAAIMTVTLQIYIICYVFDDVNQQKDSINFALYS  
SDWTQSHAQHKNLLLHAMRMNNAENLRLQVTRKKICFLSVLRNIIILRHYIFCIKLLFTH  
HAKSVFNTISAGKDVKENAYFAFFSSNNFQALII

>AcraOR10a-like

MKSIRYNSITYKNCDYLSFAYNVIQWIGVFPPSDSTKWTRLVFNFYRAIIIFIILTLFTTLM  
TVQMFVTTELARTIDIWTMFFSGLYKWIYMTVFNWEFSLKFLSALAQLQTQGSKAYGRSA

DVFTADYLKQTKKISYWYLFSGFVAGFFIIVSPLLTYSKGDRSNFQYYNDPKSYPLSCWIPF  
TLNENWMFLTIFICH SIALALIVLVYLGIDTYFFGAIYAVGGQIELLNTSLNNENNLAQFEN  
VSCTNQTSVYTEKQKMRCYSTLRECVKHHILVLDYIKNIRKLSTLILVDYVHGITSVTFAL  
FQLTISASVIETISVICFIFVSVWHQYLNNFFGEFIQKQLSVCTALYNVPWWRCDKRVRQLL  
TLMILRSIKPTLITGYMYKLSYESFISFVKALYTYMIFLDMRSASLLPILATILNTKIL

>AcraOR22a-like

MYLFNSRVLYILLSATKLCVMDNLRDEEVTHLKLFRFYHMIKLNSTKIFNYYNYNAYR  
LLTFLYVAIMNSIVIYSNIGFFVGTDQSQNINYVDLYLIMFLMTNIFFCSWRICIILKSNTIFE  
VLNVSRNLNFFTSEHCRKHNLVHLKNRDQTKITYYFFVFSTIVIQLISPIMAIMFTTDVE  
NVRLSNILNLRFPVSTHTYNQYHLIFYLIELTISIIPSYVIILDTLILSFSLAIISQQKVLRAFK  
NIGHEENSQSKCYDDFKSILEDQIQLNLTNINFMSIYTINYVILKKKIKSYYIVKPVILAN  
VAMSSTFLVITTYVFIVKFLLNLISTGDMVLFSENYESEIFIIKLGSTAFFIPAQFFLYCYLLDN  
MYHKRESVNFAIYSCNWTKMDVKFKMLLLTLRMNDANTLMIKISPKKFFNLQMFNSNI  
NVLQYYLRHVENYKFKISLIARDCKDFTTKLVSQPPRGFWVMLIG

>AcraOR22b-like

DIRQHFYIYYALVECCGISALFSTTKANNYKNNSKIDYFLMIFASTYVYLSIWKLFKCLKDR  
KNFLDLFKIGKLDFLTSKECSKYSKVQYKHRDKNLKFVNYFLFSVVILQWFIFPIVINEII  
NFENSENLKV

>AcraOR43b-like

MEHIVDMFLKKTCNCNDRSYDTMCQVFFIYFELAITLFFAVSSYLSIANSTEGLSVRLYGLL  
CFLIESHFFFFIAVRLYYLPQFRDMYQRTLKMGIPENFRQRIAIVKHHLIISNVFVSVSMLYT  
ISMDWVQMGDPFTFPFIDVLPKTTNLTIYVCKYILYLPVYIAYFETCFLNVTMYSTGVV  
KRYFQILDGQVEEAIAKDEQQLKIAIKHHQEVLKFFDDMKTAYEKPILMTIEFCGLYVGL  
TSYFSILVIQHDGILSALFEHRSVYSGNNSSFKRLISIMMTRATIPLEFKVASIFTINLNLLIKIL  
KFVYTVFNVLTSISRKLKETAI

>AcraOR4-like

MVGRSSFGSVDAMQQQPESFVLTPFQKFCIRWSVFFDSTS DRLSRIETVLSVQLSTIMITS  
VLTMTSVLIADNKALESFTYFVICVFLLAITFAIRTKRFNRAMLLMIVDEFPGYERPMED  
TLKRKMSAIRKS YGEFTMKVMVSYLTLVLEIPATAMVPLTAARLTDVKLGSQSTQMVVL  
WFPGDTTQIGTYAFSFVIQFLIVMIVKFIITGIMCSFSFFVSQMISEFQILSAYVEHAVEIVEY  
DMSTGKTTDQKLLDHVKSCVMLHHRLIDFKDQLNESYGYIILLEMFSTLYFCLSAFNMIF  
VGNRFVIAKGLLTSNYLAELFIFCMYGMVVEAHMGLRASYSAAWYSQPVRFRRLSM  
MVMSRTQTPLQLTIGKVFIANLPLFLSVLKVSYSGVNALRAANAK

>AcraOR42b-like

MATASSSEELTIVDNRLFKAISLHQILNPTHGGNKYYRIALLAIMWISLVSQSMQLVGLYFA  
VN DLQR FVFTT VVSNSFLSMSKAYVL VTNVDR LRDGLEAAQYEFTSCGS RDQRTVRA  
RAALSTIVRTFTVLSYVT CFMWAINPLSAIGEFLPVTNADGT VSRY RVTIY NVWLP VPVTV  
YNTTAVWAVLYAVEVIVCF FNVISWLLFD SYVFTMCFTFKAHFSTLSASYATIGHPDALRSQ  
TPHVGSGTYYTTVIKPVILLQIIGGSYAVITLIFLTSLYLMGFSIISTPVLKAFFGFLAVTFQL  
YLYCYVFNL IETEKTAVNFGLYSSNWTAMD LKF KKTLLAMNMNSA HRR VMK VTPK SIIN  
LEMFAKVMNMSYSIVS VLLNSRAGK

>SflaOR4-like

MDAQPRRARFHLPFQKFCVRWSVYDSSSDRLSRVETTLRVYQLTTIMVTGLTMYPILF  
EDNKKALESLTYFIICAFLLSLIVLAIRTKRYNRA MLLMVEDEFPGYGGPVPDALRRKMSA

IRSSYGRFTMHIVSYLALVVFEIPATGMVPLVAASFTDAKLGQSQTQMVMWFPMĐTSEI  
KMYAVSMVIQFFIVLTVKFIITGIMCSFSFFVNQMITEFQILATFIEHATEIVEYDRSTNRTTE  
QKLLDHLKMCTKLHNRLIFYKDQLNESYGFIIELMFSTLYFCLSAFNMFVGNKFVMV  
KGLLTLSNYLAELFIFCMYGSMVEDAHINLLRASYNSKWYAQPLRSRRSLMMVYRSQT  
PLQLTVGVKFVIANPLFLSVLKVSYSGVNALRAANAK

>SflaOR46a-like

MAMLVVCGTLSVYKGHVMVANADLIWDTLHVARYAFITCAGRDESELRRAGSLLRALLR  
AFVAVSYQTLAIWIAIPWLTDTRPVANGDGTMAEYRMNVNNLWTPLPVAVYNATAVWA  
VVYAIIEVFLITVNVFFWALFDCYLVTCFVLNAQFHIAAAYEKLAWSPSPHRGIRENN  
DGFIELDHYDNLILHDKDNQRIMMKFDFFDIVQPVILVQIVNGSFLVITLIYLTLMYFTGW  
SIKSLPILKFFSGMASLTIELYIYCAYAFNHIETKKNNVNFGLYSSNWTAMSISIKFKRTLLATMK  
MNAAHQRLMKITPISIVNLEMFSKVMNMSYSVVTVLLNSNSTQTKEME

>SflaOR49b-like

MDDDDHQNYIINLRLMKLTGFYQLINPNTSKYYGYSPYKVVATIEIMFGVFSVSLILSSY  
YYLYNTNELMNHFMLAVAIFFSTFKLFCVSRNSELIWDCMDMTSVQFLSYTGRRDALRT  
ARAKSITLSILFLLWGSVTVAWCLSPFIVDGVYLDVEINGKVRQYRNSLNVYPVGERF  
YNDHFLAFYAVEMLQVVSGHATIAYDTFVISMCIAIQFQLKTIADSYSTLCYGTVSEAYG  
NKRNIIDGNEFETALSLKLLIHDQQNMLKKIRDIFRLFEPVTVQLAAQSMILIFQAYMIFIN  
NYNGLSLVSVPIKLLLITPNIIHSFITCYLYGLINEQKESMNFALYCSDWTKINTKYKKML  
LLIMRMNNAEKLKLKVSINRIVNLEMFSSIMHTTYSIISVLAKSYGNTKTK

>SflaOR43a-like

MKFLTLAYDILQWIGVFPQWIWSKWKLWVYSIYRIMIFVMIALFTVLMTVQMFVATDLTIL  
ARTIDIWTMFLSGLYKWSCMSLFHEKFVKLTKLIEIQVQGSVAFGRRSADIFTTNYLKQT  
QKVTFGYMMMSGLVAAGFLIMSPLLTYPKGGRSDFEYYNDPRSYPLSCWMPFMIDERWMF  
WTIFISQISLIVVVCMYLGIDSFMFGAIYTVGGQIELLNWALNSIKNSLEEIGSSTDQLIQ  
YTEKQQMKCYSILRQCVKHHILNYIKMVHTLFSSLIIDYLHGITSVSFALFQLTISRGIGE  
KISVISFIALSVWHQFLNNFFGEFIIQKQLSVSVALYHIPWWRAGKSVRQLSLMISRSIRPT  
FITGFYMYKLSYESFISFVKALYTYYMLRVRNAEDKNA

>AgosOR43b

MVHYMAEMFFKAICSDDDLHGRDAMRMVFFTYGELAITLFFAVSTYLSIVHSTEDLSVL  
LYGVLCCLIQLLIFAFISFRFLYHRSHFRDMYQRSRGMEISENSNRKIAAVIKHHIMPNVFVV  
ISALYKISSDRVHIGDPFTFPMDVLPPIETTSAVYVCKYVYALPVYLTQIEVCFLYVTYM  
YSTSIMKSHFQILEKQVEEAMVNKDEHKLMAIKHHQELLKFFKEMKTVYEKPIFLIVSC  
GLYIGLTSSLIIQVIQGFIHQILLGICIVSSLECALTIICVYATNLYDLHDRILNALFQHQLLY  
SQNKSFKQLILIMMTRTTIPLEFKAGSIFTVMNLLVRILKFAYTVFNLITSINHQLIKTAV

>AgosOR10a-like

MTVQMFVTTELILARTIDIWTMFFSGLYKWIYMTVFNWEFAHLKFALAQLQTQGSKAYG  
RSADVFTADYLKQTKKISYWYLFSGFVAGFFIIVSPLLTYSKGDRSNFQYYNDPKSYPLSC  
WMPFTLNENWMFLTIFVCHSIALFLIVLVYLGIDTYFFGAIYAVGGQIELLNTSLNNENTL  
AQFENVSCTNQTSVTEKQKMKCYSTLRECVKHHILLDYIKNIRKLFSTLILVDYLGITS  
VTFAFLQLTISASVIETISVICFICVSVWHQYLNFFGEFIIQKQLSVCTALYNVPWWRCDKR  
VRQLLTMILRSIKPTLITGYYMYKLSYESFISFVKALYTYYMLRVRNTKT

>AgosOR43b-like

MPRIDAINVFLQMTGCTDSKRMLYLTYFEFLITLYYFIASYVSIYYEQSVSIQLFTLLCMLIE  
SYILLNITFRIYHKNQFREMDQYSKQLGIPDDYQSKINIITMYHLIASNMVFIFPVTYTILYD  
SVRVGDPFTPFLDVLPIKTRNLVIYACKYFVYAIHSVYIAHIELCFINTTFIYYGVVLKYRLET  
IVQTIREAVVDNDEQKMKYAVIQHQRLLIYFNTMKIVFTKPILQSMSFNAIYFGLTTLVIQ  
AIRGYINQTIVSICIASGIAAIINITYTFYGSVLLDLHDEILRVLFDNSFFYVNKSFKRSILIM  
MARATIPLTFTVGYIFTINLNLLKIVKMSYTVLNVLLSSEAIPHKMS

