

Appendix A Primer pairs used for cloning, prokaryotic expression and for gene expression analysis using qRT-PCR

Gene	Primer Sequences (5'-3')	Product length (bp)
Primer sequences for cloning		
<i>CforOBP4</i>	Forward: TTGTGGTGTGTTGGCGAGGAGTTC	523
<i>CforOBP4</i>	Reverse: AAACATTCATCTTGACAGTG	
<i>CforOBP5</i>	Forward: GAACGTTTAATGGGTAAATATAT	719
<i>CforOBP5</i>	Reverse: CGACGATGGCTCGGTTGGTA	
<i>CforOBP6</i>	Forward: CTCAAATATAGAAAATGATCCGC	453
<i>CforOBP6</i>	Reverse: ACGGACAGACGAAGCAAATA	
<i>CforOBP7</i>	Forward: ACAAATTATAATTAAGTGGACCT	637
<i>CforOBP7</i>	Reverse: TCGGAGTCTTCTTCTGCCAT	
<i>CforOBP8</i>	Forward: TCCGAGTTTTAACATTTAAATAA	737
<i>CforOBP8</i>	Reverse: TAATCGGCGAATAAGTAGTC	
<i>CforOBP9</i>	Forward: ATTTTTTTAACAATACGTTTCCTA	661
<i>CforOBP9</i>	Reverse: CATCTTACAAACCGTGCTCT	
<i>CforOBP10</i>	Forward: GGGCGATATCAATGCAGAGTTAT	801
<i>CforOBP10</i>	Reverse: TCCGCTATTTTCGTCGGCATC	
<i>CforOBP11</i>	Forward: CTCAAGTTTTATTAATTTCCCTT	757
<i>CforOBP11</i>	Reverse: GCGTATGACTTTCAAGATGC	
<i>CforOBP12</i>	Forward: GTTGCCTTTATATGGTACGGGTA	573
<i>CforOBP12</i>	Reverse: TATCATACGATCCAACATAT	
<i>CforOBP13</i>	Forward: GAAAGGTTTACAGTCACCGTCAA	613
<i>CforOBP13</i>	Reverse: ACAAAAACCGAAGCAGGAGG	
<i>CforOBP14</i>	Forward: TATTGATATATTCAGTGTGTCGG	1247
<i>CforOBP14</i>	Reverse: TGACGAGGACTTTCTGTGCG	
<i>CforOBP15</i>	Forward: TTCAACTTAAGCCTAAATTTATT	823
<i>CforOBP15</i>	Reverse: GGATTTACGGAAGAACAGA	
<i>CforOBP16</i>	Forward: TTTTTTTTTATATTTTCATGTTAT	649
<i>CforOBP16</i>	Reverse: GAGAAGCAAGTGGTGGCAGC	

<i>CforOBP17</i>	Forward: CCTCAGCAAATGCATAACTACAA	555
<i>CforOBP17</i>	Reverse: CGTGTGTCCGACTTTCAGGC	
<i>CforOBP18</i>	Forward: AGCGATAGACGGACGTCATATAG	479
<i>CforOBP18</i>	Reverse: AGTCATTTATTGTCTTTCAC	
<i>CforOBP19</i>	Forward: TGGCTTTTAAAATGAACCAGCTG	405
<i>CforOBP19</i>	Reverse: TCACAATCTGTATTCCTTAG	
<i>CforOBP20</i>	Forward: ATATAACATTCTCGTTGCTTTAC	1227
<i>CforOBP20</i>	Reverse: TATGAAACAGTCCACAGCAC	
<i>CforOBP21</i>	Forward: GACAAAAATACGTCCGTCGCCGC	593
<i>CforOBP21</i>	Reverse: AGACGACGCCAGTCCCAGTA	
<i>CforOBP22</i>	Forward: GATTTTTTTTTTTTTTACCACGT	447
<i>CforOBP22</i>	Reverse: GGCTCGTCAAATCAGGAAGT	
<i>CforOBP23</i>	Forward: GGTAATTCTGCAGCATTAAATCG	621
<i>CforOBP23</i>	Reverse: TTTCACATAAATCGGCTCCA	
<i>CforOBP24</i>	Forward: GACAAAAATACGTCCGTCGCCGC	535
<i>CforOBP24</i>	Reverse: AGACGACGCCAGTCCCAGTA	
<i>CforOBP25</i>	Forward: CAAAGTTGCGCCATATCATACT	429
<i>CforOBP25</i>	Reverse: GCAAAGACATTTAGATACTG	
<i>CforOBP26</i>	Forward: TCGGTTGGAAGAATCAGCCCACC	859
<i>CforOBP26</i>	Reverse: ACTCAAACCTCAGCCAACGA	
<i>CforOBP27</i>	Forward: ATGAATCGGATTTTAGTTATATT	391
<i>CforOBP27</i>	Reverse: ACATTGCCCTTCTCCATTA	
<i>CforOBP28</i>	Forward: ATGTTTCGTATACTGATTCTCTG	369
<i>CforOBP28</i>	Reverse: CGTGCGAACCATCTGACATT	
<i>CforOBP29</i>	Forward: ATGAGGGCATTATTTTGTGTTGC	385
<i>CforOBP29</i>	Reverse: ATTTCAAGTTGTGCAACATG	
<i>CforOBP30</i>	Forward: ATGAAATCGGTAATCGTTGTAGT	411
<i>CforOBP30</i>	Reverse: GGCAAAGTAATCCAAAATGC	
<i>CforOBP31</i>	Forward: ATGAAATCAGCAATTATCGCTTT	371

<i>CforOBP31</i>	Reverse: GAAGTTTCGTCCAAGTCGTC	
<i>CforOBP32</i>	Forward: ATGTATTTTGC GTTATAACGATTT	421
<i>CforOBP32</i>	Reverse: AAAACGACGAAGCCACGATG	
<i>CforOBP33</i>	Forward: ATGAAAACAACAATTCTTGTTTG	401
<i>CforOBP33</i>	Reverse: TCTAGGAGACAGAAATAAAA	
<i>CforOBP34</i>	Forward: ATGAAGTCCGTTATCTGTGCACT	381
<i>CforOBP34</i>	Reverse: GTAGAACCTTCCTGCGATTT	
<i>CforOBP35</i>	Forward: ATGAAGTATATCATCGTCCTTGC	393
<i>CforOBP35</i>	Reverse: CAATGTACAAAAATAGAATA	

Primer sequences for prokaryotic expression

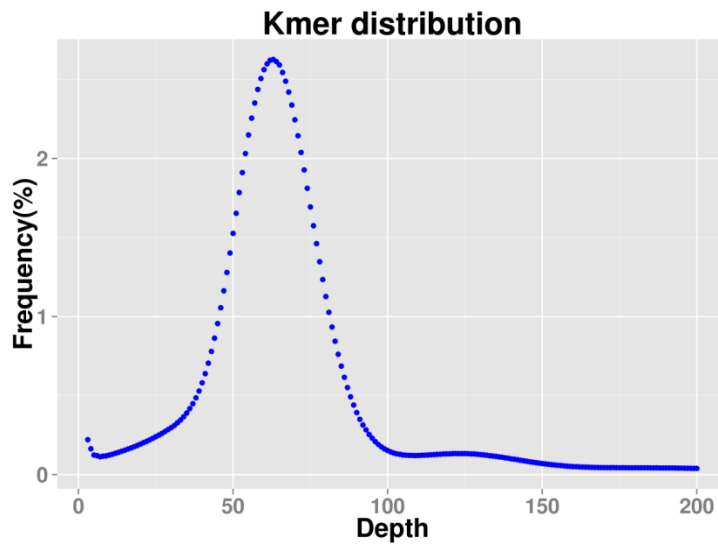
<i>CforOBP4</i>	Forward: (CGGGATCC)CAGACGGACAAGCAAAAAGAACT	348
<i>CforOBP4</i>	Reverse: (GGAATTC)TCAGAGCAAATTGATGTTGGCCT	
<i>CforOBP5</i>	Forward: (CGGGATCC)GGACAAATAGACCTGATGAGTAA	324
<i>CforOBP5</i>	Reverse: (GGAATTC)TTATTGGGGATAACATTGGAAAA	
<i>CforOBP6</i>	Forward:(CGGGATCC)GATGACCACGGTCCGCTTTT	348
<i>CforOBP6</i>	Reverse:(GGAATTC)CTAAGCCGGGCCTTTGG	

Primer sequences for qRT-PCR

<i>CforOBP4</i>	Forward: AGAGGCTGTCAAAGGGGACGAG	87
<i>CforOBP4</i>	Reverse: ACTGCTGTTCGTTTTTCGGGTTTCG	
<i>CforOBP5</i>	Forward: GCCTACTCGGGGCAGATGGG	107
<i>CforOBP5</i>	Reverse: GGCCCTCGCGCATTCTTCAC	
<i>CforOBP6</i>	Forward: CCACGGTCCGCTTTTCCTCAAG	139
<i>CforOBP6</i>	Reverse: ACATTGCACCTCGCTGCTTCTC	
<i>CforOBP7</i>	Forward: CGACTCGTCTGCTGGTTCCAAG	135
<i>CforOBP7</i>	Reverse: TTGTTGCCCATTTGACGGTTCCG	
<i>CforOBP8</i>	Forward: AACGGCAATATCAACACGCAAACC	106
<i>CforOBP8</i>	Reverse: TCTGGTCATTGGCGGAACATTTCG	
<i>CforOBP9</i>	Forward: CCCGACGACGACAAGTTCTACG	133
<i>CforOBP9</i>	Reverse: CCATGTTGTGCGGGTTCGATGAC	
<i>CforOBP10</i>	Forward: GGTGCAACAGGCGAGACAAGG	105

<i>CforOBP10</i>	Reverse: AGCTTGCCGTTTGCCTTTGAG	
<i>CforOBP11</i>	Forward: GTTGCAGGAAGCAGAGAAGCG	95
<i>CforOBP11</i>	Reverse: GGGGTTGCCTTCGTCGTAATC	
<i>CforOBP12</i>	Forward: GATCGCCGCTGTCGCCAAG	87
<i>CforOBP12</i>	Reverse: GCACTTTCAGCCAGGCACACC	
<i>CforOBP13</i>	Forward: CGTGACGCATATCGACGACTCC	86
<i>CforOBP13</i>	Reverse: ACTCGTGAGCGGCAAAGTTTCG	
<i>CforOBP14</i>	Forward: ACGCGGCGTACCTCAAATGC	99
<i>CforOBP14</i>	Reverse: GCACTTCGGCGGGTACTTCC	
<i>CforOBP15</i>	Forward: CAGGAATGCGTGGCCGAGAC	149
<i>CforOBP15</i>	Reverse: AGCTGCACTTCGCCTTTGTTCG	
<i>CforOBP16</i>	Forward: GGCACAGGCTGAACAACAAACG	114
<i>CforOBP16</i>	Reverse: GCCACGCACTTGTTCATCGAGAG	
<i>CforOBP17</i>	Forward: AACCAACACGGCTTACGCAAG	91
<i>CforOBP17</i>	Reverse: TTCCATCCGCGTCTTGCAGTTG	
<i>CforOBP18</i>	Forward: TCTACGCTGGCTGACCTGAAGG	140
<i>CforOBP18</i>	Reverse: TGAGGGTGGTCGGGTTTCTCTC	
<i>CforOBP19</i>	Forward: GCGAGGGGAACTTCAACGAGAC	104
<i>CforOBP19</i>	Reverse: AGCCTTCCGCACCAAGCATTC	
<i>CforOBP20</i>	Forward: CCCGACGATGACGCTTTCTACG	147
<i>CforOBP20</i>	Reverse: GCGGGCTATTCTGGGCATGTTC	
<i>CforOBP21</i>	Forward: TTGCCGGAGGACATCCAGGAG	95
<i>CforOBP21</i>	Reverse: TGGGTCAGCCAGGCGTTCTC	
<i>CforOBP22</i>	Forward: TCGTTGCTGGTGCTGCTAAGTG	127
<i>CforOBP22</i>	Reverse: TCGGGATGTCGCTCTCCTGTG	
<i>CforOBP23</i>	Forward: AGCCTCTTGGGCTACTTGGA	110
<i>CforOBP23</i>	Reverse: TCCTCCTCGGTAAGATCGCTG	
<i>CforOBP24</i>	Forward: TTGCCGGAGGACATCCAGGAG	95
<i>CforOBP24</i>	Reverse: TGGGTCAGCCAGGCGTTCTC	

<i>CforOBP25</i>	Forward: TCGTTGCTGGTGCTGCTAAGTG	127
<i>CforOBP25</i>	Reverse: TCGGGATGTCGCTCTCCTGTG	
<i>CforOBP26</i>	Forward: CAAGGCGACTGGAACCAAGACC	115
<i>CforOBP26</i>	Reverse: GCACCTTCAGACCGCTTTCCC	
<i>CforOBP27</i>	Forward: GCCTCAGTGTACGCCGAAACC	134
<i>CforOBP27</i>	Reverse: TTCTCGTCGAACTGGTGTGCTG	
<i>CforOBP28</i>	Forward: AGGTGTGCCAATGTGCAAGGTAC	85
<i>CforOBP28</i>	Reverse: GCTCTTCTGCTGTTTTTCACGACAC	
<i>CforOBP29</i>	Forward: ATGTGTGGAAAGCTCGTCGTATCG	85
<i>CforOBP29</i>	Reverse: TGCCTTCTTCTGTCAGCTCAAACC	
<i>CforOBP30</i>	Forward: GGCTTTAGCTGTTGCCAAGGA	134
<i>CforOBP30</i>	Reverse: TGATCTCACCAGCCAGTTCACA	
<i>CforOBP31</i>	Forward: TGGAGCAGCTTCACCAGACA	117
<i>CforOBP31</i>	Reverse: TGCACTTCATGTAGCACTTCAAGT	
<i>CforOBP32</i>	Forward: AAAGAGAGCAACGCCCAACAGTC	103
<i>CforOBP32</i>	Reverse: GCTTCTTGCCCAGACAGAGGATG	
<i>CforOBP33</i>	Forward: GGACACACCGGAAGGTCTTTGC	106
<i>CforOBP33</i>	Reverse: CGGCGTGAAAGTGAGTACCATCC	
<i>CforOBP34</i>	Forward: ATCCTTGCGAAACTGCCACCAG	142
<i>CforOBP34</i>	Reverse: CTCTTCGGACCCGCGTATAACAAG	
<i>CforOBP35</i>	Forward: CTCGCACTGGAGCATGAAGATGG	93
<i>CforOBP35</i>	Reverse: ATCATCGTTCACGGCATCCTCATC	
<i>CforOBP36</i>	Forward: GGGCTACCATCGAGAATGCGTTC	81
<i>CforOBP36</i>	Reverse: TCGTTTACCCTTCGGGCAAAAGC	
<i>CforGAPDH</i>	Reverse: CCGCTTCCTTGACCTTGCTCTTG	
<i>CforUBE4A</i>	Forward: GCCAGCGAGGAAGCGATGATG	97
<i>CforUBE4A</i>	Reverse: GCTTGGAACCTGGGCAGAGTAACG	
<i>Cforβ-actin</i>	Forward: CGTCACAAACTGGGATGACA	100
<i>Cforβ-actin</i>	Reverse: GAGCTTCGGTCAAAGAACG	



Appendix B Distribution frequency of 19-mers in the *Cylas formicarius* genome.

Appendix C Statistical information of 19-kmer analysis of the *Cylas formicarius* genome

K	K-mer Number	K-mer Depth	Genome Size (bp)	Used Bases(Gp)
19	24,314,168,078	61	368,853,960	27.64

Appendix D Summary of generated sequence reads using the Illumina system

Library name	Data (Gb)	Depth (x)	Q20 (%)	Q30 (%)
270-1 bp	13.82	37.91	99.34	98.04
270-2 bp	13.82	37.91	98.93	97.35
Total	27.64	75.82	99.13	97.7

Appendix E Summarized sequence reads derived from the PacBio system

Platform	No. of reads	Total base (bp)	N50 length (bp)	Average read length	Longest
PacBio Sequel	2,884,459	34,139,672,427	18,752	11,836	89,710

Appendix F CEGMA and BUSCO evaluation for the *Cylas formicarius* genome assembly

No. of 458 CEGs present in assembly	Percentage of 458 CEGs present in assembly (%)	No. of 248 highly conserved CEGs present in assembly	Percentage of 248 highly conserved CEGs present in assembly (%)	No. of 1054 core eukaryotic genes	Percentage of 1054 core eukaryotic genes
449	98.03%	235	94.76%	1042	98.87%

Appendix G Summary of Illumina reads aligned to the *Cylas formicarius* genome assembly

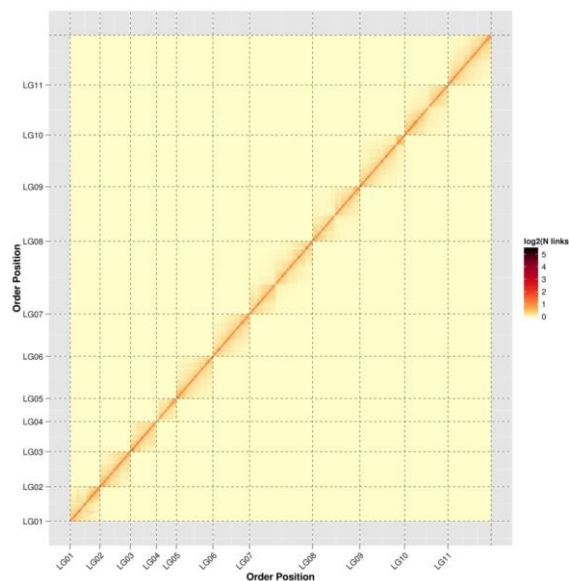
Library	No. of reads	Mapped reads	Percentage of mapped reads (%)	Properly mapped reads	Percentage of properly mapped (%)
270 bp	181,983,380	178,361,910	98.01%	177,115,944	96.04%

Appendix H Summary of Hi-C data for error correction and chromosome assembly

Library id	Insert size (bp)	Read pairs	Base number (bp)	Mapped reads	Uniquely mapping pairs	Valid interaction pairs
H01	300-700	109,601,871	32,834,123,430	197,039,172	80,043,133	32,234,443

Appendix I Hi-C libraries for chromosome-level assembly

Chromosome	Sequence number	Sequence length (bp)
Chr0	4	23,730,323
Chr1	5	24,084,616
Chr2	22	21,400,864
Chr3	24	16,147,109
Chr4	11	29,081,913
Chr5	15	29,464,127
Chr6	13	50,227,660
Chr7	14	38,047,904
Chr8	14	35,812,270
Chr9	9	34,626,698
Chr10	7	34,436,273
Total Sequences Clustered(Ratio %)	138(62.44)	337,059,757(99.42)
Total Sequences Ordered and Oriented(Ratio %)	78(56.52)	333,787,415(99.03)



Appendix J Genome-wide chromosomal contact matrix for *Cylas formicarius* showing interactions among the 11 chromosomes. The number of log₂ links was calculated as the interaction frequency distribution of Hi-C links between and within chromosomes. The

colour key of the heatmap ranging from light yellow to dark red indicates the frequency of Hi-C interaction links from low to high.

Appendix K Statistics of repeated sequences

Type	Number	Length	Rate (%)
ClassI	491,714	103,075,250	30.4
ClassI/DIRS	6,732	2,301,757	0.68
ClassI/LINE	129,821	27,870,928	8.22
ClassI/LTR	5,977	3,263,649	0.96
ClassI/LTR/Copia	2,014	801,356	0.24
ClassI/LTR/Gypsy	9,889	4,594,013	1.36
ClassI/PLE LARD	334,340	69,408,694	20.47
ClassI/SINE	444	86,177	0.03
ClassI/SINE TRIM	130	201,769	0.06
ClassI/TRIM	1,693	2,070,686	0.61
ClassI/Unknown	674	120,204	0.04
ClassII	367,693	73,273,789	21.61
ClassII/Crypton	3,940	1,124,157	0.33
ClassII/Helitron	2,751	558,071	0.16
ClassII/MITE	495	73,898	0.02
ClassII/Maverick	29,513	7,703,954	2.27
ClassII/TIR	323,939	64,780,365	19.11
ClassII/Unknown	7,055	1,086,541	0.32
PotentialHostGene	476	153,271	0.05
Total	860,541	157,509,980	46.46

Appendix L Statistics of repeat elements

Repeat elements	Number	Length	Genome proportion (%)
DIRS	6732	2301757	0.68
LARD	55504	10642243	3.14
LINE	129821	27870928	8.22
LTR/Copia	2014	801356	0.24
LTR/Gypsy	9889	4594013	1.35
LTR/Unknown	5977	3263649	0.96
PLE	278835	61058986	18.01
SINE	444	86177	0.03
TRIM	1693	2070686	0.61
Unknown	804	321973	0.09
Crypton	3940	1124157	0.33
Helitron	2751	558071	0.16
MITE	495	73898	0.02

Maverick	29512	7703503	2.27
TIR	323939	64780365	19.11
Unknown	7055	1086541	0.32
PotentialHostGene	476	153271	0.05
SSR	658	362661	0.11
Unknown	45612	8740806	2.58
Total	906151	157507930	46.46

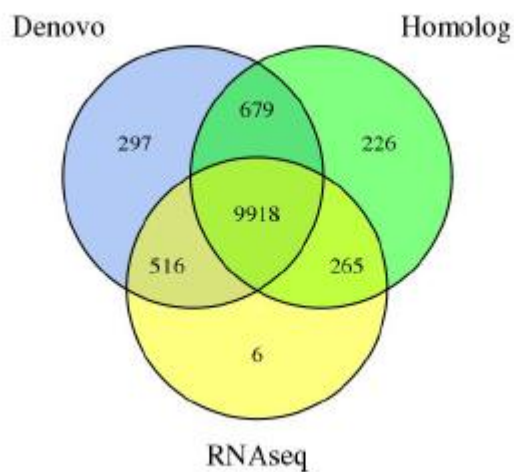
Appendix M Statistics of gene prediction results based on three methods

Method	Software and gene set	Gene number
Ab initio	Genscan	14,203
	Augustus	10,593
	GlimmerHMM	36,128
	GeneID	8,104
	SNAP	22,127
Homology - based	<i>Anoplophora glabripennis</i>	12,478
	<i>Dendroctonus ponderosae</i>	10,499
	<i>Oryctes borbonicus</i>	8,839
	<i>Tribolium castaneum</i>	10,489
	<i>Drosophila melanogaster</i>	7,434
RNA - seq	PASA	17,697
	TransDecoder	23,437
	GeneMarkS - T	35,199
Integration	EVM	11,907

Appendix N Statistics of comparison of gene sets of *Cylas formicarius* and 15 other insect species

Name	Total gene	oneCopy num	MultiCopy num	Unigene num	Othergene num	Cluster num	UnCluster num	Total family	Uni family
<i>A.planipennis</i>	11373	1566	650	264	7565	10045	1328	8589	90
<i>O.taurus</i>	14402	1519	856	1064	9430	12869	1533	9486	327
<i>O.borbonicus</i>	6730	1619	408	55	3847	5929	801	5345	19
<i>T.castaneum</i>	12841	1588	699	635	8805	11727	1114	9485	194
<i>A.glabripennis</i>	14533	1535	879	693	10165	13272	1261	9736	200
<i>C.formicarius</i>	11907	1589	634	223	8565	11011	896	9291	75
<i>D.ponderosae</i>	12102	1503	840	455	8284	11082	1020	9000	180
<i>Z.nevadensis</i>	12314	1592	619	473	7909	10593	1721	8959	161
<i>L.migratoria</i>	17566	1526	833	1667	7347	11373	6193	8185	457
<i>A.mellifera</i>	9917	1651	390	141	6519	8701	1216	7982	35
<i>P.humanus</i>	10748	1614	451	93	6391	8549	2199	7854	31
<i>C.lectularius</i>	11920	1604	527	765	7053	9949	1971	8328	224
<i>A.pisum</i>	18247	1413	1275	3064	9148	14900	3347	8403	811
<i>B.mori</i>	13165	1603	553	1250	7092	10498	2667	8151	307

<i>D.melanogaster</i>	13886	1577	641	1410	6838	10466	3420	7899	425
<i>C.elegans</i>	20174	1544	849	7688	3878	13959	6215	6153	1359



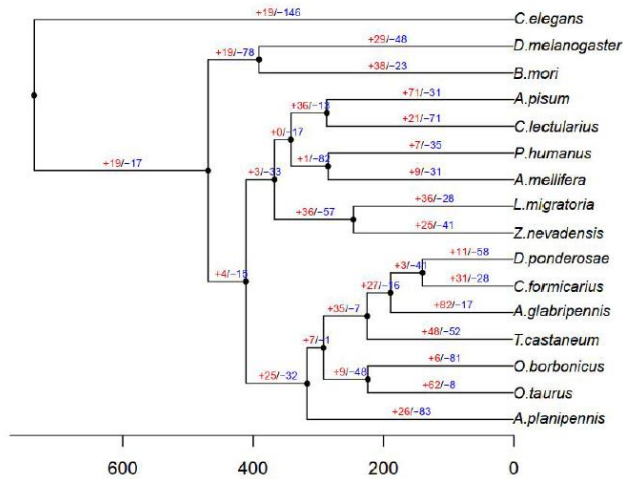
Appendix O Distribution of predicted genes by using ab initio, homology-based method, and RNA-seq.

Appendix P Statistics of functional annotation for predicted gene

Annotation database	Annotated gene number	Percentage (%)
GO	5,883	49.41
KEGG	6,183	51.93
KOG	8,166	68.58
TrEMBL	11,448	96.15
Nr	11,447	96.14
All annotated	11,469	96.32

Appendix Q Statistics of the predicted non-coding RNA

RNA classification	Number	Family
rRNA	102	3
tRNA	165	24
miRNA	40	31

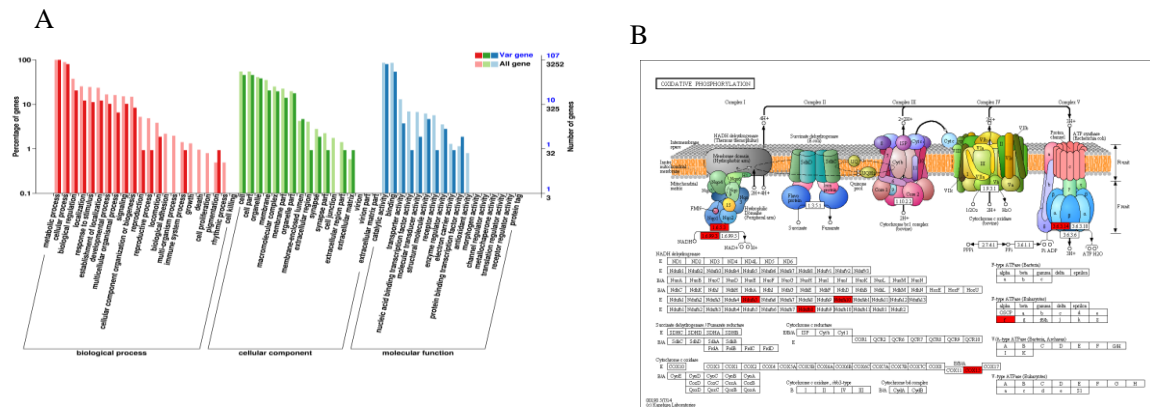


Appendix R Phylogenetic tree of 16 insect species and the sizes of expanded and contracted gene families. The 16 species used for comparison were *Tribolium castaneum*, *Tribolium castaneum*, *Onthophagus taurus*, *Dendroctonus ponderosae*, *Anoplophora glabripennis*, *Oryctes borbonicus*, *Agrilus planipennis*, *Bombyx mori*, *Apis mellifera*, *Locusta migratoria*, *Drosophila melanogaster*, *Acyrtosiphon pisum*, *Pediculus humanus*, *Cimex lectularius*, *Zootermopsis nevadensis*, *Caenorhabditis elegans* and *Cylas formicarius*.