>AgosOR2a-like

MYGSSCTDKIALSSENSATDVVGEICLTPRSDTVTLVKIGSSVIYLTVRIFIYCYLFDSINK  
KRELVNFSIYSCNWTKMDLKFKLLLLTMQMNDANQMVMKASPKKIIDLQLFASIMSTSF  
NMVPVLLKIKNSEYYKSQ

>AgosOR4-like

MVGHSLFASVDVMQQQPESFVLTPFQKFCIRWSVFFDSTS DRLSRIETVLSRVQLSTIMITS  
VLTMTSVLIADNKKALESFTYFVICVFLLAITFAIRTKRFNRAMLLMVDEFPGYERPMED  
DLKRKISAIRKSYGEFTMKVMVSYLTFLFEIPATAMVPLTAARLTDVKLGSQSTQMVLW  
FPGDTTQIGTYVFSFVIQFLIVMIVKFIITGIMCSFSFFSQMISEFQILSAYVEHAVEIVEYDL  
STGKTTDQKLLDHVKSCVMLHHRLIDFKDQLNESYGYIILLELMFSTLYFCLSAFNMFVG  
NRFVIAKGLTLSNYLAELFIFCMYGSMVEAHMGLRASYSAAWYSQPVRFRSLMMV  
MSRTQTPLQLTIGKVFIANLPLFLSVLKVSYSGVNALRAANAK

>AgosOR42b-like

MATASPSEEESTIVDNRLFKAICLHQILNPTHGSNRYYRIAILECIWMSIVVQITQLVGLYYA  
VNDLQRFAFTTUVVNSFLSLAKAYVLMANVDRRLDGLEAARYEFTSCGRDQRTVRRA  
RAALSTLVRTFTVFSYVTCFFWMLNPLSAIGEFLPMTNADGTVSHYRVTIYNWLPVSAT  
VYNTTTWALTYAVEMTVCFFNVNTWLLFDSYVLTMCFTKAHFRTLSASYATIGHLDTF  
RSLTPHASDDNFNIKTGNNNTLNCYDELINHLLDNQRIKKYDEFFEVIKPVLFQIIGGSYTVI  
TLTFLTSLYLMGFSIISIPVSKAFFGFLVNFQLYLYCYVFNHIETEKSAVNFGLYSSNWTA  
MDLKFKKTLAMNMNSAHRVMKVIPRSIINLEFAKMMNITYSIVSVLLNSRAGK

>AgosOR33b-like

MDLSNLIVIIQDHQKLTKKIHDIFDEM RPIILFQLLSESILMSLIPLVLFNNSNNGISLTSTESIK  
LLSAEIVNTGHLFSACYLFSLIDIYNDTINFALYNCNTEMNINFKKLLLFTMQMNNANNF  
KLNISTNIIVNLKLFTNLKFAVASYKTYAN

>AgosOR5

MPRIDAINVFLQMTGCTDSKRMLYLTYFEFLITLYYFIASYVSIYYEQSVSIQLFTLLCMLIE  
SYILLNITFRIYHKNQFREMDQYSKQLGIPDDYQSKINIITMYHLIASNMVFIFPVTYTILYD  
SVRVGDPFTPFLDVLPIKTRNLVIYACKYFVYAIHSVYIAHIELCFINTTFIYYGVVLKYRLET  
IVQTIREAVVDNDEQKMKYAVIQHQRLLIYFNTMKIVFTKPILQSMSFNAIYFGLTTLVIQ  
AIRGYINQTIVSICIASGIAAIINITYTFYGSVLLDLHDEILRVLFDNSFFYVNKSFKRSILIM  
MARATIPLTFTVGYIFTINLNLLKIVKMSYTVLNVLLSSEAIPHKMS

>AgosORCO

MGYKKDGLIKDLWPNIIRLIQLSGLFISEYYDDYSGLAVLLRKIYSWITIIYSQFIFIVIFMV  
TKSNDSDFQLAAGVVTLLFFTHSMIKFMYFSTGTFSYRTLSCWNNTSPHPLFTESHSRFHA  
KSLSRMRQLIIVSIVTIFTISWTITFFGESVWKVPDPETFNQTMYIPVPRMLHSWYPW  
DSSHGLGYIVAFALQFYWIFITLHSNLLELFSSFLVHACEQLQHLKEILNPLIELSATLDSA  
VHNPAEIFRANSAKNQPINGVDYNGSYVNEITEYGTKGTELNRKGPNNLTSNQEVLVRS  
AIKYWVERHKHVVKYVSLITECYGSALLFHMLVSTVILAYQATKINGVNVFAFSTIGYL

MYSFAQIFMFCIHGNELIEESSSVMEAAYGCQWYDGSEEAKTFVQIVCQQCQKPLIVSGA  
KFFNVSDLFASVLGAVVTYFMVLVQLK

>DnoxOR46B-like

MQFPVPLAVNSRPVVWALIYVIEVYVCIVNVIWSQFDCCYLVTMCFVLNAQFHMSAGY  
GKLGSGRAESTSSDITSRTDVRIKFDDVESNHYDDLISHIQDNQKLICKFDVFFEVVRPVV  
LVQIANGSYSVISLIFLTALMYLMGVPIISAPFLKFVCGLISLTIELFIFCYGFNHIETAKSVV  
NLGLYNSNWTEMDSFKKTMLAMKMNTSHKRAMKVSPNSAVGLEMFARVMNMSYSI  
VSVLLNSRS

>DnoxOR22c-like

MRFSCVADIKNVDVSIKFPNHYDDLITHIKDNQKIVEKYEIFFDVVRSTVLLQITDGSYSVITL  
IFLISIAYLNGDSIVSPTILKFVCGLASLLIELYIFCYGFNHIEDGRSTVNFGLYSCDWTKDL  
KFKKTVLLAMSMNSAHKKVMKLSPPNSIVNLEMFSRVMNMSYTIVSTLLS

>DnoxOR85b-like

MYAFSYVIQFLIVVTVKFIITGIMCSFSFFVNQMISEFQILSAYVEHAVEIVEYDQSVDKTTE  
QLLLEHVKNCSVMLHNRLIHFKDQLNESYGYIILLEMFSTLYFCLSAFMIFVGNRFVMV  
KGLLTLSNYLAELFIFCMYGSMVEDTHMGLRSSYSAAWYAQPVRFRRALMMVMSRTQT  
PLQLTVGKVFIANLPLFLSVLKVSYSGVNALRAANAK

>AlinOR1

MSINDYKPGEIFQNNLKPDKLRLKKVSYQQPDKRGTYKKVAKRLSEEEALKKGNDN  
QGLYLVLGTLRYRDSFGSWVHTIVFIIACLFMLFCLGRQTLITDDLSLLFETIHYITIIGGVLV  
IVPPMMKNQFRQKIFKIFAREVYCYDYLDEETAQEILRLRAEGNKEKQLLKAFTVMLLG  
TFAGFSVLLPGMYIINGQFFAPQREDGVIMGIPCVIWFPFRVDDKWVVTVRILLALEEYAS  
FTVVAFIIGQQTATCIGHTLLYEFKVLAGTMNKFEQRACKMDKKFIGDGTLPASQTRKYI  
TSCLNESIKHHDVLLDVEQYSSIFYVPELVILLSSTMVICLSAVSLTSDNIPLEAKAVSVIFT  
GAEMMNVFVNCYYGQILDAHNIIGDAMYESNWTSYSSIVHQVLIILSRVQKPLSLTAG  
GFAAVNLDTFAQVVKSSFSYFSLLQALKE

>AlinOR2

MTVDETLHDMVGFPLWIQNVLVYMKITGHWVGAVPGPTPLRVNILRAVGGFPVFLVLLYV  
AGANINGMVHNSDMTDISMNLIVLSTTVSALHKYSVFTNQQQALGRLGRWVKSVAERK  
ANNVPDTYADRVLKKALKAFYISGNVASPILIVKMMLTGNTFNVNPVENFPKPFLMFLIA  
VSFQAIaweavvDGCILMNSLFVFRSELVRALEWEKLNFDPHNPEISRRQLKAMVKKHV  
MLLGVKKDLKEYNNSMFGYQVFAAVFTTCALIYGCAKDTKFLGQAVIQLPTSTASLLTF  
SILCWGEEVTLFQQIHRNIYMTNWFEPREDKSIIVILEFAKNPIIFTGFTVFTCLTTFV  
ETMKQSFSLYTIKAVL

>AlinOR3

MTLKSYIKETLKWDPLGLITTIAVVAGAFNTIAPPKRIRRIFYWLSWYQTISYILFLMSAGT  
NIFTSTDFFDECLESHLFLVTAFHVFMKYLTLLFRERDFLELFDHIKRVWSSYRIHNEHFLTS  
KLSSVNITSVLIFTSIFNVVFVNVAAYLKNILDPTKVHLPIQIWPSFTKSSFLVGTIqvvl  
FTWPLFIVAMSTTFLNSISSHVEALGLALAEDIGREKVWSRDVARDFYKKHQDVISIVLRV  
NALMAGNWGFEMICASVQLTPAYRTLRAFRMNDVEVFNHAVLCLNMMVIYMIFSSGN  
RILSMGEKIHTKVYESNWHELPVKERKNVLFMLFRTTVPEYRYKIIHFDLPGFTVVNTV  
FSYMAALLRFLDSGGSEDEGALM

>AlinOR4

MGYVSSKFKSSVQEWSWEDEYSVEAMRLRYRGFHRIGFLVLDLSPKYALLSVIMCVIAA  
AVLFIVSFCLTFSCYQMSDDFEDCSGVCNLGFLCVAFSFLLNHFYRKKILDLHHMLGK  
GFHDYQEPQYFPDELEKFKKVVTQNVALIILASYVALIGFLVVVCPLIDESLGFGWTEP  
YDENGVRQLPVPIWLPPSHEGLHWFSFLFLEGFGGAMICLSIGGTALLFTCLSGGLML  
EQKLLVLSIKSIEKRAKRRYRELHKGKPGIDEDGNKIALNDDNKYQECIGYCLRQNILHHH  
KILTYTNHYLDLARSPLLFAFLVETMAIAMSMVKLNNEGSNKWGANIAFACIAIAEVANMI  
MLCVLGEVTSGSIEINDELYTKWYTFNKSNNKVLQFLLETRNPVvlaALGLVVCNMD  
QFSSVMHTAYSFFNMVKLSKLREETVTMGANT

>AlinOR5

MPPNQLLNTSKHEHDVYKRLDKLYYGMRLLLGITPHKFFGKCYFGKAILYVTVILYIL  
YGLGELLWAIIPGGILERLSSHAYVCSYCASYGVIWVYLMVKLETIHQNRIDFKSFNCNRLL  
GNTEVESILQKNINYFVKTFLFAASLLAGANVTSYILGFVVELIVQYAETGTLEEICVLSCFP  
PLWGQMIIAAANLVTLFMCFSIIMSMYIITGLSLEIETQCEILTRTMAYDEVNDDFKTFVID  
HIRLIKQTKWVWRFLFENINNSLFFSSYVCLAMQMFSLSVIKPEGYYLGVSDFCVEFIVM  
ASQCWLSSAVTNSVLSISEGVYNTPWYRKNKSNAIDVILMTQMAQRPYIQRVFLGTMKIE  
KETMIQVIQQSYSFYALLMILQSKK

>AlinOR6

MTDEHLAGVSRIYRDALGFSQLDVFLDAKPPQNGRFSWHIKRIVAQFFVCFLAPSFISLQIC  
GVLTAESQNLKQLSFDLGFLSHNVQNFVKMTYWLTBLKSVRSLCIDVSTFNVNKYRPILSS  
WVLKKETDVTRKFMNRCFLISYGNLIFWVALPTIVSICNYFRYVAGVTEGQDSYIPRLSPT  
RFPVDMSSLRNRLLVGFYEGLITMGFVYFQPIDMFSSIVNMVRTQFFILNSSLFEMPADL  
EEFWGSRIPVQDTQPPMDLRLFVEDHQRLVRYGVQLRKFLNPVLMVTVDCFNIMCSLLI  
VITEILEGDMNFTALLELISGLLVLSSLVVFTYTSTSGMLKEAEESVFEALYAHKWYGKN  
DEHKKNVIFMQIRTESANKIPMFHIGDVGRTFIEGLRMCYTYNFLKQFK