Appendix S Expanded and contracted gene families of *Cylas formicarius*

+	GF_163	PF00497.15	Bacterial extracellular solute-binding proteins, family 3
+	GF_114	PF00078.22	Reverse transcriptase (RNA-dependent DNA polymerase)
+	GF_26	PF03175.8	DNA polymerase type B, organellar and viral
+	GF_113	PF00135.23	Carboxylesterase family
+	GF_124	PF02958.15	Ecdysteroid kinase
+	GF_87	PF00370.16	FGGY family of carbohydrate kinases, N-terminal domain
+	GF_468	PF00078.22	Reverse transcriptase (RNA-dependent DNA polymerase)
+	GF_204	PF08395.7	7tm Chemosensory receptor
+	GF_60	PF00201.13	UDP-glucuronosyl and UDP-glucosyl transferase
+	GF_111	PF13843.1	Transposase IS4
+	GF_33	PF02949.15	7tm Odorant receptor
+	GF_12	PF00232.13	Glycosyl hydrolase family 1
+	GF_146	PF00043.20	Glutathione S-transferase, C-terminal domain
+	GF_515	PF13358.1	DDE superfamily endonuclease
+	GF_4	PF00664.18	ABC transporter transmembrane region
+	GF_123	PF00135.23	Carboxylesterase family
+	GF_14	PF11838.3	ERAP1-like C-terminal domain
+	GF_698	PF01395.17	PBP/GOBP family
+	GF_19	PF00089.21	Trypsin
+	GF_85	PF02949.15	7tm Odorant receptor
+	GF_206	PF02176.13	TRAF-type zinc finger

+	GF_22	PF00067.17	Cytochrome P450
+	GF_51	PF00135.23	Carboxylesterase family
+	GF_73	PF00089.21	Trypsin
+	GF_803	PF01346.13	Domain amino terminal to FKBP-type peptidyl-prolyl isomerase
+	GF_401	PF00503.15	G-protein alpha subunit
+	GF_554	PF13359.1	DDE superfamily endonuclease
+	GF_42	PF05970.9	PIF1-like helicase
+	GF_209	PF00089.21	Trypsin
+	GF_227	PF00295.12	Glycosyl hydrolases family 28
+	GF_222	PF00295.12	Glycosyl hydrolases family 28
-	GF_37	PF00089.21	Trypsin
-	GF_13	PF02163.17	Peptidase family M50
-	GF_254	PF03372.18	Endonuclease/Exonuclease/phosphatase family
-	GF_1	PF00067.17	Cytochrome P450
-	GF_50	PF00474.12	Sodium:solute symporter family
-	GF_35	PF02958.15	Ecdysteroid kinase
-	GF_45	PF00135.23	Carboxylesterase family
-	GF_134	PF13358.1	DDE superfamily endonuclease
-	GF_510	PF00151.14	Lipase
-	GF_357	PF00041.16	Fibronectin type III domain
-	GF_8	PF00732.14	GMC oxidoreductase
-	GF_95	PF00379.18	Insect cuticle protein
-	GF_145	PF00067.17	Cytochrome P450
-	GF_304	PF00188.21	Cysteine-rich secretory protein family
-	GF_226	PF00644.15	Poly(ADP-ribose) polymerase catalytic domain
-	GF_6	PF00201.13	UDP-glucuronosyl and UDP-glucosyl transferase
-	GF_220	PF00092.23	von Willebrand factor type A domain
-	GF_117	PF00002.19	7 transmembrane receptor (Secretin family)
-	GF_255	PF02949.15	7tm Odorant receptor
-	GF_648	PF14683.1	Polysaccharide lyase family 4, domain III
-	GF_3	PF07776.10	Zinc-finger associated domain (zf-AD)
-	GF_452	PF00665.21	Integrase core domain
-	GF_20	PF00106.20	short chain dehydrogenase
-	GF_122	PF02949.15	7tm Odorant receptor
-	GF_82	PF01757.17	Acytransferase family
-	GF_83	PF12796.2	Ankyrin repeats (3 copies)
-	GF_785	PF14291.1	Domain of unknown function (DUF4371)
-	GF_7	PF03028.10	Dynein heavy chain and region D6 of dynein motor



Appendix T Functional annotation and enrichment analysis of the obtained rapidly evolving genes were carried out using GO and KEGG. A, GO enrichment analysis of expanded gene families of *Cylas formicarius*. Bars are subdivided to represent different GO terms; B, KEGG pathway enrichment analysis was performed for gene family expansion of *Cylas formicarius*. The graph depicts the most highly enriched pathways.

Appendix U Comparison of the chemosensory gene families of various species

Species	OR	GR	IR	OBP	CSP	SNMP
<i>Tribolium castaneum</i>	270	219	71	50	20	6
<i>Cylas formicarius</i>	154	46	39	36	13	4
<i>Agrilus planipennis</i>	46	30	30	12	14	4
<i>Dendroctonus ponderosae</i>	79	59	55	36	11	4
<i>Anoplophora glabripennis</i>	121	190	63	60	17	4

OR, odorant receptor; GR, gustatory receptor; IR, ionotropic receptor; OBP, odorant binding protein; CSP, chemosensory protein; SNMP, sensory neuron membrane protein.

Appendix V *Hsp* genes identified in six coleopteran insect' genomes

Family	<i>Cylas formicarius</i>	<i>Tribolium castaneum</i>	<i>Anoplophora glabripennis</i>	<i>Dendroctonus ponderosae</i>	<i>Agrilus planipennis</i>	<i>Onthophagus taurus</i>
<i>Hsp100</i>	1	-	-	-	-	-
<i>Hsp90</i>	1	3	1	1	2	1
<i>Hsp70</i>	8	8	5	4	5	7
<i>Hsp60</i>	1	-	1	2	2	1
<i>sHsp</i>	17	9	17	11	9	9
<i>Hsp10</i>	2	1	2	-	2	2
total	30	21	26	18	18	20

Appendix W Sequences used for building phylogenetic trees

Heat shock proteins

>TcasHsp1

MVKSPA V G I D L G T T Y S C V G V W Q H G K V E I I A N D Q G N R T T P S Y V A F T D T E R L L G D A A

KNQVAMNPSNTIFDAKRLIGRKFDDPKIQDDIKHWPFKVINDCGKPKIQVEHKGEV
KKFAPEEISSMVLTKMKETAEAAYLGTSVRDAVITVPA YFNDSQRQATKDAGVIAGL
NVMRIINEPTAAALAYGLDKNLKGERNVLIFDLGGGTFDVSILTIDEGSLFEVRATA
GDTHLGGEDFDNRLVNHLADEFKRKYKKDLRSNPRALRRLRTAAERAKRTLSSST
EASIEIDALFDGIDFYTKVSRARFEELNADLFRGTLQPVEKALTDKMDKGMHIDIV
LVGGSTRIPKIQQLLQNYFNGKSLNLSINPDEAVAYGAAVQAAVLSGETDSKIQDV
LLVDVTPLSLGIETAGGVMTKIIERNARIPCKQTQTFTTYADNQPAVTIQVFEGERA
MTKDNNLLGTFDLTGIPPAPRGVVPKIEVTFDL DANGILNVS AKDTSSGNSRNITIKN
DKGRLSQKDIDRMVSEAEQYKEEDEKQRQRIAARNHLEGYIFQLKQAVSDCGDKL
SSADKETITRECD SCLQWLDANTLAEK EEEYEDRQKQLTQICSPIMAKLYQQGAPQG
GQMPGSCGQQAGGFGGQRQGGPTIEEVD

>TcasHsp2

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NVMRIINEPTAAALAYGLDKNLKGERNVLIFDLGGGTFDVSILTIDEGSLFEVRATA
GDTHLGGEDFDNRLVNHLADEFKRKYKKDLRSNPRALRRLRTAAERAKRTLSSST
EASIEIDALFDGIDFYTKVSRARFEELNADLFRGTLQPVEKALTDKMDKGMHIDIV
LVGGSTRIPKIQQLLQNYFNGKSLNLSINPDEAVAYGAAVQAAVLSGETDSKIQDV
LLVDVTPLSLGIETAGGVMTKIIERNARIPCKQTQTFTTYADNQPAVTIQVFEGERA
MTKDNNLLGTFDLTGIPPAPRGVVPKIEVTFDL DANGILNVS AKDTSSGNSRNITIKN
DKGRLSQKDIDRMVSEAEQYKEEDEKQRQRIAARNHLEGYIFQLKQAVSDCGDKL
SSADKETITRECD SCLQWLDANTLAEK EEEYEDRQKQLTQICSPIMAKLYQQGAPQG
GQMPGSCGQQAGGFGGQRQGGPTIEEVD

>TcasHsp3

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VKRFAPEEISSMVL RKMKETADAF LGKETKDAVITVPA YFNDSQRQATKDAGMIA
GINVLRINEPTAAALAYGLDKNLKGERNVLIFDLGGGTFDVSILTIDEGSLFEVKAT
AGDTHLGGEDFDNRLVNHF ADEFKRKYKKDLTKNPRALRRLRTAAERAKRTLSSS
TEASLEIDALFEGIDFYTKISRARFEELNSDLFRGTLEPVEKALNDKMDKSMIHDV
VLVGGSTRIPKIQNLLQNYFSGKTLNLSINPDEAVAYGAAVQAAILSGDSSSKIQDV
LLVDVTPLSLGIETAGGVMSKIVERNARIPCKQTQTFTTYSDNQPAVSIQVFEGERA
MTKDNNLLGTFDLSGIPPAPRGVVPKIDVTFDL DANGILNVS AKEVSTGKSKNITIKN
DKGRLSQREIEKMLADAERYKEEDDRQRERIGSKNQLESYVFNVKQAVEEAGNKL
SAEDKKKALKECEACIKWLDSNQMAEKEEFYKLDLTKICSPIMTKLHRGGGSSG
GGGNDGPTIEEVD

>TcasHsp4

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GADISMIGQFVGFYSAYLVADKVTVVSKNNDDEQYVWESSAGGSFTVTQDRGEP
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EEKKEEGEDKDKDKPKIEDVGEDEDEDTKKEDKKKKKTIKEKYTEDEELNKTKPI
WTRNADDISQEEYGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFVPRRVPFDLF

ENKKRKNNIKLYVRRVFIMDNCEELIPEYLNFIKGVVDSDELPLNISREMLQQNKIL
KVIRKNLVKKCLELFEELAEDKDGKFKFYEQFSKNIKLGIHEDSQNRAKLSSELLRY
HTSASGDEACSLKDYVSRIKPNQKHIIYITGESKEQVANS SFVERVKKRGFEVYVM
TEPIDEYV VQMQKEFDGKTLVSVTKEGLELPEDEEEKKKREEDKAKFEGLCVKVMK
SILDNKVEKVVVSNRLVESPCCVTSQYGWTANMERIMKAQALRDTSTMGYMAA
KKHLEINPDHSIIENLRQKAEADKNDKAVKDLVILLFETALLSSGFTLDEPQVHASRI
YRMIKLG LGIDEEEA MITEDAQGGDAPSADAAESEDASRMEEVD

>TcasHsp5

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ENLLADYDFSETLTRAKFEELNNDQFLKTLKPVKKVLEDADMTKDQIDEIVLVGGS
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>TcasHsp6

INEPTAAAIAYGLDKKAERERNVLIFDLGGGTFDVSLLTIEGIFEVKATAGDTHLG
GEDFDNRLVEYCTQDFKKKHKADISGNPRALRRLRTQCERAKRTLSSATQASIEIDS
LFDGIDYSTTITRARFEDINMDYFKKCIDPVDKVLQDAKIGKSAVHEIVLVGGSTRIP
KVQQLITEYFNGKEPCRSINPDEA

>TcasHsp7

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INEPTAAALAYGLDKNLKGERNVLIFDLGGGTFDVSILTIDEGLFEVRATDTHLGGG
DFDNRLVNHLADEFKRKYRKDLNPRSLRRLRTAAERAKRTLSCTEATIEIDALFEGI
DFYTKISRARFEELCSDLFRGTLQPVEKALNDAKMDKGQIHDVVLVGGSTRIPKI

>TcasHsp8

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EVLFCYEPYDELVLMQLQQFKGFKLVSEKDMRDDKAANDLSNLGEDSLKRSEV
NELSEWIKSKLSGKAVDVNATTRLENHPCVVTVEEMAAARHFIRTQSHQLSEDRR
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SINALLTKALEKH

>TcasHsp9

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AKL

>TcasHsp10

MFYPVFSHDMRYFLRLWRPWRQFAAPNIESSVTFGRQKFQADLDVQYFKPEDITIK
VAEDNTVTVEGKQEHQEGENYVSRHFVRRFVLP EGHDMDKLESTLSTDGVL TITA
PRIAKEAEEGRTIPITRTGKAH KSGEN

>TcasHsp11

MSLLLFQDPFESPRHPYGRLLDRYFASLLNFDDFLPLETETRGLRQRFPAPESDVR
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EGHDLGKIESRLSSDGVLSITAPRITEGGQASRNIPVIRTGQPSQHVEYDKQEDKTEE

>TcasHsp12

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KNQVAMNPSNTIFDAKRLIGRKFDDPKIQDDIKHWPFKVINDCGKPKIQVEHKGEIK
KFAPEEISSMVLTKMKETA EAYLGTSVRDAVITVPA YFNDSQRQATKDAGVIAGLN
VMRIINEPTAAALAYGLDKNLKGERNVLIFDLGGGTFDVSIL TIDEGSLFEVKATAG
DTHLGGEDFDNRLVNHLADEFKRKYKDLRSNPRALRRLRTAAERAKRTLSSSTE
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VGGSTRIPKIQQLQNYFNGKPLNLSINPDEAVAYGAAVQAAVLSGETDSKIQDVL
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TKDNNLLGTFDLTGIPPAPRGVPKIEVTFDL DANGILNVS AKDTSSGNSRNITIKNDK
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DKETVTRECDSC LQWLDANTLAEKEEYEDKQKQLSSICAPIMAKLYQQGGQGGMP
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>TcasHsp13

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>TcasHsp14

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GDGTTTATV LARSIAKEGFENLGKGANPVEIRK GIMLA VEKITETLKTLSKPVTTPE
EICQVATISANGDQSVGNLIADAMKKVGKEGVITVKDGKTLHDELEVIEGFKFDRG
YISPYFVNTSKGAKVEYQDALILLSEKKISSVQSIVPALELANMQKKPLIIVAEDIDG
EAL TTLV VNR LRIGLQVA AVKAPGFGDN RKATLQDMAIATGGIVFGDEANIVKLE
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SGSLDGLKPGNNDQAIGIEIVKRALKVPCMTIAKNAGVDGATVVAKIEQQQGDY
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>TcasHsp15

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EENDVSEL DIKVS VKDSDEEGDKLKEIMLK SCKDVVRHQLTKYISSLKEEFSKGMIL
PKKDEVKPD AVKNLSSGFNKKISMT PVVSENNKQIGLKL DVTTINITQQFCRAQEF
YDALTKIEMVTA FTRAHVKMDASKGGK FELFNGNIVGQFDEL VPGKKIVQQWRY
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AFGFGAFIV

>TcasHsp16

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PKKDEVKPDAVKNLSSGFNKKISMPVSVSENNKQIGLKLDTVTTINITQQFCRAQEF
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AFGFGAFIV

>TcasHsp17

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VAAKKQSQPSQSQPQPVEQYLKEVNPTTKTAYQRPLNYLRFNSQSALKQQEQSE
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QQKLLAAAENSQEENQSKSSLYVPQNVKKAKKQKTTPSRQSSQQYDYYPQVPPQR
PNYTPESPRYPQSLPSRNA YQKSEANYQVEDPLLYPEPKELEYQTQAPARSSKQRTT
RLPRRKP KYQTEEP EYQPASDDQGFYQPSSLYQDEPTYRRPLPRPSKPAKYEEP
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QPTAEVA VRQVGRGPSVSYRQTYPQYQYDRRQQIATPLPKTRYFNSLEYQNEEDSS
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LIVVYDD

>TcasHsp18

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>TcasHsp19

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>TcasHsp20

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>TcasHsp21

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WLSDEALKDHVAKATV SERLSDSPCALVASMFGWTGNMERLAISNAHQSDDPQ
RSYYLNQKKTLEINPRHPLMRELLKRVNDDPSDPTAKDMALMLFRATLRSGYML
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>AplaHsp1

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QQWRYKAWPEGHYSTVEITIDEKEDHTEVRLVQTGVPRGELEKIRENWERYYWTP
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>AplaHsp2

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LSDDHDLKVKPIYAKNGTLRILAPKRGEAGQELTVQTIKLGPPKILKIEKE

>AplaHsp3

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SRELLQNSTLINKLRDVLTRGVIKFLQEQQSKATDEYLKFTDYGIFLKEGIITNQNQ
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>AplaHsp4

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>AplaHsp5

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>AplaHsp6

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GDTHLGGEDFDNRLVNHVVEEFKRKYKDLRTNIRAIRRLRTAAERAKRTLSSSTE
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VGGSTRIPKIQNLLQNFFCGKQLNLSINPDEAVAYGAAVQAAVLTGDTSDKIQDVL
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>DponHsp11

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>DponHsp12

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>DponHsp13

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>OtauHsp17

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>OtauHsp19

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>CforHsp7

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AEDALRDHISKATVSERLS DPCALVASMFGWTGNMERLAISNAHQKADDPQRSY
YLNQKKTLEINPRHPLIKELLKRVNDDPSDPAKEMALMLFRTSTLRSGYMLRETA
DFAQSIETMMRKT LGVALDEPVEEEDVPEDGIPEEENGDIKEEEAEHDEL

>CforHsp27

MSGIAATRLAEERKAWRKDHPFGFVARPSKNLDGSLNLMNWECSIPGKKGTPWEE
GHYKLRMLFKEDYPTSPKCKFEPPLFHPNVYPSGTVCLSLLEDKDWRAITIKQI
LLGIQDLLNEPNVKDPAQAEAYTIYCQRNLEYEKRVRAQARAMSHQEG

>CforHsp28

MSLLPLLFDEPPYSSYWL RPSRILDQHFLGLDSDDLLQPLNLNRRILSRTPAGYLR
NWRPNASEKDSGSLVSFDKDKFQANLDVSQFKPEEISVKVADNVLTI EGKHEEKQD
EHGYISRHFVRRYVLPKNYDVEKIQSKLSSDGVLSITAPPVQSSEVEHKNIPIQTGE
PAKQIEQKKQ

>CforHsp29

MDLSLLPLMIDSGPLSPASRWAASPLITPEEFAWPTRRLLSQISQFDNSNLVVVDKD
KFQVHVVDVQQFKPNEISVKLNDDNTVTVEGKHEERQDEHGYVARSFVRRYQLPD

DVDVEKLASKLSSDGVLTISAPKKARGKTEEYREIPITRVGPVKSPETKTAEESKQ

>CforHsp30

MALLPLMFDDDLFGHPRKWSSFLEPEELCWPTATFSRGNLHHLRDLRHQLPRVD
KNTSIIVDKDFQANIDVQQFEPYEISVKLTGDNTVTVEGKHEEKEDDHGTICRHFV
RRYQLPEDCDVARLQSKLSSDGVLTISAPKKRDDKEVELNEIPIHHTWRPRLNWWP
SRSHSVSGHI

Olfactory receptors

>CforOR1

MYVAYSIAIQMTCVSSGLLMALKVPLL FETNPAAIDTTARTMVVVITTVKLAMC
QSRDVLRLISQALEEDYRISIQEDPSVRRRIYRWHSTYCNNLVKLLVGSFILLAFFTVG
TVDANILASLASGRQLNYTTEKLIAVHFWYPYDESRHYAMAILEQHVRTILSCLTIG
TVTAFINFMIVALMLRLKLLQYYFKEFQAYSPDGFVASARVGIDVGLKLVQCQKHQE
LIKSFENFNCHMKHIILLEYTLTSVMFAGQLVQLVAGERIMFNSAFIALTISQLMIFA
WNSNEIVVQSAALATALLESSWYEQPLEIQKEISFMVMRCQKPLRLTIGAFGTMDI
GAAISVGGANGSESYTASAVCPADSGEGNLTLCRRAPRTRIANPANSTPNSSSTNS
RASDLHTAVDASENTGGNHKEDTQDGPIVEREKSNRRPNIDAKLLNQKNCIVKN
CRVSQIEIDEIVSYIRKTINTSEIETQRENKEDEAKVNEDELRELKIQMKHETTSYHT
KNLLKGGK

>CforOR2

MLSFDEEFKAAPQKVFRITITLMITLWTVEIKAKLIQTARIKRIIAYILAEETKIRHSPD
EDVARCYFEQAKFCRRSNLIIFSVMTMTVATSMIVGNFVQCRQVEQHNRLRNDTISK
SFTYELYAGLDRKMAESVLEATNDLSVLIAASLVSSQLVFISCMIFATSLIKIMQI
RFRKMVVTYGGDVVVTLRDLVLEHQKVIDFVDQLNAAMKNLILLEYLLHSLNFASV
SIQFIKVGFFQISTFQT

>CforOR3

MVKILRFQLTVLKYLVFWPKDRLD SKTNRILSVSYFTLSVLFCLPILGAVLYEALNG
MKDPNIAIEATIALCDATAYYVFLCFLKNQAKIAGIVKDVNLFLNYCEAKLIEEID
ATCHKYTKYLLTYVTFGVLFNLLWPQITINQCTSARGELVKHMPCGMVTQNYFPF
DTRDTYVYWTIFFYFVNFLHICVAFSIGTSVFIGLLMHTIGQLKNCSSYFKSIFFGA
DIATKFRLSY CIRYHQTILSYAERIFSTFTSILITYVTITSFTFAVVSYQIANSKTAIEER
IRYVLLL VGWILFFLICFFAQEVIDQSLKVGDAVYHSNWHLVAGTDEIKRSLAVVI
LRTQRPICWKVKYIGTMSLFTFVYVIKTSYTFFTLLL TATDSA

>CforOR4

MASDKGYFGYIRRLMMMVGWRLLDYQTSTLKRRIYEVYAVLFQLICLSALVSLIG
ELPILFRNTNATAAMDNIGKIIATVVVIFKMTMWRSNQMLRLMRLVLHQSDIRLQ
PDSQIKAIYQRHQNYDDKFISLIVSSAVMIAVCAAGFGDVDCYLYTRQFRNLNQTQ
KPLPMNLWYPFDRNRHYVFLIDQNIRPSMACLCIGVVSASVNSVIVFLKLQLTLL
QRNFRSFDGCKGNDLKPLCVEHQKLI EFVAIFNGAMRNII FLEYTVSSLTFATVIFQI
TTGDQLVFSFTMLAYISLQLLTFAWSNEILIQSIELAKAIYESRWYDQSKSTKLLLY
TMMMRCQKPLCLRIGLLGVMDLNAGLSRLKLGYSYTSVMKT

>CforOR5

QVLNNVFETLVESVCSKFNNGRFETMYKTVEIPILTL SKYCMIFVGIWKLDLPPKNV
MSRRVYDIYSAFVRIYFPLFISSSICQFVITLGAEKSLEDLFQELSFIIIAAIAEVGTILC
QSEDFKQIIVSIIEQERRILESSDDQVISYHAAQIKFCNAINLMTIFFVIITGVFIILENA

WKRQQVEKYTNKFNNGSAEKPFIYELFYKFDPHKYSNVMMGVNYLMLLTNILLIIS
TKIVFVSCIIFASSSLRKLQVGFKKTVSISTRVLDIRQHQRVIRFVKKLNESIRYMIL
MEYLLNSVNVAAVSIQFIAATNTGNSHSYYIQYRDHKNLETQFFYAAGSNCTKHSE
LSKYSMIFVGVWKLKLLPKNVMCRSVYDIYSAFVRIYYPLFISSLCI

>CforOR6

MFLHQPCGIRPPTYFLCTTLKCLNQILHRIFTAKGLKFSSWQSVLGLKLSNELRVAE
RMCKIQDVLEPSILTLPKYFMMSAGIWKLDLPTSNYVYRRIYEIYSAFVRIYFPLLVS
SLSIQFVISIGNDKSLDDIFKELSFIIILAIAEVGAILCQGNAFKHIMSSIIDEERRIHESG
DDDVLRYHSAQIKFCNAVGLTIIVFVMGTATSIGLENIWKRLEVEKFNKEHNESAA
KPFYIYELLYKLDPYKYPNFMLFVNYFVLYVNAFPIISTKIIFISCIVFTSSSLRRLQVG
FRKTATTSTRVLDIRQHQRVIRFVEKLNDSIRYMILMEYLLNSLDVAAVSIQFIAYE
QGIPISPLTYFLYLFVQTFALGWSANEIQIQLALGDALYDSPWYEQNDQAKRLILS
MIVRSQRPLALTIGPFDTMTTASALRIMKASYSYVSLMIN

>CforOR7

MNASRTHRPSILNFSKCFMIVAGIWRFLHDPLKIYPYSAIVQSYFVVICISLAARFA
LTLASGVSNKSSEEMFKQASYIITVIIVEYAAILYQSGPLKRILSYIMEEERQMLQCT
DPEVSRNHFEQLGFCRKS NFIMFIFTCGSGASIALENVWRQLQVHKYNARFNTTLPR
PLPLELSYGGWDEEKHFALLLIAHDVWVVISMFLIVSTKTIVFSCVIFVPSILKRLRV
KLGKLAESGLRDLVREHQDVIGFVERLNNLSKYLVLLEYILNSLNVATVSVQFITY
DPKMLPAPAFYFSFLIAQIFILGWSANEIREQSLALSDALYDSLWYEQSETVRKVLL
AMMVRAQKPLALTIGPFEPMTTQSAVTVIKASYSYVTVMMSYE

>CforOR8

MCKFFQGREILKLSRYSMMLLAGIWRLPWTKSSSLNKVYRFYSAIQIYFPLFLTSMT
VNCAQMLRNKDHSQTVFRSFAMMITLFIVEVKAILFQTASVKRIIAQVMDEEKSILD
YDDREITRNHSNRVRFRCRKS NFIFGFNFSSGVAMIAGNIIARFQIDRRNEMLNATT
AKPFIYDLYYATLDPEEHPTFLIFVNYVSLSVAGFMISTQVVFVSCIVFAASMLETLQ
VKFKKPAGFKDDASLRRLISEHQHAIRFVEMLNDSTKHLMLLEYLLNSLNVASVSI
QFLVSENASLAFPIHFGLLLVQIFVLAWSNEIKVQSSGLADAIYECLWFERTEYS
KLLLLIAIIRSQRPLVLTIGPLGAMTNESALTIMKASYSYVTLMANSYR

>CforOR9

MLLAGIWRFPWTSNVLLAKVYQFYSAIQIYYPVFLTSMSVGFAMMLGEQVYSVS
VFRSFGMMITLFVVQVKVILFQTRGVKRIISQVMEEERPILSDDDGQIIRNHSKRVR
CRISSMAIFGFNLSGVAMTSANIARFQIGRRNEMLNETTAKPFIYDLYYPALDPQE
HPTFPMVVNYISMPVAAFVSTQVVFVSCVFAASMLETLQVKFKKSAGFEDDAT
LRLRISEHQHAIRFVEKLNDSKHLMLLEYLLNSLNVASVSIQFLVSENVSLAFPIF
HFGLLLQIFVLAWSNEIKVQSLELADAIYECPWFERSEYSKLLLLVAIMRSQRPL
VLTIGPLGAMSNESALTDTEISVLPNAMLLAGIWRLPWTSSVLLAKIYQFYSAIQI
YYPVFLTSMSVSFAKMLGEQIYSISVFRFLFGVLITMFVVEIKVVLVQIGSVRQVIAQV
IQEKLIFDSGDARIIRKYSKRQVFCRIYSMAIFSFIFSSVAMIWTNIMARQRTERHN
LMFNESTVKPFMYDLYFPSLDTDKYPTFPMVVNYLSIPVAGFMISTQVVFVSCVVF
AASMLETLQVKFKKSAAFEDDATLKILISEHQHAIRFVKNLNNSTKYLLILLEFLLNS
VNVAFVSVQFLVTKPGAPLAIPAIHFAFLVQVFCLAWSANEIKTQSLELADALYEG
LWFERSENTIKKLVIMITRAQRPLVLTIGPFGFMNESALTIMKAAYSYVTLMANTY

R

>CforOR10

MTISHRRSEILKLSKYSLVVAGVWRFSWTKSPSLQIFYRFYSVLIQIYYPACTSLAT
RFAISSVRETPSDISTFFRTFAMTITLTIQIKVVLVQFQTRAVKQIIRQIMDEEKSILGSN
DEEILQRYSQVALCRIWNLAIFWLIFGSGTGMLGNVLQRLQTKESRESNRTIPKP
YLYDFYYASFVVEEHSTILTLVNYAYMVVSGCMISTQVILVSCMMFASSMLKTLQ
VRFKKASCYDADILLTLKRLVMEHQHVIRFVKLNNSTKHLMLLEYLLNSVNVAS
VSIQFLVTKPGASLAFPACHFGLLVQIFSLGWSADEIRMQVRHFASKFSRVSLNLS
KSLGLADALYESSWFEQSENAKRLVLMITRAQRPLALTIGPLSAMTNQSALTIMK
ASYSYVTLMANSYG

>CforOR11

MANLPPQILRVSKYCMVVAGTWRLSLASRHEVLQKIYSLYSACARAYFPIMLTSM
CLQTVREKSTKSTEEMFRILSYIILLFIVQIASLMCQTGKFQKVLVRVASEERSILNSC
DWNLLRFHSRRAQFCRTFNILFSTSGAVVCIILENWFLRRSIDRHNVLYNESQDK
PFAIGLYSHSLDRERHATLLVAINDLCLCMNTFAVVSTKIVFISCMIFAPSMKKLQI
EFSKLNHRDSDVVSCLKMLVVDHQEVVGFVETMNESVKYLILLEYLLNSLNFVAVV
SLQFISFETKLLPSPILFFYTLLVQTFVLGWSANEIQVQSLAIADALYESLWYEYTER
AKKMLLIMMRAQKPLALTIGPFDAMNTGSALAIMKASYSYVTVMIDG

>CforOR12

MPINKPCTTLRFHHISKTMTTILTLKCGMIAAGIWRFPVTTRPSFQILYALYSICIQV
YLAIFVVSVMVIRFAILSIHENHPTKESVDLLFTAFAYLISFLVTQIKAVICQTKPLRRII
CYIIIEEENLSNSGDEEILAYHRRQIALDKKINWAIIFYFTALLGSAIVSNAFLRVSIG
QLNSASNSTVRRPFVYELYYYKVDTEKRASILVILNAFSVLVAILMGVSTQSIFLTCI
IFASSVLKALQVKKLKMVSGDNDMAVTLAHLVKEHQRVVRFIKQLNEAVKHLML
MDYFLNAMNMALVMLLFLEAETGMQFASCVFYSGRMMVIIFALGWTSNEIKVQS
QGLADAIYESGWYERPLSVRRLHMMILRAQRPLALTIGPFDEMTIQSSLTIMKAA
YTYGTVMQMOKYQRE

>CforOR13

MPEVLGFAKYTMIGGGIWRAPFSKNPLVRKTYSVYSVAAQMYFLTFTLLFCTKVIV
IIREKIAADILFRVLSYTLSLIIAQAKSLICQTRRVKQIFTYILEEETKIVGCGDDEVLD
RYARRVKVGNHINLAIFSFTSALGLGAIENIQNRLEIGAYNLAHNETLRKPFLEYF
YYGQLDTEENSTALMWNLYCTVIAAIVCISTQIIFLSSIVFVASVFETLQIRFGKLV
DASKDTVATLKSLVVQHQRRAIRFVEELNDAMKYLMLMEYVLASFNIASVLIEFITE
KELTAMFLFGRSCYSAWLITNIFALGWTSNEIRVQSAQVANSIFETRWYEQSEEAK
RILFIMLMRSQKPMVLSKGPFGDMTIETSLTMMKAAYSYVSLMSQEYK