>AlinOR8

MSLRTNAADGKNHLLDRDVEGLTGLNTFGIKTFWHILDYFHTTGKRHWLMTTYIVM  
YHLIGGYCLLGFAAVFFIDQEDIPRMAAAIMNPLIATQAIFKCWTFSYSTAEYLKLFVLLK  
KNFMSCVPPEKKLAVDEVTKKNIGLTNQFVKYAMRWNCFTLSMVSFMPYLRSQAFREFF  
HLGVGPIVPNKVFENEYPFEWNSSPTYEIIWFYEQICAFLAVVTSSAYQAILLYFVMAIVGH  
LKVLGFVMGNMKATDFTSDSNETMDETAKAKSYKQLVLCIRDHGKINEAGDLLAERYNT  
FLTFHIGIAIVVGIAIFNCTVATELADKIKFGIMCVYGLLEVAIYCFGQLENACDDVLRQ  
VYSCEWERMDPKFRKAAQLMMVRANSPICLRAGRLYRVNLETLEAIQQLVYTSLTMLS  
MVQ

>AlucOR2

MVLVPYLKPQKERNAAVDRGYDITGMFYARLAGLYPDLEIGWRYWFFGSYQILVVVAYF  
YYVLAYVIANVIAIKYMDVELIGSTLCFGSYTYTYALIALTFYIKRSKIDKLLEIIGNELYIYQ  
CPLSQKQLKIRNEETTRAKNFGRYSFFVPCVALTHMSVPAIHGFKGEYSSIVNGSAPINK  
YTPLPVWTPVQATSGMSFFVFWCQLCPGFVEFLIFHGSCTFFVGVCVLVSEIKILLESLN  
SITDRAKYLYHVKGGRGSDIDNLYDDPIYQQCMVDCLKENVHHIKIKEFRNLFDIISYCI  
FFIFGGAATTSTPPYTIKIMESGDTDCKLYSAGVVMGHTFLSVYLLSRYCKFGQNFSE  
NSKLLEAFYCTPWYNTMDYRKILIAMSNSQTLQIKGSVVGVSLSAAFLDVIKSSYSL  
LNFLATAGS

>AlucOR7

MIPFVFKRDDSVDHEVVKGYQSTYNYIMRFCGLYPDFRGFWYYISGAHLNTVHLAYIWFL  
AAYMISTYYAFAYRDM DLLSYELCYGLVTIWF TVTHYTIYKRDQLDSLFRKVGRGFFTY  
EKPIDSEEEAIIDECNTNCRKTFQKTLALTTIAFWTCIIPPLPKAVMDYSSIVEGGVPVNK  
HLALPTWNPYPTDTHLTWYTMWMYQALAGCTEAYIIGATCILYCNFTIINRELKLLRFSL  
GNIKNRAIHAFKMRGYSQLGQKYENSQYQVCLVHCIDESIKHHIELKQFHGAIQNLLGF  
PIFAIFSGSALTISSPMFMLQMIGEH EESSFTLVMNIFQYTIIIFGFTYFLANYCLFGQSITDE  
SALLHFAFYDTPWPEAGLNFRKVLGMHHSRKPVLTAHGLASASSETLVVMLKTVYSY  
FNLLAAT

>AlucOR12

MKFIDKLAEEEDDELIEILKGNYWHFLYSMTFIRWKRPRIAIALISAYAIWIIVHLVIGIYSI  
YLAADERNWAVVGLVTHHMVLGALAIYLPICNTGGFREVMADMHRTFTTDIGQQYSGGN  
MYAEQACIDIKKDVRQRQTFVYYINPALVAAAGSLALAGPFLTKWFSGMENPYSPNGLSLK  
LPTALYYPFPTDSGVVFYAIVLTVISGTILGYLILAPQLVFINLSQNLKRELRFVGYSMETL  
VRRAMRMTFENNWKRKVTTEL DVDDTEFQQNV ELSIKETIIHHHQKASKLLSTAQSVKG  
PLAASYIFGLVTIAISLYNITLALKTNDIGSLTFL LLSSEVIGTFINCGLIGSELTEQSEDVTE  
KLYFIEWYNFSVKNRKMFFT FQTAITQPYEIKAGGVTPMNMETFS DIMNSAYSFFN ILQTIE

>AlucOR18

MSFSFV EKYQLSPETEK TMVTEYSYL VGGLLINYRPKVIISIAQTSIFIGLITSYTIIFIIS  
TAKSSNFVAFSQNLNYASLCCICLGLYFAGLSHRSAFVRLMEIHD DFYDYGDSFDNAEVA  
MWKSSLRTFKIIIVVGIPTYLIIIAVSIVLG DYIDTALGYDSTD E DYLGEIYQKAPLN LWYPF  
VVTNMFLRVAVTLSQMTTAAILATT LATGDVMMFLGQTV ALQLRILCLAATKMDQRAN  
LMYEKGLARSSSGDKEDLDGCYKLCIKQLVQHH LIKEFYKTYYTIAKWPTAIAFMNGSL  
MIAMSIVAMNGNEETP STYI STYLLVAE VLSM WLLCET QNVNTWSEKLFMDTYEFNW  
NGLSVPNKKM LLIFKENIKKPLLMMAGGLTPINRDTFATIMNTS YSYVNLLRASERRSND

>AlucOR30

MVEKS NFHV KRAQLFKAYNSIHWL TLKWFYEDYPVEKLWSDKRLWI HLSIVIICQSSITM  
FKVFHLISEENFFIFLTS LTSFLV IVLV A RTYI LYQFPTFRQLYFKPEVFC NLHRPTRSL ALL  
TEAITHSRKVG MWCLVLFITFDVAFLVLP IVPPILEIIDGTNK TYDELIPQYPSINPV SLSWLS  
KELKYAFDLVMAFNTIPWVG FVVVYYTVVQLFRAQHKIMMTAMLPGPPVPGDG REPLE  
LKLWIQDH ALIRKL VYKLRNTISP ALAGTICVN VFTV GLNMLA VSSPI GSDAPMTRYLY  
YFSFGTYSALSIFDIFIHCWLASEITNCGEDLSY ALLKSDWQNDLKRSHHHYVLPLMLCKK  
QIRFTGLGLIPVLT TETIRV SYFTLLRK TD D

>AlucOR46

MGYRVYPQQDLSDP SHMFSQLNALKSTTMWKP DNQYYIPFMILFAVN VFV LAIC TVGL  
LLKG C STKDLVDRSEAMDI FT LTGSAL YK MVFFLYHYEQLVDMVTCGLALVRNLPEGWT  
KNCGLLSRIHYTAGFLVLLI WGLAPILKVMYGETTWAEMKLINTYDPFDSTGFLFFLYIT  
GQYVLVLSAVIYMAADCYLFTSIYVAVGALQYIVDQFENMRDLNNNNKHTVADTMHDCL  
QECIEIHVHVL DYL RKT DKL FKSMILADV VHAV ISLSFAMIL QTSE SKGIFEGV KMVLFVQV  
CFVHQFLNSHFGQELIDKQDNLAKQIITDIPWTDASRKFKKSYYIMLTCVREP FKLSAWNV  
YFLQYATF LEFSKTM IQYYMVLQE VQDEAEVS

>AlucOR56

MVEDLTVKDLAGTYLLPHSVAYMHFTGHWIGAVPGPTPFRV KMYRAFGGTFTWLIVIATA  
IASLNGMLHGSGMSDIS MNLIISTSISSLHKY SVFIH QEQGLGRLGRWMKRA NEQNKISEN  
PDT TTD RILKKSLV SFY SGIVA ASLLV KIV VTG YTNALI PGLDQRYQPL LILVF MEAFSFS

SLSLEVIMDALILMNSLFVFRRELNVDEWRKMNYKSDNPQQFRQLKTNVQNHVEL  
LTIFQDVKNYCNSMFGYQVFAIVFTTCALLYGMAKDSGFDKAVLVQMPTSLASFLEFFIL  
CWCGEIQHGQQVHTSIYDTNWYEAPLREKSMТИVLEFSKNTIQLTGFVFKADLKTF  
VESMRQSFSLYTLLQKLV

>AsutOR4

MVLVPFFIKPQIGRNAAIDRGYKLTSMFYARLAGLYPDLEAGWRYWFFGTYNFVYVAYV  
YYVSAYMIANVIAVKYKDFELIGSTFCFGSYTYVYALITIMFLIKRQKIGRLLEIVGNDVYK  
YRRPPTKEEILIKESESMAIVYGRYTFYIPCSVALMQMAVVAIHLGEYTSIVNGSTPID  
KYSPLPVWTPVEATTGLSFFVLYWCQLCPGFVEFLFHGSCTFYIGVTCALVSNLKLHHSL  
GRIVDRAEYLYDIKNGKYDHQRKIPLNTELFDECUMECLKENVQHHVEIIKFHHLFQDIVG  
YSNLFISGAAVTISTPPFTIKAELGDRHQLTAGIVMIGHAFLSLFLLAQYCKYQGSIEDE  
SEKILESYFTPWFKAASKSFRQVLVVAMSNSLKP LEIKSAVGISASAATYMSIICKSAYSML  
NFLVTAK

>AsutOR6

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AYGKSFYGMVYADIENVGQVLCGLGTIVIYCISSIYIARKTDMDDLTMVKGFINYNR  
GVTEQECSIIDEMEKVTHRYAFGSTVMLTTISLVMGLLPVIRGLKGQFTSVTNETAPINKY  
TPLPVWMPYDCNSVGIFIFTFIFQMVPGCMEYAIINACCILYVGLAQQLSGNLKILANSIRDI  
HTRALIMFDNEGGETVSKNTSELYANAHLKCMNACLNENMEHHVVKLIEFFNKFQGVAGF  
SMLAIFSGTGLIISTAAYSLLIAQTGGDKELLITNIFVWTFYLLVYTFLMVYCYYGQEVT  
DKNDEILPALYETPWLEADLPFRRSVLISMSPYQRSMQLSAMGLIYSSYATVLDIKAFTSY  
LNMLMAVQ

>AsutOR9

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LGVGPIVPNKICENEYPFEWNSSPMYEIIWFYEQICVFLAVVTSSAYQAILLYFVMAIVGHL  
KVLGFVMENMKATDFTSDSNETMDETAKAKSYKQLVLCIRDHGKINQAGDLLAERYNTF  
LTFHIGVAIVVGIIAIFNCTLATELADKIKFGIMCVYGLLEVAIYCFCGQLLENACDDVLRQV  
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VQ

>AsutOR10

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VLGFVMETMKASDFTGDSFQRMDESAKAKSYKQLIKCIKDHQKINHAGDLLAERYNTFL  
TFHLGTAIVGIIAIFNCTFATELADKIKFAIMCVYGLLEVAIYCLCGQLLENASEGVLQVY  
SCEWEEMDPKFRRAAQLMMVRANKPICLRAGRLYRVNLETLGAIQQLVYSSLMLSSMV  
Q

>AsutOR46

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YIISAYYGFVYNDMELVSYNICYGLTIIFLVGHGSV ру KRNHLDRLFETVGKGFFTYEKPL  
DADEQAIVDECДМКCKTAKRNILLTMVLTWTCVVPLPKALKGEYSSVAGGPINK

HLPLPVWSPYPIDTPLTYWSMYALEFTAGITEAFIIATTCTLFCNLCTIVSRELKLLRLALRR  
TRS RANYTFKMRGYSYLAGSNYAKYKLFQQCMVHCIEECIKHHIALKKFQEEFQGFMGF  
PIFAIFSGTALTISPMFMLLTMEAEDSFLVLMKILQYSSIIFSFTCFLSSYCLFGQMITLESS  
LVHFAFYETPWIDGDLDFFRKVIMGMIHSRKPFILTAKGLAAASSETLVDISKTIFSCFNLLA  
ATQ