>CforOR14

MLKLSRYSMTVAGIWRSPFPYNSIYQIYSSFVRICYLISLALMYAYLFDIFAAGGTAI
DEPADFIFTCIAYLISLTVVQIKAALCQSDKFLRLLRRIQEAEDDLFRLNEPEIASFHS
SQVRFARKINLVVFFNFCTAELIIANLFQRTAIEEHNRFVNTTLEKRFVFWYGYGS
IDTEAHEMLLLVVNGFSLTLAACMTFATHCVYFSSTFFASSLLGALGIRLKKAAASY
AEDGLVRLIKDYQDVIEYVQYLNASTKYVLMMDYALNSLNMALIIFLFLKVDTYA
QWLSVVSYAGYLMTNIFATGWAANEIKMQLRLSDAIYESSWYNYDKELKRHLL
MVMIRAQKPLVLTIGPFGEMVLQSSLTIMKAAYSYSMIMIYKY

>CforOR15

MKVVHRSILNFSKYCMISVGIWRPLPTNINVIRKTYAIYSIFVTIYIPLFLTSMCIHFI

LALVSQNETLEDLMKEFSYIIITLMTETA AAVICQRNNFKGIIAYVLDEENNILNSGED
ETLHHHTQQKFCYNVNL TIFVFPIC TAASIVIENASVRSQIGQYNREHNDTLDRPFP
FELYLYKFDKNKHQAAMLLVEYVSHWMIIFRIISTKNIVVSCVIFTSPILKRLQVRFK
RMSMEEGGTFESLKDLISQHQNVIRYVSDLNHSIKYVIFMEYLLNSLNVA AVSVQFI
SDKLAISPLFYFAYLFIQT FVLGWSANEVKVQSEALGDALYESLWYEQNDRVKRMI
LYMIVRSQKPLALTIGPFDAMTTASAVRIMKASYSYVSLMVN

>CforOR16

MMNIVDRRILNFSKYCMIFVGIWRLRLPIESNTRKTYEISIFVKIYMPLYLLSMCI
HFILAVGSKNETLEDLMKEFSYVLVSLITEIVAVLCQKRTFKQIISYVMEEEKDILNS
GEEETLYQYKRNLNFCIAVNLA VFIFPVCTAASISRTQRHVGGTFFVPLYLYKFDKN
NHQIIVMFVERVWQVLVVVRAISTKNIVISCIIFTPSILKRLQIRFRQLSRQEGDTFEL
LNDLISQHQKVIRYVSELNDSIKYVILLEYLLNSLNVA AVSVQFISNKLAYSPLFYFI
YLFVQTFVLGWSANEVKVQSEALSDALYESLWYEQNNRVRMILYIILRSQKPLTL
TIGPFDTMTTASAVRCRRIVGLDTVFYFHNYRDGREKCIRISAEIFPVIMILCGELYIV
VLIFETSVLAGLSPLQPSFYLLP THEIANCEYIRIYELAIK YLSQILVVLRIISTKNIVIS
CIIFTSSEALSDALYESLWYEQNGRVRMILSMIVRSQKPLILTIGPFDTMTTTS AV
RIMKASYSYISLMVN

>CforOR17

MNHARPHQSILNFSKRFMMTSGIWRLPTINCPTIAKIYAVYSTTIQTFYSIVAVSFGI
QFASTFDKFAKNSEAVFKEASYIITLVIIEYASIVCQRKNMRNIMTFILHEEHIFEN
EDEDVRKTYLGHFKFCWKSNAVLF AFTCCSGAAIVLENLVLQLEVHKLNRELNET
RPKPLPLDLYYWQFDPDKYDTFLLIVHDVWLTNTMFLIVSTKTIVFTCIIFAPSIMTR
LQMKLNTLKEGEVWSSVKKLAREHQKIEFVEQLNDSIKYLILLEYLLNSLNVATIS
VQFITDDKMIAGLVFYLSFLVQTFILGWSANEIKLQSTALSDAMYQTSWYNQSR
YIQKMLLTMMVRSQKPLAVTVGPFEAMTTQSALTMKASYSYVTLMMNNYDKR
YQL

>CforOR18

MIPTFLNRSILNFPKRFMVVTGIWQPVWTTANPKLRKLYAVYCAFVKLYFMIFVTC
AFAEFALTLTKNSTSRMLNQLSFVIPMLTVLYAML VCGTDNFRRVISYITEEETHL
STCDDEEILKLHSRHLRIGK FVSTILVFTVASTGTAIVLENLYRNLPTLKRSSGGNDTI
EVDTIFDVYYFGIDKSKHAVAFVLVNEIVCVFNTTLT LAVKSIMLTCMIFAALSA
LRIRFRKVDKEDVGLSLKHLIVQHQRVIGYVDDLNDLVKHILFEYVFESLTVAAV
SVQLATCEPKLMPPTASYLCYLLLQILMLGWTNEIKVQSLALSDGLYESPWYRQN
ESSKR VLLVMTRLTQKPLTLTIGPFGAMTMSALAVIKGSYSYVTLMKNNYK

>CforOR19

MTGSERPQNSILD FPKRFMVVTGIWRASSITRNSAAQKAYIAYSVFVKFYCTLFVAS
AVIEFTLSVLSSENSIEFRQLSYIISMLTTL YATMVCDTINFRRIISYIEDRGNRLASCGD
EDILKLHSRLMKTGKLVSTALGLAVASTGSAVILENIWRNVIAIAYNSGGNGTAEI
AFILDLYYFGLTTRKPATAFILVNECLSVFNTILTLATKSITLTCMIFASYALQEIQR
MRKIGTDVDVDLSLRVVSQHLDVIGYIHDLNDLVKYLILFEYLFESLNVAVLSVQ
LAAYESQTLSSASYLSYLLLQIFMLGWTADEIKMQSVALS DALYQCPWYEQNESS
KKVVLVMIKLTQKPLTLTIGPFD SMTMQSALAIKGSYSYVMLMTNGYQ

>CforOR20

MVAKQAERSILD FPKRFMVVTGIWRTSSITPHPTMQKVYVAYCIFIKLYYTLFVALL

IEFGRSLASTNSVEFRQLCYIISTVTIFYATLVCDTVNFRRLLISYIEDRVSRVAGCDD
EEISILHSRQLKIGKLVSTILVLTVA STGSA VVFENIWRNVVNMKYYSGRNETADIV
SIVNLYYFGISRRPKIVFVVFVDEFLCVFNTTLTLATKSITLTCMLFASVALQELQIGFR
RIGSDRDVKNLMEQVISQHRELIRYVELLNMMVKYIILFEYVFESLNVA AISVQMTK
SESQTLLSLALYLT YVLIQIFLLGWIANEIKIQSVALS DAL YESPWYEQNESSKKVIL
VMIKQAQKPLTLTIGPFDAMTLQSALAIKASYSYVTLITNSY

>CforOR21

MADTRTERSILVFPKRFMVVTGIWRASSITSHPTMQKVYVAYCIFIKLYYTLFVTSLI
TEFALSVASTNSVEFTQLSYIISALTMFYATLVCDTVNFKRIISYIEDPVSPLARREDE
EISKLHSRHLKMGKVSTILVLTVA STGSA VVFENIWRNVVNTKHHS GTNDTALSI
ANLYYFGIFRRPKIVFAFVEDFLCVFNTTLTLATKSITLTCMIFASYALQELQLGFRI
GAERNVKNLNEQVISQHRNVISYVNLNRMVKYLILFECVFESLNVA AISVQMTKS
ESQSFLSLALYLSYVLIQIFLLGWTANEIKIQFILHSQSVALSDALYESPWYEQSESIK
KVILVMIKLAQKPLTLTVGPFAMTMQSALAVTHLYEKFNFSTVPTGMFNSRSSRH
LIRMLL

>CforOR22

MARSFLKFSERIMILTGIWHPALITGKSALQKLYLTYVFKLYFALFFTSASMELF
LSVGPGRSSPRLFKQLSYIIPSLSIFYAKIACGT VNFRRIVSYVKEKEKLCFCEDENI
SNLHSRCYRIARLVNMILITVA STGIA VVLENLWRNINTLPFNSTSEIVSIIELHYFGI
SRKPAMVVFVLL EEFMCVFNTTLTLATKSITLTCVIFAGYALKALQIKFRNIGQDGDV
NSSLNHVITQHQDVTRYISRLNVLKYLILIEYVLES LNVA AVSVGLVTNGSQT VLS
SVSYLSYLLQIFLLGWTANEVQVQSIALSDALYECSWYEQNESSRKVLLLMIAFT
QKPLKLTIGPFDAMTLQSALTVIKGSYSYVTLMTNN

>CforOR23

MPILKRLQVRFGKWEADDAGLLTLLKEFAKQHQHVIRLIKNVETSLHQDLSVVLSL
VQFTISTINGKDADQMFGQLIYVIAVMNGGIGALLYQRVDFKEIINYITKDDKDVGF
ITKLNKSIKYLIFMEFLNLSLNIAAVSIQIFTEKTM LASPILFFGILFTQTFVLGWSAN
EIKVQSLMLADALYRSPWYEQNETVKKMVLTMIMRAQTPLVLTIGPFDAMTTQSA
LAIMKGSYSYVSVMLNNYQ

>CforOR24

MTTIKRRSIVSFSKWFMSVGMWTLDDLPTRNALCKVYALYSIFISFYFATFVSSICI
QFAITLTTQTTDLETFKQLPFVISLLITHYVTVIRSSKFTEITNVVNEENLISISDDED
ILNSHLEEVRFNDALSAIFFALTACTGATLILENFWHNMEVARYNREKNVTLDRPIL
LHLYYFNVNKRKHETLVLAITEVALVFNTLIIFSTKVIIFTCAAFASSALKNLQIRFR
VGLRCD DALTNLKL LIVEHQGVIEFVKNLNESIRYLLLLEYLLNSLNVA AVSVQFLT
YNRQMLLTPAFYFCFVLVQIFILGLTTDEIKVQSVALS DALYDSPWHDQHNLRRIL
LIMIARTQRPLRLTIGPFNAMTMESALAILKASYSYVTLMKHGYQ

>CforOR25

MAATAKPKSILSFSKFFLLFVGLWKLELPFRDPAAIKIYGLYSVFNAVYFATLALSIS
IQFGISVATKFFEPDTFKQLSFVIVILTTYVTVL VIRSGRFTDLVARVEQEEKLMYC
ENREILLFHLREISFSNSVNM AVFILCLCTAATLLWENFTSNMNVASYNAKHNASLE
RPILLDLYYFNVMHKHETLVLVVNEMVLGFNTFVIVSTKVIVYTCITFAASTLKCL
QIKFRKGLRQKDALINLKV LIMEHQGIAEFVKNLNELIKSLLLLEYFLNSLNLA AV
SVQFLTCDAGMLVTPIFYLCFVLLQVFILGLTTDEIRVQENYQQLALS DALYDGP

WHYQNEEVKKMILIVLTRTQRPLELTIGPFNPMTMQSALAFNLDINSLAKALTDTA
FSISYEIIQNRFLPYIRETTI

>CforOR26

MATIAKSKSILSFSKVFLLSVGLWKLKLPFRHPAATIVYALYSTFITLYFATLAVSMS
IKFGITLTTNFADPDIFQQLSFLIVILTTHYVTVVIRSDGFIDLISQVEREEKRLMRSEV
GEIVNSHHKEIRFSNVVSATFVVLTSCTGASLIWENFRSNMAVVGYNRKNNASLER
PILVDLYYFNVNKLHHENFILVVTEIVLCFNTLVIASTKMIVYACITFAASALRCLHI
RFVKILNEFIKFLLLLEYFLNSLNCNEYFQQEARLLLIPAFYLCFVLVQVFILGLTT
DEIKVQSLALSDALYASPWHQQSEEVKKMILTVLTRTQRPLELTVGPFNAMTMQS
ALAEDAKKLSIPAFSLCFVLGQIFILGLTTDEIRVQSLALSDALYDGPWHHQNEEVK
KMILIVLTRTQRPLELTIGPFEPMTMQNKTANYFAFQILKASYSYVSLMAQTAQ

>CforOR27

MATIAKSKSILSFSKILLIAGLWKLKLPVKHPAIIIVYALYSTFITVYFATLALSMTV
QFGITMATKFAGPDTFKQLSFVIVLIVTYIITLVIRSRSTDLVARVEIEEMRLMLE
DDEMLLSHLKEIRFSNVVSTTFLVLTIVTGATLIWENFWSNMKVVTYNRVHNASLE
RPILFDLYYFNVNKHKHEDFVLMVTEVVMANFNTIVVSTKGIVYACITFAVSALKC
LQIRFRKLGIRQDRALADLKLHVVEHYRIMEFITNLNGVIKNLLLLLEYFLNSLNLAA
VSVQFLTYDPKLLLAPACYLCFVLIQVFILGLTTDEIKVQSLALSEALYDSPWHNQ
EEVKKMILTVLTRRRPLELTIGPFNPMTMQSALAILKASYSYVSLMAQNSQ

>CforOR28

MAAAPKRRSILSISKIFLLSVGMWKLELPFRHPAAVKFYVSFVKLMPGYFAMLALS
MSVQFAITLTTNFSNPDLFKHLSFVIIIGTAYYVTLVIRSDGFVELISRVEREEKRLAR
SEVAEILLSHLKVIRFSNAVGTTFALSICTGAALIWENFWSNMKVLNYNKKYNTS
LVRPILIDLFFNLNKRKHETLMLIVTEIMLVFNTHVVSSTKVIVYTCIMFAASALRC
LQIRFRKLGRLQEDALADIKLLIQEHQEVIEFVENLNKSIKYLLEFYLHSLNVAAV
SVQVLTYSKMLMRPACYLTFVLVQVFILGLVTDEIKVESLALSDALYDSPWYNQ
NKTCRKMILRIVMIRAQRPLELTIGPFNPMTMESALAILKASYSYVTLIAQNAQ

>CforOR29

MWKLQPIEYRIATKIYAVYSAFINIYFPTFVASLCIQFAISVSSDFDQDMFKQLSYAI
SLLITYYITLVTRGDRFTEIVAQVIEQEGRMLRSEDPEVLGSHLNEVRDDWRILLFFF
TFTIGTGLTVILENFWYNMEVAIYNKKHNTTLERPITIDLYYFTMNKRKHETLVLIIT
ELAVIFNTVIIFSTKAIVFTCIMFASSALKELQIRFRKVGSCREDPWRKLNLDLVVDHQ
KLIEFVRKLNVSIFLVLEYLNSLNMAAVSIQFLMSQNKTLTPAFYFCFVLVQVF
ILGLTSDEIKVQSLKLSDSL YHSPWYNQGRVKKNLLIVIARAQRPLELTIGPFNP
TMESALAILKASYSYVTLMMHGYYQ