>AsutORCO

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FLVCFILETNSDEMAAVTITLFFLHSVTKFTYFAIRSKYFYRTLSAWNQVNShPLFAES  
NARHRAAALSRMRKLLMIIGVVTILAVFGWTTVTFLDDPVWDKTDPDNVNETISVEIPQL  
MVYAWYPWDAKTGMYFMTFALQLYWLFITLAHSNLLDVLFCFVIFSCEQLKHLKEILQ  
PLMELSAALDSVPNGDLFKSGSAGSNIALISNGDGGNDFDVRGIYSSQRDFSGFQRGM  
TNGTTVGPNGLTKRQELLVRSAIKYWVERHRHVVKFVASIGDTYGTALLYMLTSTVTLT  
LLAYQATKIEGVDVYASTTIGLVYTLGQVFVFCIHGNELIEESSSVMEAAYSCHWYDGSE  
EAKTFVQIVCQQCQKSLTVSGAKFTVSDLFASVFGAVVTFMVVLVQLK

>MsanOR2

MTKTPRVAAVFTAPESSEDLTIVDNKLFKAICLHQLLDPTNGSNRYYGLVLMFMSVSLG  
MQIQLVGLYFAVNDLQRFAFATTVSNSLLELFKGYVLVANADRLRASLEVARYEFTTCGS  
WDQRLVRQSRAVLSTVLRTFTVLSWFTCFIHALAPLFAMDEYLQVTNAQFTVSTSC  
NVWLPVPTTVYNTTIVWTLVYAFEVIACFVNFIWLLFDSYVVTMCFTNAQFTVSTSC  
MNIGHRDHCFRSPSPHASEGASDDNDILNCYDELINHIKDQNQLSIKKCDDFEIIPAIIFQII  
GGSYSVITLIFLTSLYLMGFSIISGPVLRSSFGFLSLTFELFLYCYVFNHIETEKCKMNFGLY  
SCNWTAMDLKFKKTLLHAMNMNTAHRVMKVTPMSIINLEMFANVMNMSYSIVSVLLN  
SRPQK\*

>MsanOR43b-1

VDATSAFSKLETEKLSH SVCQWKRVIAHMVYNFFQKTGRSDVRRYATTCVEFFSYFELVVI  
LIFVIFAFLSVVYSNEDLYNRIYSFSWLCFEANVFAVILIRLYYQSKFRDMDYDRSQLIGGTLG  
NYRRTLVLVYYYFVTSTALVIVPLLYVISFDSEAEMGDPFSFPVADALPKKTGNVTYVCK  
YIVYSFILYAAHLENGFVN GTFIYFTGVVKKYFQILDVEVQEAMVN KDEQKLKIAIKRHQE  
LLKLFIDMKTVYDKSILIIIEFCGLFNGFNGYIMIQCIQGVIPH KILGFSIACILASLLTMSIYCI  
CGSNIYLYHDGLLKS LFEHNSCYSKNNSFKKLVIMMMTRATVPLEIKAGSIFAINLNLLVKI  
LKFTYTVFNL NLLTSVNRQIKENSAI\*

>MsanOR43b-2

MADIVDTFFQYTGWSDDH SFVATYSAILTYSIDLAVFLFLIFTFWSIVYWTEDLSIRIYCFL  
WLFIVVHMFVSIYSRLYYQSI FRDMYRHS LIVGLPENYRRKILIVI YYFIVSNVYVYIPMVY  
TIAFDSVQMGDPFTYPFMDVFAVKKPTITVYLCQYIIYAIPVYLTLEGCLLNTFMHSTGV  
MKRLFQTLDKQVEEAMIIRDEQKLKIAIKQHQUELLKFRKMETVYEKQILLSIEFCGIYIGL  
TCFIMIQVIQGVIHPLLGLCIGSIFEGLASITVYCIFGSIMHDLHDGTLNSLFNQQSCYFRD  
KSFKQLVVIMMARVSIPLEFKAGSIFTINLNLFVKILKFTYSVFNL NLLTSVN\*

>MsanOR46a-1

MMDIRDDQNNLFNITLAKYMGIYQMLDPQTTRFRGLNVYHIVMIFIILFLCVFAVIINISVV  
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CKERSV FITTAITFLYFTSFV IYIVSSLTLLNDIIPVKNRDGSISNYQHNIINLYLLVSGDTYNA  
HYNIFYM LEVLILVFVIIPYCIFDFVTVLCLAIRCQWQMCTAFESIGHTSLGDNLSLVDCG

EEKKKLPNKHDLIYDELKTIIMNHQAVKKYDKFLTIFQQALLQIVVCLTFIILWICFILV  
KINMMFNQKKFFSA\*

>MsanOR46a-2

YMGIDFLWKSENTLYVIYKAYFIVRYSKDIWKCLSITRYDFTSFKYQNRHILDYWRKRLTR  
LTTIYAIMHLTTVSSFLISLAFTKYKLPVKNHDSIGYYRHNVNMNLYIIVSDETYNAHYY  
MFYIIETLFVSLVTSIFFTCLLLITLCFSICCQMVCISAFESVGHKSLRDLDSPIGDDYTAE  
NIKIPSNEHDLNYNELKTIINDHQAVMEKYEMFLTLFRRVILLHIFVSSLALITLLTIIMSFS  
NDDRYKTSEVVIGKLLCCIPSIFFDIFVVSYLFGNIHNDHNSMVFALYGSNWTEMDMKCK  
KLVLLTMKLNNA

>MsanOR64

MDIWKNKKHLFNIKLSKIITLYQILDPETVKYHGRNIYHIVIACTMLCTSIVLMIGVLSGLN  
YFKSNIPLSMNFFFISFGAYTIYKIWFTIHHSNDIWDYLSITQYDFTSIGNRHRHILDRWRE  
RLTWLTNIYAILVLMLTVYFIAMTSAFSEDKSLIKNHDSIGYYRQNVLNLYLIVSDETYNT  
HYYTIFYIVEASVFVYLSIYFCLFDILLITLCYSMCCQMIVCSAFELVGHRSLRDHSPIDQ  
SVGNISTNEHDLIHEELKTIIMDHQLVMKKYEDFVSLFRRMILLHIFVSSLVIVLIFTITMSF  
SSDERFKTSTNAVHKLFVFIPPTLFQIFMVCYLYGSMHNQKDAAIFALYSSNWTEMDMKCK  
KLILLTMKNNANQKK

>MsanORCO

MGYKKDGLIKDLWPNIIRLIQLSGLFISEYYDDYSGLAVLFRKIYSWITIIIYSQFIFIVMF  
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AKSLSRMRQLIIVSIVTIFTTISWTITFFGESVWKVPNPETYNTQMYVPVPRMLHSWYP  
WDSSHGLGYIVAFVLQFYWIFITLHSNLLELLFSSFLVHACEQLQHLKEILNPLIELSATLD  
SSVHNPAEIFRANSAKNQSINGIDRDYNGSYVNEITEYGTKGENESNRKGPNSLTSNQEVL  
VRSAIKYWVERHKHVVKYVSLITECYGSALLFHLVSTVILAYQATKINGVNVAFASTI  
GYLMYSFAQIFMFCIHGNELIEESSSVMEEAAYGCHWYDGSEEAKTFVQIVCQQCQKPLIVS  
GAKFFNVSDLFASVVLGAVVTVFMVLVQLK\*

>MsanOR4

SYQAVVKINKMTSIIGKKNYQRKFYQTLMTLAFFLDTSQYRFISRFIMQFYIFDWMLVSL  
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PNAAYKENIKTFKSLISIPLAISLSIAFGPLVSTFNDIGKLPLDNRAHFVLFWPKIVDTNKPS  
MYGIYTLQVIFTISLYISVSLNLGFMVFLNELTQFEMLLDGINDAFKFKMDKQFPSLFID  
CIRHHQIIKFLDDLKSYFKWMILIEIIVLQVILSILYNLTKVNASIGYKMKVGGSLFNILPI  
CFHCHIGEVVLSLHKRLSNHIYNMTWYDMPNKNKQLIVIMFQRTQRDLTLSSALFSSEKA  
SRALISKVIKVY蒂LVLLKT\*

**File S4.** The amino acid sequences of 39 ionotropic receptors (IRs) from 9 Hemiptera species.

>SflaIR25a.X1

MLTMYTLIRTTILWITNLLDVGWSQNLQTINILFISDRNNLVAEETLNVALNYIRRNPRL  
MLDGIVSVKIGGDDASEILETLCVNYNASIRNNKPPHLVIDTTINGVTSEAVKSFTAALALP  
TVSASYGQSGDIRQWRNLDGEQQKYLIQISPPADIPIEIIRSIVVAQNITNAGIMFDDTFVMD  
HKYKSLLQNIPTRHIIASIDDTTSIKLHLSRFRDV DIVNFFVLGKLSIJKSVDHANSNLFG  
RKYAWHVTQDKGSLKCGCSNATILYVKPEPDAGSREKLSNLKTYGLTSTPELKAAYFD  
FYYRSLLAIRSMMNSVEWPTNMTYTTCD EYNEENPLPRRNIDLRRYLKDMTEPPSYAPFLI  
DTNGHSYEEFTMRLEKVTVLNSQS VSAENVGSWKASLNSPIVKDAANMSHFSAVTVYR  
VVTVLQNP FM IQV DDE DGKGVVKFKGYCIDLIEEIRKLIGFEYEIYIAPDNNFGNMDENGQ  
WNGMVKEV KRADIALGSL SVMAEREN VVDFTV PYYDLVGITILM KKPKTPTSLFKFLT  
VLENDVWM CILGAY FFTSFLMWV FDRWSP SYQNNRN KYKD DEEKREFNLKECLWFCM  
TSLTPQGGGEAPKNLSGRLVAATWWLFGIII ASYTANLA AFTVSRL DTPVESLDDLSKQY  
KIQYAPLNGSATMTYFQRMADIETRFYEIWKDMSLNDLSEVERAKLAVWDYPVSDKYT  
KM WQAMKEAKLPNTLEEAIERVKSSKSSSEG FAYLGDATDIRYQVMIDCDLQMV GDEFS  
RKPYAIAVQQGSP LKDQFNNA ILLLNKRKLEKLKETWWNMNPERIQCEKQDNQSDG ISI  
HNIGGVFIVIFVGIGLACFTLAF EYWYKYKKSSKVANTMNPQM VIGRGEFTYPIIPNYE  
TSGMRSRNIIQGLRRSISQSTPKQQ

>SflaIR25a.X2

MFDDTFVMDHKYKSLLQNIPTRHIIASIDDTTSIKLHLSRFRDV DIVNFFVLGKLSIJKSVD  
HANSNLFGRK YAWHVTQDKGSLKCGCSNATILYVKPEPDAGSREKLSNLKTYGLTST  
PELKAAFYFD FYYRSLLAIRSMMNSVEWPTNMTYTTCD EYNEENPLPRRNIDLRRYLKD  
MTEPPSYAPFLIDTNGHSYEEFTMRLEKVTVLNSQS VSAENVGSWKASLNSPIVKDAAN  
MSHFSAVTVYRVVTVLQNP FM IQV DDE DGKGVVKFKGYCIDLIEEIRKLIGFEYEIYIAPD  
NNFGNMDENGQWNGMVKEV KRADIALGSL SVMAEREN VVDFTV PYYDLVGITILM K  
KPQTPTSLFKFLT VLENDVWM CILGAY FFTSFLMWV FDRWSP SYQNNRN KYKD DEEK  
EFNLKECLWFCM TSLTPQGGGEAPKNLSGRLVAATWWLFGIII ASYTANLA AFTVSRL D  
TPVESLDDLSKQY KI QYAPLNGSATMTYFQRMADIETRFYEIWKDMSLNDLSEVERAKL  
AVWDYPVSDKYTKM WQAMKEAKLPNTLEEAIERVKSSKSSSEG FAYLGDATDIRYQVM  
DCDLQMV GDEF SRK PYAIAVQQGSP LKDQFNNA ILLLNKRKLEKLKETWWNMNPERIQ  
CEKQDNQSDG ISI HNIGGVFIVIFVGIGLACFTLAF EYWYKYKKSSKVANTMNPQM VI  
GRGEFTYPIIPNYETSGMRSRNIIQGLRRSISQSTPKQQ