>CforOR30

MLEGTGNMAADSGRHSILTLARYSMTSVGFWKYHSQKNPLKLFYSTYSGFIVLYF
MTYTISVGIKQVITVSAASTVDSEIKQLSFISSLIPMYVVMVCRSSGFNEIISLVRREE
QSIITSDDADILKSHLKQIRRSNAVNGIFSACCTGFAMALENYRPNVKVARYNRE
HNTTLERPLLVDLYYFKLNTQKHADLLL VVSEICFIFNTLILSSKLCVYTCVIFTSSL
LKKLQIRFSKTGLRQEHKLAALKSLVMEHQNVIEFVDKLNVSIRYLVLELYLLNSL
NVAAASVQLITYDKKMLLMLFFYVSFLLMQVFIMGISANEIKVQSITLSDALYSSPW
HEQSEATKKVLLIMIARTQRPLMLTIGPFGPMAIESALAVCKASYSYVTLMMQNVH

>CforOR31

MHCAKPSCCNKSFVVTHTMAIGTKRQQSILTLAKYSMTLVGFWQYPSQKYPLKL
LYSIYSAFFVIYFMTYTCVCIKFAITLTTASTFDSEIHKQLAFTLSILMTMYVVMVCH
SSGFNKILSYVNEERSILQTEDFDILKSHLQQIRNCNNLNAIYAVFTFGTGFAMALE
NYLQSIEVARYNSDRNTTLERPQLVGLYYFGINPYKHADLLL VISEICILFNVLIMLS
SKLGVFTCVIFGISLLKKLQISFRKMGVDRENALAVLNRLVDDHQRVIAFADKLNA
SIKYLILVEYILNSLNVA AVSVQFITYDKKMLLLPFFYLFFLLIQVFIMGIGANEISVE
SVNLSNALYFSPWYEQSEAAKKVILIIIARTQKPINLTIGQFRPMVIDSALAVRHMAA
GTKRHPSILTFARYSMSSVGFWKYPNQKYPLKLFYHFYSAFFIFYVVTYTVSACTQF
SITLTAASAFDSAMIKQLSFVITILISFYVIMVCHSKTFNKNISHIVREERSMLQSDDA
DVIKFHLQQIRNCNAMNAIVSILAFGTGFAMALENYLINVKVARYNKDHNNTTLERP
LLIDLYYFKIDKHKRADLLL VFAEMSFANTLIMLSPKLSIYACVIFTSSLLKQLQIRF
SKLGLGREDTLTSLKHLVREHQIIAFVIQLNASMKFLILLEYLLNSLNVA AVSVQFI
TYEKMLLMPCFYIFFLLVQVFTMGISANEIKAQSLALSDAIYSSPWQE QNESVKKI
LLVIGRTQRPLMLTIGPFGPMVIDSALAICKASYSYVTLMMHNVQ

>CforOR32

MTELP SILTPAKIFMTSVGFWKYPQKYPKYFYKLYSAVVFYFFLCAICLYIKFII
TVSTTSTLDPDINQLAYVISYLMTTYVIMVCRSASFNDVIYDIAVEEQRMLKSGDD
DILKSHLQHRRDNYINFLFAIFTIATGFALAWENYQQNIVIARYNRDHNNTTLERPLL
VQLYYFKINKHKRANMLLVASEISACSVLMILASKLSLYSCIIFASSVLKMVEVKFR
KIGLGENPLAVLKRLVKEHQRVIAFVYKLNKSIKYLILLEYLLNSLNVA AVSVQLI
TYDKKMLPTPVFYLCFLLIQVFIMGISTNDIKIQLALSDAVYSSPWHEQSEATKLL
LTVIARSQTPELLETIGPFGPMLIESALAVCKASYSYVTLMMHNVQ

>CforOR33

MVDHQ SILTPTKTFMTSVGFWKYPHQKYPARYFYNLYSALFVYFSLYAMCLYIK
FIITMATTSTLNPEVIKQLAYVISYLMTTYMIVVCRGASFNDVIADIVLEERRLMAY
GDGDV MKSHFQHIRWDNWIILLFAVFTIGTGFALALENCLQNVERARYNRHNTT
LERPLLVELYYFKINKHKRANLLL VASEISLACNMLMILASKISVYTCTIIFASSILKIV
QIRFRKMGLGQADTLTALRRLVGEHQRVIGLFEIPIRHQRLILIDRERIINYEWVANE
KNAMLNFPKFFMTGIGIWRDLKIRYAVLKKLYALYSVIMQAYFLVFMCSLDLEFF
LTCTNDKNPSELFQQLSYVIALSVVTITSLWQKEEIREIIHMLEEEKTIAGSEDEPV
LDTYLNQVRVSGKINVAIFSLSGVALSILLETWRRQQVNKINATRNETLEKPFPL
ELYGYDFDRERYSTLLLVTQGAACFSINFMVTATKVMFFTCIAFASMVLKTLQIK
FRKYGSRNHDPSRELTALIVEHQRIIRFVTNLNESMKYIVLLEYLLNSLNVA TVSVQ
LIVFQTKAASPIFFLGLFAQIFVLGWSANEIKVQSAALANALYASRWPDPQPEFAQK
LILVMIVRSQRPLELTIGPFDAMTTQTALRILKASYSYITLMKNNYDQ

>CforOR34

MENRQILALSRYGMIVAGIWRLPFTSRAAVRKFYALYSAFVHVFFAAAFVASMLLRF
LILVAEKSSAELLFGSFAYLISFYITAIKAVLCQSSEFKRILSYIVEEERMAMSDNQE
LFRCHLVQIRFAERINLGIFSITVGLSVSAVMANAMQRANVEEYNRSYNASLEKHF
VYELYYAKVNTEDHERLLAILHAFTTAWILFVGSSTQCIFITCIVFASSVFKTLQIKL
RMLSTEDALKNLRSLVVEHQNAIFGVKLNSSVKYLMLMDFLSSLNIGLVLILLR
AENTTQFTTSFYACRLITIIAIGWCSNEVQIQSLGLSDAVYESPWYEQTEDVKKILL
MMIVRVRKPVALTIGPFDEMTLQSSLRIMKAAYSYCGIMAKKYN

>CforOR35

MFARELTISGHPHVVTNADDERNIYLEGSMPLFQKQSQNLVKVAPAPTDIFYKTELR
GGKINAFENESYEFSIVINYLPVLRTRLRILGLLPVANSDRGYFVTIHWIVYSVLLLL
FIMGYTAFIQLHKVEEAKAGEGRFEEAVIDYLFTVYLIPIVTNVIGLYEAKKQAEVL
NQIISFEKIYNSTTKKKLDLFLANKPLLLSIALPIIGSGIMVVTHVTMSNFVVKVIPPY
CYINVVTYMLGGAWYIYCNIIGKVATIIAEDFQQALKNISSIKIADYRSMWMMLS
RIIRNVGNSFGYALLFLCLYLFFVVTLTIYGLLSQIQSGMGTKDIGLTITASSAVMML
YFICDEAHYASACVRTNFQKKILLVELSWMDDDSQQEINMFLRATERNPTDMCLC
GFIDVNRNLFKSLLATMVTYLVVLLQFQISIPDDSLPDNNNTTTT

>CforOR36

MLASKDDAIVRNYLSRVQFCDKCNRIMSVFMLGAVTSIMAQAIWKRREVSEYNVR
YNTTLELPLPFKMYFNLDRKHPKLVFVLNFLAIPINAINFLSTKSILYSFVLFAPLT
WKQLNFRIRKISVRDDGVSSVFENYVSEHQEIIFSTDLNDSVKYLILMEYLLDSLIV
AMNSMQFITFPFCLGRNKHIQKQPSGAKRNQLESTGLSRDDKQEISTDKSISESQS
WGNITPQTKMEDKEVSRSAVWDKNSDQEKESQRSATPSENTPESLRWGNNSDQD
EIDENFSSELQEDRKKLIVFKNIYKEMLEKDNDNEVSQEFWRVENITKTQRKNTR
HQLKAVTKIDSTDHYEGDKVILGKNGTKVSKTLFATINWSKYTSATRRLLSAFFSR
KVMATHSLTGKPSAFLDTKEAKLQLDPLIVGDIIEIVCRKCNVVKSEVRGAITSKC
ADENKLYKKSERLKCKS

>CforOR37

MTLAGIWKLELPDPFQSRWLYPIYSITIHAIYVSLPLLLAFNFPYLLENDPGEANES
LSKILYGVLLIAKVLSESESSKCLLVRAIREEAALNQYGDNFAKRIYQEHVLFENR
LNKFVVSATVAVFLWEVGKYSKTMPSHSELFRFARIAMTLAGIWKLELPDPFKA
NESLSKSPYGILLIAKLLSYQSESAKCLLVQAIREEATLNEYGDDFVKRIYEKRMTR
CNRLNKFIFISATVVVFLCEVGIPLKPREVENAFVILRMAPHLEIFRFARITMIVSGI
WKLELCPDFKHCSRVIPIYSVMVHVITYTSFPLLLLINFPHLVKNDPSEAMETISKILY
GILSIVKLFYSQSESSQCLLAKAIQEEGHLNDHGDDFVKRIHELHVSVCNVFNKIL
MSVVFVGGSVLCEFGIADSYKFHRLPKNESVNVAKPLPLPFWYPFDENKHHVWVLV
EQLLTIVWCALLFISVQIFSNSALIYMRGQLKILQKSFKEFHQNMVEGDSNSGLTAL
KHICVKHQNLIGYINTANRAFRSVVFFEYGISSAMLATALFQVAVAGRVTTNVIHV
SVLTSQLLLLAWSSDEIVAQSLELAPAIYQSNWYECDKDSRILIRIMLMRCQKPLSID
IGSFGAMTVRSAMSELFRFARITMTLAGIWKLDLPPFEWISQVYPIYSVVVHVIVY
ASLPLLLTMNFPYLLENDPIEATESLSKILYCVPLIVKLFQSENSKYLIIGANAEEA
RLYQNADNFVKSIVHEMHVLYCNRLNKLILMSVAFAGFLLCELGIVDSYKFHKLKLVK
NESKIMVKPLPLPFWYPFENENKYHVWVLTEQLLTIVWCAISIVSVHTFSNSVFIYTR
GQLKILQSHFSNFHKNIVDGGNGVVGLKELCVKHQNLIAAQVYGVVEKEENPVKAK
TRLSTVWTTFFLELWARATDRFLTRHDVVDMTFFNLSKKHLEAVTKKSK

>CforOR38

MDGEYELPPLGQHSFKTSHRKESAILRTMSHSELFRFARIAMTLAGIWKLELPDPFK
GFTRIYPIYSIMLLVVNLPYLLKNDPSEAKLLSYQSESSKLLVQAIREETTINQYGD
DFVKMIYEKHMTRCNRLNKFIFISAAVVVLLCEVGIAESYKFHRLRKNENQTLAK
PLPLSCWYPFDENKYHIWILIEQLLTIFCAGLSYINTVNRAFKGVVFFEYGISSVILAT
SILQVTAGGNITYKLTHLLGVTSQLLLLAWSSDEIVVQSLELAPALYQSKWYECSK
ESRVLINIMLMRCQKPLTIDIGLFGPMTVQSAMTAIRDEVDLLQNGDDYVMKIHEK
HVFFCNLLNKFFWLSTAGAASLLCEIDIQWSLKFTF

>CforOR39

MTLAGIWKLELPDALKGFTWLYPIYSIAIHAIYASLPLLLALNFPYLLENDPGEANES
LSKILYGVLLIAKVLSESESSKSLLVRAIREEDALNKYGDDFEKRIYQEHVLFVFCNR
LNKFIFVSAVAVFLLEWEAGITESYNSHRLRQNESQTFKPLPLSCWYFPFDESKVHI
WILIEQLLTIAWCALLFVSVHMFNSMLIYMRGQLKILQYNFSNFFENIVQKDTNDS
FPALQFLCEKHQNLIRYINTANCAFKGVLFYFEYGISSIVLATSIIQISAGGNITYKLTH
LFGVTSQLLLLAWYADEIVFQSLELAPALYESKWYECRKRKESRVLISMMLMRCQKP
LSIDIGSFGAMTVQSAMTRLKLAYSYSVMTK

>CforOR40

MRGGAIIDAKCRIAMILGTIWKLGTPQQSKAFPVVYQAYSILAHVIYVSIPLFLTMN
FPRLLKTDAGKGFETLSKILYCVSMVIKLFQFQSRSSSTSLAQAIRDEVDLLQNGDD
SVMKIHEKHVFFCNLLNKFFWLSTAGAASLLCEIGLVGSYRVHRMNKKNATLNK
PLPLPFWYFPDENKYHRWVLEQFLVILWVGFPVATVQMFSNSVMIYMRGQLKIL
QSYFSNYNENITYVGDNLKTLKGLCVKHQHLIRYINTVNSVFRSIVFVEYSISSIMLA
TALFQVLAGHNVTYNITHIFVIISQLLLLAWSTDEIVSQSVELASALYSSKWYECERE
SRILIFMLIRCQKSLSIDIGSFGPMTLRSAMSRLKLTYSYSVMTS

>CforOR41

MVYSMPILMVANFPSLLQTDINSAIEGASKMLYCGILAVKVYLYESHRCRDLLARA
LEESRLNAINDGDVTRIIYKEHVRYCHILSKLFYISTVTSSATLCGTAIINSYSFSKNG
DAVGNMPIPLLFWYFPDRNRHCIWVMAHQLLTVVVGNYALPVIVYYNSIMIYVR
SRLRILQHYFRNYDKYSMLNGGLTTLETLSKLCVKHQDLINYVEDVNRSLKNTVFL
EYLGSSIILATILYQVIESEENLFPNMSDSKELFHFARLSMILTMWRQDPPPFYKSV
NFLYRSYSIVLHVILFSPALMTANLPDLLRSDANSDLLSRAMEEESRLYSINDEDVI
RIYKGHVRYCHLFSKFFISTMVSSSTLCEIAIINSYKFSKNAEAVGDKPTPLLLWYP
FDKNRHHIWMVMAHQFLTMVVGNCYASAVYLYNSIMIYVRGRLQILQHYFRNYK
KYVFHESSTTTLETLRALCVKHQDLISYINDVNRSFKSTVFLEYSITSAILATVLYQVI
ELLVMAPNTKLFARITMILGTIWKLEMPHRKGRHIYPVYSMATHVIYVSIPLF
LTMNLPQLLKTDLGAELETLSKILYCVPLMTKLFYQSESSKLLSKAIKDETRLLQ
SGDRTVVNIYADHVFFCNLLNKFLWISAAGAGSLLCEIGIVGSYKYHKLNIENETL
PKPLPLPFWYFPDENKYHICVLFQFLVIVWCGLSVAAVQIFSNSMMIYMRGQLKIL
QNYFRNHHKYLSVNVVGNNGSLNTLKLKCVKHQYLIRYINNVNGVFRSIVLIEYSIS
SVMLATSLQVIAGHNVTYNATHISVITSQLLLLAWSSDEIVVQSLELSSALYESKW
YECERGSRLIGIMLMRCQKPLSIDIGSFGPMRIKSAMSRLKLSYSYASVMTS