>SflaIR2.X1

MSADAMLTNGGGPCWLLVTVVWSLHVLDSSAAVAALPPVIRIGAIFTQEDKDSTTEVAF  
KYAVYRINKD KAILPNTTLVYDIEYVSQQDSFKASKKVCRLLESGVHAIFGPSDSHLAGHI  
VSICESVSMPLLTIADGVTDLTGRHFVTDMFPAREHLGQA FRDLINFLNWTKIAIVYDDE  
EGLLL VQNL MKMSKADFYIRQVDQHTHRQVMREIKNHIFNIIVDIHP RNINGFFRSILQL  
QMNDYRYHFLFTFD LETFD LEDF KYN SVN MTSYRIV DDE NHRV NVL REMERF QRVGQ  
NMLHKSGIIRAEPALMYDA NVFANSIGSFEGSSDSMKSANISCKSSNRWANGTLLYNRLN  
AVVIEGLTGRVHFDEGRRS DIKLDL LKLHQEKVKVGF WTPSTGINITRHSV FYGQQSSNV  
TLIVVTRVEKPYVMIKEDKNLTGNSKYEGFCIDLLHRIASQVGFHYAITLVPDNKYGAYDP  
TTKQWNGIVRELMDKKADLAMASMTINYARES VVDFTKPFMNM GIGILFKVPSNEPSKL  
FAFLNPLATSVWSFMLLAYMAVSFSLFFLARFSPYEW RPHT EENYREN RFTISNCFWFIAG  
VSLKQDAGITPKATSARILGGIWWFFT III PSYTA NLRTVERLQKPIQNVAELSSQE KISF

GTLEGGSTMSFRDSKIPYQKMWKFMEKYPVFVSTYEETKKVLGGNYAFLMESTMID  
YAVQRDCNLTQISGLLDSKGYGIATPKGSVWRDKLSAVLELQEKGVIQMLYDKWWKNA  
ADICIKDEKVKEFKPKPLDLNDLGGVFVFLCGLTVAVIIALEFCWHSKKSTDQQQSVC  
TEMAEELRYAIRCDGKHKATLKRTCNGCSPITTYVPAPMHMNHVTSQIDNVPMMELTkp  
SISIDHEDK

>SflaIR2.X2

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SMPLLLTIADGVTDLTGRHFVTDMPAREHLGQAFRDLINFLNWTKIAIVYDDEEGLLVQ  
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HFLFTTFDLETFDLEDFKYNSVNMTSYRIVDDENHRVVNLREMERFQRVGQNMLHKSG  
IIRAEPALMYDAVNPFANSIGSFEGSSDSMKSANISCKSSNRWANGTLLYNRLNAVIEGLT  
GRVHFDEGRRSDIKLDLLKLHQEKVKVGFWTPSTGINTRHSVFYGQQSSNVTLIVVTRV  
EKPYVMIKEDKNLTGNSKYEGFCIDLLHRIASQVGFHYAITLVPDNKYGAYDPTTKQWNG  
IVRELMDDKKADLAMASMTINYARESVVDFTKPFMNMIGILFKVPSNEPSKLFALNPLAT  
SVWSFMLLAYMAVSFSLFFLARFSPYEWRFHTEEYRENRTISNCFWIFIAGVSLKQDAGI  
TPKATSARILGGIWWFFTIIIIPSYTANLTALRTVERLQKPIQNVAELSSQEKISFGTLEGGST  
MSFFRDSKIPYQKMWKFMEKYPVFVSTYEETKKVLGGNYAFLMESTMIDYAVQRDC  
NLTQISGLLDSKGYGIATPKGSVWRDKLSAVLELQEKGVIQMLYDKWWKNAADICIKDE  
KVKEFKPKPLDLNDLGGVFVFLCGLTVAVIIALEFCWHSKKSTDQQQSVCTEMAEELR  
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>SflaIR2.X3

MYTSHRWSNLIRRNSITCAIFTQEDKDSTTEVAFKYAVYRINKDKAILPNTTLVYDIEYVSQ  
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DMFPAREHLGQAFRDLINFLNWTKIAIVYDDEEGLLVQNLMKMSKADFYIRQVDQH  
RQVMREIKNKHIFNIIVDIHPRNINGFFRSILQLQMNDYRYHFLFTFDLETFDLEDFKYNS  
VNMTSYRIVDDENHRVVNLREMERFQRVGQNMLHKSGIIRAEPALMYDAVNPFANSIG  
SFEGSSDSMKSANISCKSSNRWANGTLLYNRLNAVIEGLTGRVHFDEGRRSDIKLDLLKL  
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EGFCIDLLHRIASQVGFHYAITLVPDNKYGAYDPTTKQWNGIVRELMDKKADLAMASMTI  
NYARESVVDFTKPFMNMIGILFKVPSNEPSKLFALNPLATSVWSFMLLAYMAVSFSLFF  
LARFSPYEWRFHTEEYRENRTISNCFWIFIAGVSLKQDAGITPKATSARILGGIWWFFTIII  
IPSYTANLTALRTVERLQKPIQNVAELSSQEKISFGTLEGGSTMSFFRDSKIPYQKMWKF  
EKYPVFVSTYEETKKVLGGNYAFLMESTMIDYAVQRDCNLTQISGLLDSKGYGIATPKG  
SVWRDKLSAVLELQEKGVIQMLYDKWWKNAADICIKDEKVKEFKPKPLDLNDLGGVF  
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GCSPITTYVPAPMHMNHVTSQIDNVPMMELTkpSISIDHEDK

>SflaIR2.X4

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AREHLGQAFRDLINFLNWTKIAIVYDDEEGLLVQNLMKMSKADFYIRQVDQH  
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YRIVDDENHRVVNLREMERFQRVGQNMLHKSGIIRAEPALMYDAVNPFANSIGSFEGSS  
DSMKSANISCKSSNRWANGTLLYNRLNAVIEGLTGRVHFDEGRRSDIKLDLLKLHQEKV

KKVGFWTPSTGINTRHSVFYQQSSNVTLIVVTRVEKPYVMIKEDKNLTGNSKYEGFCID  
LLHRIASQVGFHYAITLVPDNKYGAYDPTTKQWNGIVRELMDDKKADLAMASMTINYARE  
SVVDFTKPFMNMIGILFKVPSNEPSKLFAFLNPLATSVWSFMLLAYMAVSFSLFFLARFSP  
YEWRPHTEE NYREN RFTISNCFWIFIAGVSLKQDAGITPKATSARILGGIWWFFTIIIPSYTA  
NLTALRTVERLQKPIQNVAELSSQE KISFGTLEGGSTMSFRDSKIPIYQKMWKFM EK YPSV  
FVSTYEEGT KKVLGGNYAFLMESTMIDYAVQRDCNL TQISGLLDSKG YGIATPKGSVWRD  
KLSLAVLELQEKGVIQMLYDKWWKNAADICIKDEKVKEFPKPLDLNDLGGVFVFLCG  
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YVPAPMHMNHVTQS IDNVPMMELTKPSISIDHEDK

>MperIR25a

MFMTRIHIFLLWLTVYTNGEAYKIGILTQSEDDTNFQLKSIMTNVN SIEPILNDPSYNITN  
KFC SIASNNTLATIDLLIPSCIPCWKISNANSMAYFRTDFSYIQPTIQLIESFVTWLNITKEITFI  
FTNQEYANQAVTYLTSGKSSLRAIVLSHTSNEIDQLKNTKIGRHALIGNNLDQYVQIIN  
QEKLKLDESWIITNDTTKLKLESSVTLMKFTSWENGYTNKMRARTLFNFIIYYFLGSVS  
RDRSKLSCDLISDV L VLEKRKEIEDKLNSYENKSELQYDIDTNRMTYNEQAMIFRVSQDG  
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KEMNFKYELVVVKDKFGSLDPETNQWNGLIGGLVEGELDIVAALTMTSEREEVIDFIAPYF  
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VERMQTPVQSLQLARQSRINYSVIDGSDAHFFRN MKMAEDILY NWK EIALNQTNNR  
KDFRVWDYPIKEEYGQILAIAIEKTGTVPNRSVG YQMVL DNEQGEFALIHDSSDIEYEVYN  
NCNLTEVGEIFAERPY SIAVQQGSLIQEEISR KILD LQDRFFELLNAKYWNASKVSMCPNA  
DDSEGITLESLGGVFIATLVGLLIALITLAFEVVYFKHKRAKVAEVSVNNTIHKDKLMYG  
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>MperIR2-like

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>MperIR1.X1

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>MperIR1.X2

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>MperIR40a.X2

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>MperIR40a.X1

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>ApisIR1

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>ApisIR3

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>ApisIR2

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>ApisGluRDelta-1-like

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>MperGluRkainate-4-like

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>RmaiIR2-like

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>RmaiIR1.X1

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>RmaiIR1.X2

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RQ

>RmaiIR40a-like.X1

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EGGILSKITEEEYQKLNDKLMGSEKFDAASVVI EPVLEGSEPQQEDDDKQLTIAMSMKTL  
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>MsacIR40a.X1

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AMRVCVITS PRPGFYQIYYSQASARPGYGSTLKMVNWWSAMDGLVRFPPLPPPQVYKN  
FEGRYFNVPVLHKPPWTFVEYLNDSFRVEGGRDDKLINLLADKLHFQFRYIDPPDRTQGS  
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KLMGSEKF DATPVVI EPVLEGSEPQEDDDKQLTIAMSMKTLQGAFYVLAIGSILAGFLLI  
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>AlinIR1

MIREWMNMFTA AFLLACA HVASALPEVIKIGAVFEEGDEWSRYA FEA AIIKI INEDESTLP  
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ARWDGQQRSSCLVNLYPHPSVLAQVAADMVRTWDWGFTVLYDDFNALRKIGELVKV  
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GAPEEAPAEEEEEYEIPPIE ALLIYDAVN LVAEALHNLDIVEPREIDCRQNNAWESGYSVINF  
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>AlinIR8a

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VMFLKAVERNLRVYDDRWILVFLDNEHNSFDRKTLVKRVTLATPTIDANAANFAENVAE  
TLEEVAKTSGIDLSPVPAQCCEGSSTAACKDLTVFQEKLSEIVEKKPWLDWRQESTMALHL  
DMDWTAESSKGKEKLFIGSWNSKKGLTIAGNVTKIPRFFRVATGYMVPFAYPVIDPSTGAPK  
LDDKGNEVWEGYCIDLINRLAEDMDFDYELTSYNFGRKLPNGSWDGLIGDLASGRVDII  
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ESLSGKYWNSTMKGKCDSSDEDEGITLESLGGVFIATLFGVLAMLGLGIEIVYERKAKKN  
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RDQLY

>AlinIR21a

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FNDTEDPVASKLYESVERVPNLYSGLRNVTRNVHSWRQSAFLGSRRLEYTVKTNFTPDE  
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SGKLLTMHKGLKGAPEADRELNLDDTQGMFLLGAGFGIGLLVIIIEISVWSSEQRKNRQFG  
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>AlinIR25a

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VKTFSRALGIPTLSASYGQEGDLRQWRALEVEIAKYLLQINPPADIPEVVRVSIVLQNISSA  
GIVFDDSFVMDHKYKSLLNVPARHIMGRVRNIQEIRNQLTRFKELDIVNFFILGSLSTIRN  
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VEEPEITSVFYFDFFLRGLLAAKALIEKAPWPKDYNKTSCNYDENHDFIRKDLDLSSLR  
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MRNFSAVTVYRVVTVKQKPFVIETFENGPKYSGYCIDLLEDIRSFVHFYEIYVAPDNAY  
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>AlinIR75d