>CforOR42

MSERMRLFHFAKLSMTVVCMWRLDRPPLSKFANLMYQLYSVVLRAILCSVPALM
AVNFPSLLNSDPNSVVKAYSQSNKCRDLLAKATEEESLYDIDDDDVTRIIYKEHV
RFCHMLSKLFYISSILSSSTLCAIAIVNSYKFSKIVDGVGEKPTPLLFWYFPDKNRYHI
WVMVHQFISILVASCYVLPNNVYYNSVMIYVRSRLRILQHYFRNYPQYALSGRLTT
LQMLNVLCVKHQDLINYINDVNCVSRDAVFFEYNVISVILATILYQVVQGDTLFN
SIFAFVVCIQMLAWTSDEIALQSSSLGAALYESKWFDQSQESKVLIGIMMGCRK
PLSISIGPFGPMTMLSAMSRLKLAYSYSVMTS

>CforOR43

MSLTVSMAVDIPNVLRTDPDKAIDSISKLTYCILLFAKVLSYPNISREILPQALS YERC
IYDQHHSATVEIYTKHVNFCHTLSKFFYVSTMFTGTAFSGFGIINSLQFHKHNTNSN

QTLNKPLPLQLWYPYDKNRHHVWALMHQVVSISVWTIFIISLQVFSNSTLIFLRSQL
KVLQNQFRNFKHVGDEHVLDRGRAVIKSLKALCVAHQNLLRYIQVVNEAFKA
TIFFEYAVISLILGMVLFQIIAGLEASLNSTFGFVVISQLMLLSWTTDEIVVQSSSELAS
ALYESKWFEQNKKSMLFIRFMIMRCQKPISIDIGPFGPMTMFSAMSRLKLAYSYTSV
ML

>CforOR44

MWFKFKESFPVNSFLKMESRKELFRFVIITLKLGMWRLDISHCSKLSAYFYMIYYI
ILTVISFYFTISMAIDIPYILRTDPEAAIDSISKLIYLALLLVKVVFYPRISKEILLQAMS
YERYIYMQNDSATLRIYSKHVKFSHVLSKFLCTTTLFTAIAFCGFGILNSYKFHRLQ
RHANNTLQKPLPFLIWYPYDENRYHVWALTQQSISMFLVLTNFIITTQIFNNCVHIFIRS
QLIIFQNYFRHFDQYWKGDNGSVVENLRRLCVKHQNLIAYVHGVNDAFKATVFLE
YAVISLILGMVLFQIIAGLDASLNSTFAFVVISQLLLLAWATDEIVVQSSKMSTALYE
SKWYDLRSQTMILINFMIVRCQKPLSIDVGPFGPMTMFSAMSRIKVAYSYTSVML

>CforOR45

MICLSLTVPMIAIHPSMLQTNTTAAIDITSKLLYCVLLFAKVVSYPYISEELLPQALCF
ERTLYSEGDSVALAIYAKHVRYCHGLSNFFYTSTIFTGTAFCGFGIFNSYQFHRLHE
SANVTLKKPLPLMQWYPPDENRYHVWALAQQVVSITVCAMRFDEHSCETGPLAE
GLKSLGIKHQNLIRYINRVNEAFKATVFLEYAVISVILGLVLLQVIAGMDASLNGTF
MFVVSSQLLLLAWTADEIVVQSMKLATALFESNWWYVHDTDELVGSIKFMIARCQKP
LSIDIGPFGRMSILSAMSRLKLAYSYSSVMVQKIRR

>CforOR46

MAILKGNRRIRDYFDYNRSFMKALLLEPPGSSKFDAIYTFSAIVHFSLVCMSSVLET
LALYFSPYDDFSSAMLNIGILSLHLVSVNRVLGWFIVRKKFHAIVDVVKRSSFLENW
DDLRRFKTEKMAAAKIRSLLSGCYGLYVFLNITLSYFNYHERTYEKFNPALNKT
SVYRKYVYPLWYPPDTSLSDGYYMVGFLYQPYAFYSLVASFCCIDCHVLNTILHLK
CQVEVVGRAFNMDGAVGDDRNSQCRIKEIRVVQCIQELQMIYRAARRIEDLQST
QFLIQNGLAVFIMCANSFRVTSSMIKVDLEAESIFLSTMIFVVMMAEVFNTCWYCYGF
TLELLNLPARIYEMDWLSYPVPLRKKLLFCSARLQPPFYFSLGKWTFTMGMYITIL
KMSYSFYTVIWRTAPE

>CforOR47

MCKVRNAKDAPILLLSKYFMVCAGIWKQLPTKNGVFCVYGIYSAFVGIYFPLFV
SSLCIQFVASIGTEKNLEDLFQQLSFIHFSIAEVGALLCQSKDFKQILSSIVEEERQILM
ATDDEVSRYHATQIKFCNAINSMIIVFLGTGTSIILENFWKRRQVVEPYPNECNGSA
QKPFYELYLKFDPKYKPNVMLSLNYFMLFINVLLIISTKVVFVSCIVFTSSSLRKL
QVFRKTSATSTSLVELIREHQRVTRFVGKLNDSIRYMILMEYLLNSISVAAASIQFI
AFEQGFPIPLLYLVYLLVQIFALGWTTNEIQIQ

>CforOR48

MADCGGIQQSFKLHKSNGTHVEKSLPLSMWFPDENRYHALALTYQIVELFWTAL
FTTSLKLAEALYESRWYDLNKRIKSILYFMMLKCQSPLGITVGPFGMLTTDDAKS
TTRHASGEIDTMKGRRLFEMTKKLMISGMWRSKLMEGSHLTKTLYLAYSILVQFL
YATHLLSYIINFYLLYSENFDDTIENISKMLYVMLLILVKVILCQSRGLMELVEIAGSE
EVSLENSGDVSMRMIYGYHRKQFYKIMYTIVSYTVTLFFKLSILGIQNSYRSNKLYK
HVNETVGKPLPLSMWFPDENRYHYLALTYQVVQLFWTALFTVTVYAVSNSLAIF
LRAKLIKQHLRNLNSNPPDDENELKMLCLEHKAISWSGRLNSSFSWLILLEYSL

TSLMLATVLVQIHEGNDEIFHTVYFFLIFCQLLNICWNANEIKCESLELAGALYESR
WYDLNQRVKNLLKFMMLKCQSPLGVNVGPFGLTTDDANSRLKLAYSFLSIMTGR
S

>CforOR49

MKGTGLFDITRMLIISGAWRSGLPKVSKLLNVFYVGYSAVIQFSYFLYFLCYAVNF
YFLYFEDFDKAIENLSGNTFVLLLVAKVLLCQKNRLISTLKQAHREELDVYREEDR
SVREIYEHHLKYFYKLIFTIASYNGIVLLKLYIVGIGGSYQFRKIHRHDNVTLEKPLP
LPLWYFPDHNRFHVVALTFQLVALVWSALFNTMVYAVSNSLAIFLRGKIKIFQYRL
RNFDRCNLYVNRDDSGSLLEVCLFKKLCREHQMIRMTRCLNASFRSLFLLYESLT
SLLMGAVLVQIHKGVDLFFYVTYFFLIFCQLLNICWNANEIKYESLELVPALYESN
WCERSNQVKTMIKFMMLKCQRPLVLSVGPFGPLTMDDAVSRLKLAYSFLSIMSGR
S

>CforOR50

MSAERELFKTTKLLMVFSGLWRLELSNSRRFVRSAYKLYSLSLQVFFNSVIISFVLE
FCRLVSNIDIDTAIKILSRLIYVALLTMKLTLCQSKSMRKLLSIALQDESDIYRQHDSEI
RRIYTKHVKYCNKITTAITICSFVLDIYLTEIGIEKSYKFSHNTANSSLERPLPSPLY
PFDNRKYHVCALTYQIETFLTAIYSGSVQGVSNVTIFFRAQLQILQHQLRHFDRFE
FAQSDGEIGNHLRILVQKHQDLIKWFDQLNQLFKKILLEYSVSSMLMAAVLIQIFQ
GEDVMFNGIYFCFIFGQLTILSWNANEIKIQSSELSQSLYESRWFECRQAEKMVIRIM
MMRCQKPLTLTIGSFGAMTADVALSRIKLAYSIVSLVSGGSGV

>CforOR51

MEYLLNSLNVA AVSIQFITYDRKMLASPIFYFSFLFVQTFVLGWSANELQVQSSALA
EALYNPWEYEQNKVKKALLTMLIRCQRPLTLTIGPFDAMTTQSALMIMKASYSY
VTLMMNNYN

>CforOR52

MKKMIHSGRSILNFSRYCMSFAGIWQYTLPTRNVILQKTYAMYMVLIKAYFPMFTI
SINVQFFLTVVNKNASEKTEDEVYRDLSYVVIYSILLVQFVVIFGRKTRSNYMVSFIT
KEETDILASEDTQIVDYHLRQIRLCRCGNWGLFMFSCGTASAMALEMFLARDQVG
KFNREFNATKEKPLVFDSYFYKLDMEKYASCLLVCSVISLVINVFIIVSIKTFEFCIIF
VPSILNKLQVRFVKIMNSGDDLWNAVGEIVMEHKRIISFVENFNESIKYLTLELLELL
NSLNVA AVSIQFIKNEGEVAASPIFHFLIFQTFVLGWSANEIKVQSLKLADALYHS
AWYEQNEKIKKSILLMIIRAQKPLVLTIGPFDAMTTNSALRIMKASYSYVSLMMNN
L

>CforOR53

MRTSLEQDPPKWRDAYVVPKMLQVCGIWPTRHTSNLTTMFRILFFAVSLVFDMT
ILVELKILITSKDYEALSTHLSTLGLYIGYTIAMIFKGQERKFTQLLDTLEAPIFDDFP
SNLVTFKTECISLSNGISTFYISCVAAASITLYLNRPLYTEFSLPISFSFDISICFNMLNISL
INVASAQLDILGETVSSFLFKRHPNFEEMEKVHLIKCAKKHVAVIRFVDQIEEVFTYI
CMTRCLSSIVSICNGVFQLTHTGNLYSVAFLFNIAFVFDVLFEGIYCWFAGLLTIKS
LAVADACYNYNWLLSSENNKLLLIVLTRSQKPLFTTAGKFARLSMASFLSVLKTA
YSYFALMQSLYERNEFEECL

>CforOR54

MYPTKNPPQKWEQAYSVPARFLKLAGVWHQDSWPAAKRIQHILFFILCVLFDVAI
YMELANLVTSNDYEMLSEHLSPVGFYTSYTIIVVFKANGKKFKKMTSSLESSVFN

DLASSSLKIKERCIFESNRLSTFFLSTVGC SLVIYLARPLYSNYS LPI SFSYSVNGIKYF
LVYSLQIVSVIYLITGISLVMLNISLLNIASALIDVLNQSVAGLGQLSGVGVLVQRHS
VIIRFVQEIDEVFTYISLTRCLTSIISICNGLFQLTHTRKIPSVTFVFNVVYVFNVLFEIG
IYCWFATALTEKSLTLTDACYNYDWPEESLSNQRSLLMITARSQKPFYVTAGK FAR
LGVGSFLSLVKMAYS YFALMQSLYEKTEDLRTL

>CforOR55

MSIKNGVSDISEDFVGVGTGFGNAMFLCILFQINAKRWSQLFNEITD TTQFGYPAR
MPQSVKKANFCALLYVYCNV GCLVYGLASIFDTSRCERLNKEKGIHEICGTVSPL
WWPGDEIDPMTKLF FIIWQAFSAFYVPGGGILTFLPWEGSEIIQAKIDHLKELFKN
VFDGDNRDQMAKRLKFCIRYHHHILKISENFNF AVKKL VGQLSFIGA IILTCIGTQM
LKES SIGATLHFLGYVVS VTLICLAGQKMMDATYGIQDAVYDSKWHEADPKVAM
DLKLILMRCQKPVYMDA VPFGVFNYNLLIIIFKTTY SYLTLINNTT

>CforOR56

MTLVGFWKYPHQH LTKFFYNLYSLLIVLYFFLYTSCLYIKFIITVSTASSLDPDNFT
QLAYVIGHMMATYVIMVCRGSNFNGVISEIAVAENRILEEGDDDILKSHLQLIRWD
NWINLLFAVFTIGTG FALGLENLLHNVEIAHYNRDHNTTLERPLL VQIYYFKINKHK
WANSLLVISEISFACT TMLKQLVAEHQRVIAFVDRLNASIKFQILLEYLLNSL NVA
AVSIQLITSLAVSDAIYFSPWEEQSEAAKILLTVIARA

>CforOR57

MVEHRSILTVAKMFM TLVGFWKYPHQH LTKFFYNLYSLLIVLYFFLYTSCLYIKFI
ITVSTASSLDPDNFTQLAYVIGHMMATYVIMVCRGSNFNGVISEIAVEENRILEGGD
DDILKSHLQLIRWDNWINFLFAVFTIGTG FALGLENLLRNVEIAHYNRDHNTTLERP
LLVQIYYFKINKHKWANSLLVISEISFACT TLMFLACKVSVYTCIVFASSVLKMIQIK
FRKMGLGKENPLAALKQLVAEHQRVIAFRFVDRLNASIKFQILLEYLLNSL NVA AV
SIQLITSLAVSDAIYFSPWEEQSEAAKILLTVIARAQIPELTIGPF GPMVIESALAIC
KASYSYVTLMMTNVQ

>CforOR58

MTSIEHILDMPKLCMISAGIWRLPLPVENVILK KTYTVYRKFVRVCFPIFLASLCIQC
TLTLDDKNSSKTTEELFKQLSYFITLLIVEVATILWQRDEVLR LISFVYEEEEKIFRSG
EKIIIQAHLKQVHFCKNSNWIVLVFTLFEVEKYNREHNATLPVPFLFELYCYKFD AE
KHA AVLHYVNDFAAIIINGFRIVSTKTIF FSCIMFVPSVLKQLCIRFRKMGT YEDDIFV
ILRHLILEHQEVNRFVKKLNDCVKYLILMEYLLDSL NVAATS IQFITYDRKMLASPIF
YISHLFVQTFILAWNANESLALADAIYD SPWYKQTMGVKKSLLTVILRAQRPLLLTI
GPFDAMTTQSGLAIMKASYSYVTLMMN NY

>CforOR59

MPRAKSYFSYIRRLMMIIGIWRIQNGEELSTKEKRLYHIYAATFQVISTSGGLSVLLE
IPTLIKRTSVFSPVLDNVS RV TMYGLIVFKMVMWRSKRMFDLLNIALEYDSQLAV
HADPKIKEIYKQYLDY GDTVISIIFLSGVLIGFGIGIIGDINCYKYFMENKGRNVSGNP
LPLNLWYPFDKNKYYTMVLVDQNI RPTMCCLCIGVVGASVNSVVVFLTLQLKLLQ
YYFRNADTFRIDDEV FEDIVERNLKLLCVKHQELIAFAEELRQTLKNIILIEYAVSSA
SIAILILQTIASGELVLNLTMLTYTVLQLLIFAWNCNEIIIQLTEFSSTALPIMLSTQRY
FRFIRQLMMIIGMWT VQTGELSTLKKRLYQVYAITFQVICTSGSLSLLAEVPALIKTS
SITSAAGEVLA VMDNVGR LMIYVVMFKIFMWQSKRMLNLLSIALQQDSELAGET
NPKIVKIYK KHV SQANNVVTIIFSSGILIGIVALIGDLN CYMYFKNQKGS DLKENPL