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FGASGVIMREDRRKHVDYTVDFEFKTGIFKQPSLSSVSNIYLLPFSRHVWAACGGLLF  
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>AlinIR76b

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FILITAFYTANLTAFLTLSISTLPIKEIDDVAKDNRHWFALQGGPIEHAIKDKEDEKLRLRD  
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LTEKPFLVRSLAFAYGKDSDLPLDFNPLIERFIESGILQHKLNLDPDAVICPKDLGNKERKL  
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>AlucIR21a

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VFTKETEIGAESIREYTSRNTMTLLIAPTSVYMVRQFLGTLAGDITNLLIVDPMIRVKLL  
SQKVGQVFKECDILIYSHEFASDLSGSTTPIVTAWRRTQFTRQVQLFPSKFQGLGGIHLT  
VAASEIAPFVFRKRGQESGAGYTIKWGDIEIRLLNIVSQMLNFTVEYKEPELIEEEDVAQA  
VIKEVLAKKANLAVGGVYLTPERINGLLFSIPHTRDCASYISLSSRALPKYRAIMGPFLWDV  
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FGDLTLKQRAFNKLKEHGEALYNCLLAPAKSGIYFRERRVSSAFGEYVTRPYTPWPRSSIP  
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>AlucIR25a

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ALGIPTLSASYGQEGDLRQWRALLEGEIAKYLLQINPPADIPEIVRSIVKLQNISSAGIVFDES  
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RKPYAIAVQQGSPLKDQFNAILQLLNKRKLEKLKEKWWTENDRKECDKQEEQSDG ISI  
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>AlucIR41a.1

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VDKPGRNPKIFLDQWSSYASFRHDANLMIDFIQNLQNKTLCIMTFDYDPYTHFEPLDGTEI  
KLIQEFCKKHNCNSLVAVDDGHYWGDFENGTSGLAGMVDGRADFGAAAVYLWLPYF  
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KYTRFAEAVQKRRMFLDKLDCIFRALGLAVLQPSTPLVPHIRHLFTSFEFLFLIASIYA  
AELASYLTVPRYEKPIDTLIEYSDSGMIWIGEHESWTYSLRGMTDPEIVNIVNNYLICSHEK  
LMKLAAPTGEYGLIVERLPGGHYTEQDHVTDDIVAQSHMMAENLFGSPPVIAVRKGSPYRK  
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>MsanIR25a

GDTMFVTRIHIFVLWLTVYTNGEIYKIGVLTQSEDDKNFVQLKSIMTNYNISIEPILNDPSY  
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KEITFVFTNQEDADQAVTYLTSGKSSLRAIVLSHTSNEIDRLKNTKIGIRHVALIGNNLDQ  
YVQKINQEKLKLIKLDGESWIVTNDTTLKFISTVTLMKFTSWENGYTNKTRAKTLNFIFY  
FLDHASRDHPKLNCDSIDVLMLEKRKEIEKLLNSYENKNEFQYDIDTNLMRYNEQAMIF  
KVIPDSVPNHLGTWTINGGLEMKYDASTVVSRRFFRIGTAKSIPWTFMEDVWKGYCIDL  
IEKLSKEMNFKYELVVKDKFGSLDPVTNQWNGLIGGLVEGELDIVIAALTMTSEREEVIDFI  
APYFEQTGISIVRKPSRKTSLFKMTVLKPEVWLSIVAALAMTAVMIWILDKYSPYSAQN  
NKTKEYQFRHTLVESFWFALTSFTPQGGGETPKAISGRVLVAAYWVFVVMLATFTANLA  
AFLTVERMQTPVQSQLQQLARQSRINYSVIDGSDAHNFFRNMKMAEDILYNVWKEIALNQT  
NNRKDFRVWDYPIKEEYGQILAAIERTGTVPNRSVGYQMVLNEQGEFAIHDSSDIEYE  
VYNNCNLTEVGEIFAERPSIAVQQGSLIQEEISRKILDLQKDRFFELLNAKYWNASKVSM

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>MsanIR40a

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ADFLSNTIKSLHGRGVTTTHALLSEDHVQSLLIDIRRAVADGHHTSYIVLSTSTLMENLLS  
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GSSLKMVNWWSAMDGLVRFPPLPPPQVYKNFEGRYFNVPVLHKPPWTFVEYLNDNSFR  
VEGGRDDKLINLLADKLHFQFRYIDPPDRTQGSGLDGSSMQGVGLIWIQREADWFVGD  
LSITYERNLVVDFSFLTLDNEAFLTHAPGRLNEAFSLIRPFHWSVWPLLITVIFVGPILYIL  
VDTTDGHPQGKSMLYWKCVWWSVTVFLQQAAIPSENNKIRFVAGLFMLSVTYVIGDMY  
SASLTSILARPPKEPPINTLKESEAMRDGLQLLVEVQSASQAMLENTGVYEELSQLVT  
RQREYLIGSTEKGMLVRDNKNYAVIGGRETFYYDIKRGFAQHFHLSEKLNTRYSAIAFQR  
ACPYRDNFDDVLMRLFEGGILSKITEEEYQKLNDKLMGSEKF DSTSVVIEPVLEGSEPRQE  
DDEKQLTIAMSMKTLQGAFYVLAIGSILSGFLLIEMRSHDKFEKNKRTKRVEAPFVHIRK  
VPNKFQNRLYDLKE\*

>MsanIRDelta1a

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AQISQYGYKYYFEETEDSELRKLYMTKMVPNGNSFKVAAEGIERIRTEFGFQVEVMSAY  
KIISKQWREEEKCGLGEIQLFKIPLLSIALVKKSGHKDIFKQKLQQMEVGLNKRIASQWIPP  
KPSCGSSSRAKQYISVSVKETYLTLAIFGFVCISLLFILEVLQHAWMNRGSKKN\*

>MsanIRDelta1b

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FAQMHYDLNLILQDQLNFKIDL GIVNSSGWD MGNA SFSQLTSQLQREECDFSGIGAFIRND  
RMTVIDYTVGTFYRQAAALFKQPLSSVHNICILPFNF EVWMVTLFTFIGFTILIAFLSRMT  
RRFKENE EALNVLD SVTIVHGAICQQGYTMNLNAGSIRVAIFVLFLTAVFLFTSYSASIVAL  
LQSPSNSIKTINDLVESSMTFSAQDNPYNDVYFGETDDPLLRKLYDKMKPYGSQKFTLAS  
TGIARIRTEFHAFMIDFVSAYKLISQLWREEEKCGISEIQLFKLPM LALAVVKRSGYKDILK  
QKLIHQQEVLKNRIIRR WIPAKPICDSSN RANQF VS VSIKEIYPM LQIYGF GLCISI LIL FFEI  
AYNTYTCRSEN LHSNTYFSILRF MYNKR\*

**File S5.** The amino acid sequences of 19 sensory neuron membrane proteins (SNMPs) from 10 Hemiptera species.

>MperSNMP1.1

MGAPTTLVIGIIFLLFGVFVGWFAFPKMIHKKILES KALNPRSNMRQMWSHPPYADFKIY  
LFNVTNPEEAQKGEKVIKEVGPVYQEWEKEENLIDDIDADTVEFSKNTFVLDEMSTLP  
LTGDEIIVMPLAMIGMVTMTKIMKPAALGLVNKAIPYLYPDQTSAFMMGTANDIMWNG  
LDINCTSGEFAAVAICTQIRQNSASLHKISKDHFKFSLFGVKNGTIESNR YTVKRGYTTPATE  
VGQVIRFNDKHQEVWPGEECNKIYGTDTTIFQPFIKDTNLASFSGDVCRLAPDYVQET  
KYNGLNVFEYSAILVKPEEKCFCLNQKKCLPGALDLTNC SAPIIATLPHFYKSEEYLNN  
VDGLHPDAEKHRIQMYFEPMTGSPLLGYKRLQFNIFLKESKISVMKTLNEDEKLIPFW  
VEEGIALNKTWTNQIKNKLFLPITIMKYVKYIFVAFGIVFIILAVIVNYNSVKTMEVTPKY

>MperSNMP1.X2

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VEFSKNTFVLDEMSTLP LTGDEIIVMPLAMIGMVTMTKIMKPAALGLVNKAIPYLYPDQ  
TSAFMMGTANDIMWNGLDINCTSGEFAAVAICTQIRQNSASLHKISKDHFKFSLFGVKNGT  
IESNR YTVKRGYTTPATEVGQVIRFNDKHQEVWPGEECNKIYGTDTTIFQPFIKDTNL  
ASFSGDVCRLAPDYVQETKYNGLNVFEYSAILVKPEEKCFCLNQKKCLPGALDLTNC S  
APIIATLPHFYKSEEYLNNVDGLHPDAEKHRIQMYFEPMTGSPLLGYKRLQFNIFLKESKI  
SVMKTLNEDEKLIPFWVEEGIALNKTWTNQIKNKLFLPITIMKYVKYIFVAFGIVFIILAVI  
VNYNSVKTMEVTPKY

>SflaSNMP1-like.X1

MGAPTTLVGIVFLSMGVFIGWFAFPRMIHNKILESKAINPRSPMRQMWEHPPITADFKIF  
LFNVTNPEEAQKGEKVLKEVGPYFYHEWKFKEDLEDDSKSDTVEFSKNTFIFDEMMLT  
PLTGEIIITMPHLAMLG MVTMTKMTKPAAI GLINKAIPLLYPDQTNAFMTATANDIMWNG  
LDINCTSSEFP AVAVCTQIRQNSASLHKINNNHFKFSLLGVKNGTVESNR YVVNRGLKMPM  
DVGVIRFNGKHKMDVWPGEDECNR IYGTDTTIFQPFIKDTNLASFSGDLCRSLN TDYVQ  
ETQYNGLKVFEYTAMLVKPEEKCFCLNKKCLKGALDLTNC SGSPIIATLPHFYKSEEYL  
KDVG DLSPKDENHRIKMYFEPMTGTPLLGYRRMQNFNMFLKKEPKITVMKTLNEEEKLVP  
LFWVEEGIALNKTWT SQIKNKL YLPITIVKYAKFVLVALGIVFIILAVV LNYNSVKTMEVTP  
NI

>SflaSNMP1-like.X2

MNVPCSVVVNPVVLSKAINPRSPMRQMWEHPPITADFKIFLFNVTNPEEAQKGEKVI  
LKEVGPYFYHEWKFKEDLEDDSKSDTVEFSKNTFIFDEMMLT PLTGEIIITMPHLAMLG  
MVTMTKMTKPAAI GLINKAIPLLYPDQTNAFMTATANDIMWNGLDINCTSSEFP AVAVCTQ  
IRQNSASLHKINNNHFKFSLLGVKNGTVESNR YVVNRGLKMPMDVGQVIRFNGKHKMD  
VWPGEDECNR IYGTDTTIFQPFIKDTNLASFSGDLCRSLN TDYVQETQYNGLKVFEYTAML  
VKPEEKCFCLNKKCLKGALDLTNC SGSPIIATLPHFYKSEEYLKDVG DLSPKDENHRIK  
MYFEPMTGTPLLGYRRMQNFNMFLKKEPKITVMKTLNEEEKLVP FWVEEGIALNKTWT  
QIKNKL YLPITIVKYAKFVLVALGIVFIILAVV LNYNSVKTMEVTPNI

>SflaSNMP1-like.X3

MRQMWEHPPITADFKIFLFNVTNPEEAQKGEKVLKEVGPYFYHEWKFKEDLEDDSKSDT  
VEFSKNTFIFDEMMLT PLTGEIIITMPHLAMLG MVTMTKMTKPAAI GLINKAIPLLYPDQT  
NAFMTATANDIMWNGLDINCTSSEFP AVAVCTQIRQNSASLHKINNNHFKFSLLGVKNGT  
VESNR YVVNRGLKMPMDVGQVIRFNGKHKMDVWPGEDECNR IYGTDTTIFQPFIKDTNL

SFSGDLCRSLNTDYVQETQYNGLKVFEYTAMLVKPEEKCFCLNKKCLKHGALDLTNCS  
GSPIIATLPHFYKSEYLKDVGGLSPKDENHRIKMYFEPMTGTPLLGYRRMQFNMFHKKE  
PKITVMKTLNEEKLVPLFWVEEGIALNKTWTSQIKNKLYLPITIVKYAKFVLVALGIVFIIL  
AVVLNYNSVKTMEVTPNI

>ApisSNMP1

MGAPTTLVIGIIFLLFGVFGWFAFPKMLNNKILESKSLNPRSNMRQMWSHPLSADFKI  
YLFNVTNPIEAQKGEKVIKEIGPYVYHEWKEKENLIDDIDADTVEFSKNTFVDEMSTLP  
LTGDEIIVMPHLAMIGMVTMTKMMKPAALGLVNKAIPYLYPDQTSAFMGTANDIMWN  
GLDINCTSEEFASVAICSQIRQNSESLSHKISKDHFKFSLFGVKNGTIESNRRTVKRGYTSPAT  
EVGQVIRFNDKHKMDVWPGEDECNKIYGTDTTIFQPFTKDTNLASFSDICRSLTPDYVQE  
TKYGLNVFEYSAMLVKPEEKCYCLNKKCLKPGALDLNCSCGAPIATLPHFYKSEDYL  
NNVDGLSPQVEKHKIQMYFEPMTGTPLLGYKRLQFNIFLKRESKINVMKTLNEDEKLIPF  
WVEEGIALNKTWTNQIKNKLYLPITIMKYVKYIFVVFGIVFIILAVVVNVNSVKTMEITPKY

>DnoxSNMP1

MGAPTTLSVIGIIFLLFGVFGWFAFPKMIHKKILESKSINPRSAMRQMWSHPIYADFKIY  
LFNVTNPEEAQKGEKIIKEVGPYVYHEWKEKENLIDDMADTVEFSKNTFIFDEMSTLP  
LTGDEIIVMPHLAMIGMVTMTKMMKPAALGLVNKAIPFLYPDQTSVFMMGTANDIMWNG  
LDINCTSREFAAVAICTQIRQNSASLHKISNEHFKFSLFGVKNGTIESNRRTVKRAYTSPATE  
VGQVIRFNDKHKMDVWPGEDECNKIYGTDTTIFQPFTKDTNLASFSDICRSLVPDYVRET  
KYGLNVFEYSAILVKPEEKCFCLNQKKCLKPGALDLNCSCGAPIATLPHFYKSEDYLNN  
VDGLSPNVEKHKIQMYFEPMTGSPLLGYKRLQFNMFLLKESKINVMKTLNEDEKLIPFW  
WVEEGIALNKTWTNQIKNKLYLPITIICKYVKYIFVIFGIVFIILAVVNVNSVKTMEVTPKY

>AcrasSNMP1

MGSKSLNPRSTMQRQMWSHPPISADFKIYLFNVTNPEEAQKGEKVLKEVGPyVYHEWKE  
KENLIDDINEDTVEFSKNTFVDEMSTLPLTGDEILVMPHLAMIGMVTMTKMIKPAAGL  
VNKAIPYLYPDQTSAFMGTANDIMWNGLDINCTSGEFAAVAICSQIRQNSASLHKISKDH  
FKFSLFGVKNGTIESNRRTVKRGYKMSPLEVGQVVRFDHKMDVWPGEECNRIYGTDT  
TIFQPFTPDTNLASFSDICRSLSPDYLHETKYGLNVFEYSAVLVKPEEKCFCLNQKKCL  
KQGALDLNCSCGAPIATLPHFYKSEYLNNVDGLSPEVEKHRIQMYFEPMTGTPLLGYKR  
LQFNIFLKESKISVMKTLNEDEKLIPFWVEEGVALNKTWTNQIKNKLYLPITIMKYVKYI  
FVALGIVFIILAVVVNVNSVKTTEIAPKY

>AgosSNMP1

MGAPTPLTVIGIIFLLFGVFGWFAFPKMLHKKILESKSLNPRSTMQRQMWSHPPISADFKIY  
LFNVTNPEEAQKGEKVLKEVGPyVYHEWKEKENLIDDINEDTVEFSKNTFVDEMSTLP  
PLTGDEILIMPHLAMIGMVTMTKMIKPAAGL VNKAIPYLYPDQTSAFMGTANDIMWNG  
LDINCTSGEFAAVAICSQIRQNSASLHKISKDHFKFSLFGVKNGTIESNRRTVKRGYKMSPL  
EVGQVVRFDHKMDVWPGEECNRIYGTDTTIFQPFTPDTNLASFSDICRSLTPDYLHE  
TKYGLNVFEYSAVLVKPEEKCFCLNQKKCLKQGALDLNCSCGAPIATLPHFYKSEYLN  
NVDGLSPEVEKHRIQMYFEPMTGTPLLGYKRLQFNIFLKKEPKINVMKTLNEDEKLIPF  
WVEEGVALNKTWTNQIKNKLYLPITIMKYVKYIFVAFGIVFIILAVVVNVNSVKTTEITPKY

>RmaiSNMP1-like

MGAPTTLVIGIIFLLFGVFGWFAFPKMLHKKILESKSLNPRSTMQRQMWSHPPISADFKIY  
LFNVTNPEEAQKGEKIIKEVGPyVYHEWKEKENLIDDDIDEDTVEFSKNTFVDEMSTLP  
LTGDEILVMPHLAMIGMVTMTKMMKPAALGLVNKAIPYLYPDQTSAFMGTANDIMWNG

LDINCTSGEFAAVAICSQIRQNSASLHKISKDHFKFSLFGVKNGTIESNRYTVKRGYKMSPL  
DVGQVVRFNDKHMEVWPGDECNRUYGTDITFQPFIKRTDNLASFSGDICRSLAPDFLQE  
TKYNGLNVFEYSAVLVKEEKCFCLNQKKCLKGALDLNCNGAPIATLPHFYKSEELYN  
NIDGLNPEVEKHRIQMYFEPMTGTPLLGYKRLQFNIFLKESKISVMKTLNEDEKLIPFW  
VEEGVALNKWTQNQIKNKLIPITIMKYVKYIFVVFGVVFIIAVVNNSVKTMEVTPK  
Y

>AlinSNMP1a

MGAPLRLGVAGGALFLFGSVFGFWGFHKFLNSQIAQTVQLKGNEMRDTWATFPVALEF  
KVYLFNLTNPEEVQNGGKPKVQEVPYFFDEWKSKGNFEDDSAEDTVSFNMKAVWYFQ  
KDRSEGLTGDEMUTIPHVVFSMIAQVERDKPGALPMLAKALPALFNNLTSPFIAARAMDI  
LFDGLPINCSSKEFGPKAVCTLINANPKGLIKSPELFLSFFGPKNGLDEGRFTVKRGIND  
PKEVGLMVKYNNTKLDVWAGPECNTLSGTDSTIFPPFIDDSEDIVSFSPDLCRSLGAKFR  
YKITYKGVPGNHYTADLGDMSANEDEKCYCPTTCLKGAMDITKCAGAPIILTLPHYY  
LADPSYLDEVEGLHPEEEKHQIFLNFEPIGTPLGARKRLQFNKSHPVKKIPFMKSLPTTM  
IPLMWIEGLELDQKFIDILNANLFRVMKIVGVSKWVMMLLGLGMGGFAFLYYKRKGE  
AGQPSEKSPTPKTVQVESISGKF

>AlinSNMP1b

MPSQKSESRNSESKMSQYPRVSQSKPTKGSRATSPVFSNLTERMREMPIKEAPPRQF  
GKFGAAMVAGGVFGWVAFPYILSFAISKMVNLAPGGEIHDIWKDIPQSLDFNIWIWNVT  
NPMEVQNGGKAVLQEVPYRYIEWKKVLDLIDNPADDEITYSSLNTWYFQKDRSYPLTG  
DEIVTIPHPLMSMVAEQDFPPAMMTVLNAIIPRIYGKLD SVFMQIKAKDLLFDGYPID  
CTSRDLIGRTVCVAVKANSKPLVKNGRNKYLFSVLGK NATPEDVRITVKKGTVN TYDIG  
KVVKVNGNPMNSVWKDECNVLDGTDATIFPPYRSADNV SIVAYATDICRSIRGYIGEGSY  
NGVRGHQYAVDLGDMSSNPKDVCYCICKCYKKGTVDLTKCQGAPLVGTLPHFYLADESY  
LDGVIGMKPDREKHQITFIMEPITGVPLLARKRFQFNVDHMPIRFVNVTKNIRPTLF PILWV  
EEALDLGPELMGFLQARLLNLTLDIVKWTLIVVGAGIGIMGIVKHQMEKEQRKKHERG  
ASVSPAPSNASQERLVGQSAFRSDSEFSFKSSEMLMDPARLTGASKTTPPLIPHPIPTPPQ  
VFTLERSLQERLSPVEGIPPEVPPSRLSVVTSVTPVEESAPAAGAQPGSKPASGSKKK

>AlinSNMP2a

MMRNGWTSVDLRMGNIHINRVLYLGAFGAVIFIIGLFFATSGTDMMINSKIKKGIVLEEGSE  
GLKRFQKTPFPLEFKVFLNITNTDDVMMGGKPVLTEMGPYTYDLYKEKPELKFKDGM  
EYNMTYQHFNAQKSRGESDMVTGLNVPLLTGATMVEQTFPMLGLFLNNAIPFLFPN  
DIFVTTVKDLDGILLRCNYTSGPAMPICNGLKGRAPPTIWREEETKNYRFAMFRHKN  
TSEGPyKVKTGKGDVTEVGQIVEYQHRQTLKNWDKNSSCTIIGTDITFGPLKNPHDDL  
YIFVPDVCLSFTANYVNTSIQNGIPLNKYFAAEKNMASYSKDPDNLRCRAKDEGVRHCL  
KGVIDASPCQGAPVIMSNSPHFLDADA EYQNAVVLKPIEKKHTFVMLEPKTGAPVEGR  
KRMQMNLKVKKVNSITLLENVTERIIPLLWIEEGTRLEGPLLQELQKLYHVMGLLGTFSW  
VLLVAGLVIMGIAGVLYLKVRHLFCAGTQIVAPVDSIGGAQKMNTFGVTNQGSDDYQE  
HGYPGTAIYPQLGDGQKGKNGDLVHTVAHPQAR

>AlinSNMP2b

MPSLNFnELLELGPELLRDNYAMRLNRTVDELLFSGITTHCPPNASLSAATVCSILRHFP  
GLKSLQKYPNGDMNVGIMRFKNDTLSDTYEVYRGNHDFDKIGQIVTNGQQSVDNWY  
DECNKVAGSYGETLLKPFLLTEDSTMVKVYGS DLCSSLPGF KETSSYEGVDSFKFGPQKKF  
LGSVV DYPEN CYCPGSIDGITLGQGCMKAGAMEFSACQAVPVVLSPFH FYKASSHFQNA

VGGLDPDSDKHESYIHLEPITGIPLKGVKRIQINFQMKGTPAMKITKNARDTLIPFLWVEEV  
AALGDDQVNLLKDMLLKMLKILSIVRWVLIAVGSLMVLVGCVMSFLSARKEHRHQY

>AlucSNMP1a

MGAAPRLGVTGGVLFGLGSIFGFWGFKLNSQIAQTVQLKKGNEMRDNWAKFPIALEFK  
IYLFNLTNPDEVQEGGPKVQEVPYFFYEWSKGKLEDDPSDDTFSNMKAVWYFQKD  
KSEGLTGDEIINIPHPVVFSIMTVERDKPGALPMLAKALPALFNNLTSFVSARAMDILFD  
GLPINCAKESFGPKAVCTLINANPKGLVKKSEFLFSFFGPKNGTLDEGRFTVKRGINDPK  
EVGMMVFNNKTLDVWSTDECNQLTGTSTIFPPFIDDSEDIVSFSPDLCRSLGAKFRYK  
ITYKGVPGNHYTADLGDMSSANEDEKCYCPTTCLKGALDITKCAGAPIVTLPHYYLA  
DPSYLDEVEGLHPEEKHQIFLNFEPIGTPLGARKRLQFNKSHAVKKIPFMKTLPTTMIP  
VMWIEEGVELDQKFIDILNANLFRVMKIVGVSKWVMMMLGIGMGGFAFLYYKRRGAA  
GGSEKPPPTKTVQVESISSGKF

>AlucSNMP1b

MTSHKSESRSKMSKMSQFPRSTKLSREQGSRAKSPVFMNLTERMREMPIKEAP  
PKKFGKFGAACMVAGGVFGWVAFPYILSFAISKMVNLAPGGEIHDIWKDIPQSDFNFWV  
WNVTNPMEVQRGAKPVLQEVPYRYIEWKKVVDNPADEITYSSLNTWYFQKEKS  
YPLTGDEIVTIPHLPIMSMLLVAEQDFPPAMLTLLNAIPIYGRMDSIFLNIKVRDLLFDGY  
PIDCTSRLIGRTVCAVKANSKPLVKNGRNKYLFSVLGKNGTPEDVRLTVKKGMNTF  
DIGKVKINGSPLNTVWKDECNVLDGTDATIFPPYRSADNISIVAYATDICRSIRGSYIGEGT  
YNGVKGHQYVNVNLGDMSKNPKDACPVCVKCYKKGTVDLTKCQGAPLIGTLPHFYLADE  
SYLDGVIGLKPEPEKHQITFIMEPITGVPLLARKRFQFNVDMHPVQFVNLTKNLRPTLFPVL  
WVEEALDLGPELMGFLQARLLTNLTLDIVKWTЛИVVGCGIGIMGLIKHQMEKEQQKKHE  
RGASVSPAPSNASQEQLIGQSAFRSDSEFSFKSNEMLMDPSQLTGMSKTPPPIPHPHMPT  
PPEVFTLERSLQERLSPEVGGIPPVEIPPSRLSIVRDMSPINESSVPGVPSEPNPVSGKSRKSM  
K

>AlucSNMP2a

MQRNGWATVDFKMGNISINRVMYLAGFGAIVFLIGLFFATSGTDMMINAKIKKSIVLEEDS  
EGLKRFQKMPFPLEFKVFLNITNPDDVMMGGKPILEMGPYTYDLYKEKPDLKFVKDG  
MIEYNMTYQFHFNHQKSHGSESDVVTALNVPLLTAVMVEQTFPMGLGFLNNAIPFLWP  
NVTdifMSVTADLLFNGVLIQCNYTSGPAMPICNGLKGRAPPTIWREEDTKHFRFAMFRH  
KNKTTEGPYKVKTGKDDISEVGQIVEYKRNLTKNWDKNSSCTVIRGTDTTIFGPPKNPH  
DNLYIFVPDVCLSGASYVNTTVQYGIPLNKYTSDENMASAARDPDNLRCRAKDDDG  
RQCLKDGVIDASPCQGAPVIVSNPHFLADPEYRDGVVGLNAIEDKHKTFLMEPRTGAP  
VEGRKRMQMNLRVKKVASITLENITERVIPLLWIEEGTKLEGPLLQELQKLYHIVGFMGT  
FSWVLLAAGLVILVISGALYLKVRRFCFSGTQLVAPVDSSGVGAQRMNTFGVTNQGADD  
YQEHGYPGATIYPQLGGSQEKGNDMPR

>AlucSNMP2b

MNVGILRFRNDSLSETFEVYRGNKDFNKIGQIVSIDGKRSLNHWYGEGCNKVAGSYDESL  
LQPFLTQDSISNVYGSIDICTIONPMSVVGMSYKGVDCLKFSPDKKFLGSVVDYPENFCYCP  
GSIEGITLGQSCLRTGAMEFAACQAVPVVLGFPHFYRASSRYQNAVGGSPHQDKHESFVA  
LEPTTGIPIEGAKRIQINFQVKGTPAMTMTKNAPDTLMPFLWLDEQVELGDEQLSMIKDTL  
LKMLKIFNIVNWVLIAVGSLMVFVGCLMSFLSARRERSHPD

>MsanSNMP1

MEVGQVVFNDKHKMDVWPSDECNKIYGTDTTIFPPFITHDTSLASFSGDICRSLNPDFVR  
ETKYNGLNVFEYSAMLVKPEEKCYCLNQKKCLKPGALDLNCAGAPIATLPHFYKSEDY  
LNNVDGLSPDVGKHKVQMYFEPMTGTPLLGYKRMQFNIFLKKEPKINAMKTLSEDEKL  
PLFWIEEGIALNKTWTNQIKNKLFLPITIMKYLKYIFVVVGIVFIILAVVINYNNSVKTVEITPK  
Y\*

**File S6.** Transmembrane domains prediction of MsanORs.

>MsanOR2 | TM

MTKTPRVAAVFTAPESSEDLTIVDNKLFKAICLHQLLDPTNGSNRYYGLVLMAFMSVSLG  
MQIIQLVGLYFAVNDLQRFAFATTVSNSLLELFKGYVLVANADRLRASLEVARYEFTTCGS  
WDQRLVRQSRAVLSTVLRTFTVLSWFTCFIWAFLAMDEYLQVTNADGTVSRYRVTIY  
NVWLPVPTTVYNTTIVWTLVYAFEVIAFCVNVIWLLFDSDYVVTMCFTNAQFRTRVSTSC  
MNIGHRDHCFRSPSPHASEGASDDNDILNCYDELINHIKDQNQLIKCDDFFEIIPKAIFQII  
GGSYSVITLIFLTSYLMGFSIISGPVLRSGFGFLSLTFELFLYCYVFNHIETEKCKMFGLY  
SCNWTAMDLKFKKTLLHAMNMNTAHRVMKVTPMSIINLEMFANVMNMSYSIVSVLLN  
SRPQK\*

II  
OOOBB  
MMMMMMMMMMMMMMOO  
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II  
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>MsanOR4 | TM

SYQAVVKINKMTSIIGKKNYQRKFYQTLMTLAFFLDTSQYRFISRFIMQFYIFDWMLVSL  
AAAFTILEENSTTLIMELIQYIIVGIYFSLIFVVIFKKEAIMSNYDCIQTKFIQWSNKRALH  
PNAAYKENIKTFKSLSIPLAISLSIAFGPLVSTFDIGKLPLDNRAHFVLFWPKIVDTNPKS  
MYGIYTLQVIFTISLYISVLSNLGMVFLNELTTQFEMLLDGINDAFKFKMDKQFPSLFID  
CIRHHQIIKFLDDLKSYFKWMILIEIIVLQVILSILYNLTKVNASIGYKMKVGGSLFNILPI  
CFHCHIGEVVLSLHKRLSNHIYNMTWYDMPNKNQLIVIMFQRTQRDLTLSSALFSSEKA  
SRALISKVIKQVYTILNVLLKT\*

II  
OOOBB  
MMMMMMMMMMMMOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOMMMMM  
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II  
>MsanOR43b-1 | TM

VDATSAFSKLETEKLSHSVCQWKRVIAHMVYNFFQKTGRSDVRRYATTCVEFFSYFELVVI  
LIFVIFAFLSVVYSNEDLYNRIYSFSWLCFEANVFAVILIRLYYQSKFRDMYDRSQLIGGTLG  
NYRRTLVLVYYFVTSTALVIVPLLYVISFDAEMGDPFSFPVADALPKTGTVYVCK  
YIVYSFILYAAHLENGFVNNGTFIYFTGVVKKYFQILDVEVQEAMVNKDEQKLKIAIKRHQE  
LLKLFIDMKTVYDKSILIIIEFCGLFNGFNGYIMIQCIQGVIHPKILGFSIACILASLLTMSIYCI

CGSNIYLYHDGLLKSFEHNSCKNSFKKLVIMMMTRATVPLEIKAGSIFAINLNLLVKI  
LKFTYTVFNLLTSVNRQIKENSAI\*

>MsanOR43b-2 | TM

>MsanOR46a-1 | TM

MMDIRDDQNNLFNITLAKYMGIFYQMLDPQTTRFRGLNVYHIVMIFIILFLCVFAVIINISVV  
YYWTNDMLLSIDFIWKGMIMLYACCPIWVIVNYSNDIWDCLSITCYGFTSYSLRYRHILDRC  
CKERSVFITTAITFLYFTSFVIYIVSSLTLLNDIIPVKNRDGSIISNYQHNIINLYLLVSGDTYNA  
HYNIFYMLEVILVFVIIPYCIFDFVTVLCLAIRCQWQMCTAFESIGHTSLGDNLSLVDCG  
EEKKKLPNKHDLIYDELKTIIMNHQAVKKYDKFLTIFQQALLQIVVCLTFIILWICFILV  
KINMMFNQKKFFSA\*

>MsanOR46a-2 | TM

YMGIDFLWKSENTLYVIYKAYFIVRYSKDIWKCLSLTRYDFTSFKYQNRHILDYWWRKRLTR  
LTTIYAIMHLLTVSSFLISLAFTKYKLPVKNHGSIGYYRHNVVMNLYIIVSDETYNAHYY  
MFYIIETLFVSLVTSIFFTFCLLITLCFSICCQMQVICSAFESVGHKSLRDLDSPIGDDYTAE  
NIKIPSNEHDLNYNELKTIINDHQAVMEKYEMFLTLFRRVILLHIFVSSLLAITLLTIIMSFS  
NDDRYKTSEVVIGKLLCCIPSIFFDIFVVSYLFGNIHNDHNSMVFALYGSNWTEMDMKCK  
KLVLTTMKLNNA

MMMMMMMMMMMMMMMMMMMMIII

>MsanOR64 | TM

MDIWKNNKKHLFNIKLSKIITLYQILDPETVKYHGRNIYHIVIACTMLCTSIVLMIGVLSGLN  
YFKSNIPLSMNFFFISFGAYTIYKIWFTIHHSNDIWDLISITQYDFTSIGNRHRHILDRWRE  
RLTWLTNIYAILVLMLTVYFIAMTSAFSEDKSLIKNHGSIGYYRQNVLNLYLIVSDETYNT  
HYYTIFYIVEASVFVYLSIYFCLFDILLITLCYSMCCQMIVCSAFELVGHRSLRDHSPIDQ  
SVGNISTNEHDLIHEELKTIIMDHQLVMKKYEDFVSLFRRMILLHIFVSSLVIVLIFTITMSF  
SSDERFKTSTNAVHKLFVFIPPTLFQIFMVCYLYGSMHNQKDAIIFALYSSNWTEMDMKCK  
KLILLTMKLNANQKK

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>MsanORCO | TM

MGYKKDGLIKDLWPNIIRLIQLSGLFISEYYDDYSGLAVLFRKIYSWITIIYSQFIFIVMF  
VTKSNDSDQLAAGVVTLFFTHSMIKFMYFSTGTFSYRTLSCWNNTSPHPLFAESHSRFH  
AKSLSRMRQLIIVSIVTIFTISWTITFFGESVWKVPNPETYNTQMYVPVPRMLHSWYP  
WDSSHGLGYIVAFVLQFYWIFITLHSNLLELLFSSFLVHACEQLQHLKEILNPLIELSATLD  
SSVHNPAEIFRANSAKNQSINGIDRDYNGSYVNEITEYGTKGENESNRKGPNSLTSNQEVL  
VRSAIKYWVERHKHVVKYVSLITECYGSALLFHMLVSTVILTILAYQATKINGVNVAFASTI  
GYLMYSFAQIFMFCIHGNELIEESSVMEAAYGCHWYDGSEEAKTFVQIVCQQCQKPLIVS  
GAKFFNVSDLFASVLGAVVTYFMVLVQLK\*

II  
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