PLNLWYPFDKNKYTLVLLDQNRILTCLCIGVVGASINSIVMFLKLQLTLLQHOF
RIVDKFEAVEYNLKFCLKHQKLIIEFVEGFNESAKNVILLETVSSITAIIIIQLISSGQ
FMLNLTLSSYTSLQLLLFAWNCNEIIVQSTALANALYESNWEQSKSVKRILQIMM
CRCEKPLRLRIGMFGAMDLDAGVSRLKLGYSYTTLVKN

>CforOR60

MRHASFSDNPDHVMHSFVKRTMLIIGIWPANFRFIIIYNLYFYTSFLYYILYNMTLMI
QVFATWNQDMINAAGNAAVAIYILNIYRVVIFRSLRFRALIHQTEMKERQILTCSS
DTIKGIFTKNVAFTRRLVRIYVAIGTTGISLYYASPLVEDALLPLPFDNSTGVQPRRLI
FSSWFPFNPNLHYWTSYFLQFVAGFYGYIVHCGAFYITMLTFVTAQLKILRHLFA
NFTAYCDEYSKTHNFSDEENRNIVLKALIREHQHVIRFVWEMNDCMKLFTMMDFII
SSFQLSLVLIQVLGSSKITERFAAFSYFLTLNTQLLFLYWNAHEITVQSEKIAVSVFA
GDFYNYPGNVTKMLQMVIIRAQKPLVLTIGPMGHVKMDAVFQIFRALYSYICLILR
H

>CforOR61

MQIKNYFFKISEGYRPOHMRFVRKSMLAVGIWPTNLEGLKASIYGKYFLASIAYYLI
FDSTILIEAARRIHGGDIIDCFGILIVYNSLYRVKIFKSPTFQKLILHALAKEQQILNC
RDDEIKELYKRNVRGTTKFTYTYVIGTVGIVMFIVCPFIDDIVQPLGYSNDTGWWQ
RHEIFPNWFPDRDRYYVTAAYVLQFAAGCFVNEINHMQWYIFLDFSVSSFLAVV
VFQLLQSTSSVEIMASCSYFCTLSTQLFLLYWNGHEIVTQHENIAECVYKSDWPSYD
AKTRIMQMTMVRQAQKPLKLNIGPLGYVKVDALIQ

>CforOR62

MIFANIVQRHEISQYNKKYNTTIPKPPYELYYMTLDEEKYGTFLVWFNDFSILVAG
FLVVSTQVIFISCIIFASSLLRMLQIRFKKMIGFTVNISVTLRELILEHQRVIEFVNNLN
ESMKYIMMLEYLLNSLNMAMVSFQLAAEHNILIASVLFYFGLLVVQTFIRGWSAN
EVKMQSLGLADAIYESPWYEQNHAACKTMIIMMRAQRPLGLTIGLFDVMTTQF
A

>CforOR63

MYQPVKGCPFYSAVSFLKRLQFYPSASKYDERKFFLRAFIWVFLMINITDLLIHTTI
NMREKKNVDFGDITGNLCTMTCVCFTHHKKWAHVFEVSLTNHEKFGKPNYK
KVTERGNVIVALAVLYAIIIGIIFYTVLSQLPSTVNTCLQVNEVNNLDEVCGLFNPAW
WPAKYRASSAVTRMWFYQVTTVFVLLSPSLLFFCLPWEAASHAVARLEHLRTDY
LNVFKINSDEIKYTKLRLWIEHHQEILRVSAAALSAATKLTIGHMSIAGIIGCLGTQA
LREGIPKSIIFIMGVLVGCFFVCHAGQSIVDETLGVSYTAYGVSWFKCDVKIQKAVL
FIIMRTQKPVRLLETIPFGAFDYALYLLIVKTSYTYLTVLNQKM

>CforOR64

MIPYDYKKYFERDFNVAKFFGCWVNDGRAESKYYKYFVMVNLFVILYNIILTIE
WFANSKSVKLFAQMGYVNLICTMGQVKSTFVFIHRSDFRNLVELFNEDLFQPRNEA
ELTTLNHVLSVFSRFRKRLISLTCVSFTSSILTPLFYSGDGLPLEAWYPFDLSVKMN
FKLAYVHQFCITYISFINMYSVLDVSGFAHFVGLQCDLLCLRLEAIRIGDYQEQKE
KLVNVCVHHYRLILKFLKTTEKVFVKIYFGQLFASTTALCMDLFLLSLSTEPKTFEFFY
LVVYLLAVANLLLVPWFSTEMTRKSENIPFAAYSCDWVDSSNSFKKELIFFIRRAQ
RPLKIFYAVDFFEISVETVFKIIRTSLSYYAVLNNLNMEEKYY

>CforOR65

MELKPILKLAANSMILAGTWPLPLPTKNLALRKTYAVYCRLIHIFFSIFLLSLYIQFG

LKVNDGNSDENREGLFSQMSFLISLLIVGVTHILYRRKNARLVIKYIMKADANIARS
KDEDVLRVYHSRQIQFCRRLSFGIVSLSVWMGISMFLETHLQRLEIENFNKGNNRSIE
KPLTFDMYFFNLDRAKYETLLCISYVLLPLNCLLFTSSKIIFSCIIFPASVLKTLQIR
FRKLGVAGGDMLANLKELIAEHQQTWFIQKLNDSVKYLIFLDFLLNSLDIATVSIQ
LITLEKNKLASPMIFFGLLIVQTFVLGWSANEIKTQSLALGDSL YESSWYEQSEVVK
KMILTVLIRMQRPLVLTIGPFDAMTTESALAIMKGSYTYISVMLNTY

>CforOR66

MAEEKLMKFAKYLMIAATGMWQLEFTESSGLKAAYYAYSVYHQVNFATFTASLTV
GMVIVANGGNINLTSESMGITIIVVILAKLTICKTAKVKRLVNESINGEKIIFSSGNP
ESIAVYNVQIKYSRVINVMFAFFMSFMVALSMLVANLAVRDKIDRMNAKMNESIAK
PELYWNWFPFDKDEHRTGTNVIYAYCLYNAALTNSAAQVFFVSTITYAGAQLRVL
QISFRDIGANDSADIFEKVERLIEKHQGVDFVVDLNGSMKYLMLLEYTLSSLNVA
SVSIQVTSVEPSVTSLAFPIIYLCLLVFQVFLGWYSNEIKMQSLALGDAA YKSQWY
EQNDKVKKLLIMMIMRSQRPLVLAIGPFGAMTTQSALTARRHFSVVRDFTMSFLD
HEGGLLVRNPHEEFSLNNDVVAGLVNDK

>CforOR67

MKVDNYFTHIRLLMVIGIWRVEDPDTSILRKRIYRVYSVCFQSLCYSVLFSLLAEIP
SLLKSDRTAAVDNGNRFIMYTSHIVFKMIAWQSKRMVALLGVLFQRNREMQAASL
IDPQIRRLYQRHARFNYKIMFVLFVFGAGTVLTVSLPAVELMEIYEFLVSSEKANVTEK
PLPLRFWYFPDRNKHYVVALVDQGIRPTLSCFCASVTSACLNSLAIFVRAQLKMLQ
YYFQYFHRDEEAFVTLKCLKVRHQRLIKCTIEFSESLKYIALMDYTVCSATFALLV
VQITIGKDVITSLAVLSFITLQLITFSWNCNEIILQSTELTNALYESDWYDQNNQNAKV
LIHIMMMRCQRPLSVHMGWLGVMLEAGISRLKLGYSYTSIAKN

>CforOR68

MLTAELLPTIFIFSQKIFTYKIYMRSMIYSILIGIVLLCWEEYYMLLNKDLFSFSQYAP
YHYLCVYNMCCRFAIVWKHSDPTAIALFKSICWSSDSVDLKTQQNIRKDANYVDN
LFKMQLVSAFLCTVIFHVDFVRLREMSISIFYVSQYFPHLETAVIFAEITLWIYGLG
MIQCPFMLFYIIHTVYQLEMFNAYITKTRSVGYKFSAESAAFQKLQRKRLIDLDR
QQEIKRMTVLYLNIFSNSAFFYTVVAMLTSLAVLFYIFYDDSEHYRAHMLLLISLYT
TVMFVVMKYGQRYEDEFENVFLNLSSEPWYDWNTPNRKIYMTMLMKSQKPETVR
MGKLADLNCVFGKNIFQGIFTVANMFNSLQN

>CforOR69

MDTISKIIFSLIVAIAKATMCQKKKIVHLLSAAALKEEFICLDKKSILKIYRRHMSLCN
KFTLFLVSVGTAGGYMLVTGYVAIFDFYYSKHLNSTLKRPMVLMQFWYFPDINR
YCVWTIADETMTILYSVICSSAVNTFINTTIIFLRAQLIMLQNNFRNFDKVNRESAG
MSLKRLCIKHQNLIQYVDSFNNSLRVYMLLEFSIASVMLAASLFQIFAGKDVIFSCIY
VLMCSGQIIVLAWNSDEILAQSLELATALYESKWFDQTKRTIALIEIMIIRCQKPLTL
SVGPFGLTVDVAASRFKLAYTYTTIMTGLSE

>CforOR70

MDTISKIIFSSIVAIAKARICQEKKIVNLISEALKEDECICVYKKSURLKIYEQHMSLCS
KLTLFLMVSSTAGGYLLISGYVAIFDFYYSKHLNSTMERPMVLMHFWYFPDINHH
CLWTIADETMAILYTVICSSAVNTFINSTMIFLRAQLIMLQNNFRNFDLDSQGNSPGS
NLRRLCRRHQNIQYVDSFNESLRFVMLLEFSVASVMLAASLFQIFAGKDVVFCIY
VLMCSGQIIVLAWSSDEILTQSLELGTALYESKWFDQTKRVIAVIQIMLLRCQKPLT

LSVGFPGPLTVDVAASRFKLAYTYTTVMTGTLSE

>CforOR71

MSVKNRLFDGAKLMLMLGGIWKLKSNTSSTLYGIYSVLVHTQCIITPVLLFANVPF
LIRKDLNAAMNTISKGIFSSIVVIKARMCQTTKIVRLISAVLEEEQRICSDQNSKGFK
TYTRHTNFCNKLALFIVVSIVSTGGYVLVLGYVAIFKYYTSPSPNSENSTEEKPIILN
FWYPFDINRYYLWTVADETVAAVYTMIWSTAVNTFINSIMVFLRAQLITLQYKFSH
FHKESPEQASFKSLKALSVRHQDIIQYVESFNESLKYVLLLEFSIASIMLATSFLQTF
GIDVAFNCAFIIMSSGQIIMLAWNSDEILTQSSNLADALYQSNWYDQSNEAKILIRT
MLLRCQRPLTMSIGPLGPLTLDVAASRFKLAYTYTTSVITGTLSE

>CforOR72

MTSPTEHDLTQVYHMEKQLMLLAGFYPKPKDSNQFVYYLSCVVVFSIEVYFELSM
TLYVVNEMDDVMKIAETLLFLMTQTAFLAKLINFAYNKDKLSALEAILKTELFQEM
TRTDFQKFQANVSKSRKILLFYCSNAAASVSGYVLIPFFEGRSTHRLAVPSFNPWDV
KEYYYSTHFFQVLCLTIGATLNSIVDTMFASLCTIFYGELRILKRCFRNLDSLPPGI
VRRQLKRNALFHLEILKVANLTERFFTYGILVQFLSSIFVICFTGFQMMLIPTLSSDF
HFVVYLACMLSQVAIFCCYGHFVTNESSDIGEAIYLSNWYMSDLSVRKDLLIVMEN
TKKPILLTAGKFLPLILRSSYSFLAVLQQME

>CforOR73

MSASEKNCLDLTLRLYRIFLIVPDDGSEDNPGIWFYIRLAIISLCCMLTYLSTIAHLG
VSVQRNLDVEKDFDLVILLSLAGAYWFNAFFFKNTKTLFKLRDSISKFTSSIKPPEW
DILTKKMNFYSFLHLIYIFFAIHTYVIFSVFDPSCERINRQKNLTELGLLAPAWFPIQ
ISETYKMPIILFQYL VFLFSFIVCAFIAWSDAEIIQYIIFRFRHMOKQLITAFERNK
MRKKFTAAIKYHNEIIRMVNLLNDCFASTILLHVLLTGAIIGCSFFRMFYGHISPTSM
LFIGWVNGLSMSTISGQKLMDESEELFNILLTADWYKFDNEIKKDFIFMLLKCRNPI
TSQALIAPMNYSLLLAVLKGSYSYITLLSKAV

>CforOR74

MADAGEIMKMSKYGMIAAGLWRLPLNQPTVVKKMYVLYSVYVHVVFVTLFLLLM
IQFIILCTKNDSLKELSDQRFTVFSYFISTLTTQVKLLIFQSNNVWLIISYIMDEEKLL
AQVNLDILSYHRRQV SFERWINTVIFSLSAFLGLATVVANGIQRHQIEKHNRFYND
LPKPTLFLYYCNIDTEKHNTMLAISNTMWWIIIIVISTPTQGFYLACITFASSMLKAL
QIRLSKTDVEKNLDETLEILIREHQRIIAFVKNLNETVKYLMMDYLLNAVNIAGV
VLILLEAADGIEVASALFYAGRLVVIVFALGWTSNEIRIQSQALADAIYETPWWEQQ
NKIQKVLHIMIMRGQCPLAITIGPFDDMTIQSSLTIMKAAYSYGTIMSQNYR

>CforOR75

MFQTYLSIWQMSKYGMIAAGLWRLPLNQPTVVKKMYVLYSVYVHVVFVTLFLLLM
QFIILCTKNDSLKELSDQRFTVFSYFISTLTTQVKLLIFQSKSVRLIISNIMDEEKLL
LIHQSILSYHRRQV SCERWINIAIFSLTSFIGLATIVANGLQRHEIERHNRYYNDSPK
PMVFPLYCYCNIDTEEHSTILVILNVMYVIIIIFISTPTQGFYLACIIFASSMIKALQIQS
KIDEEGNSLETQILIREHQRIIAFVQNLNETVRYLMMMDYVLNAVNIAGVVLILLE
ASNGIQFASALFYASRLVVIVFALGWTSNEIRIQSQAIADCIYECPPWWKQHKKVQK
LLHIMIMRSCPLAITIGPFDDMTIQSSLTIMKAAYSYGTIMSQNYR

>CforOR76

MTDSGEIMKLSKYIMIASGTWRLPLNQPAFMKKLYFLYSVYVHAQYALFLLSLIIQF
IILCTQDELSKELDDQRFKVFSYVITTLTAHIKLLILQDKSLWTLILSITQEEKLLTLI

DKDILNNLRRQVFLERWINMLIFSISAFIAVALIVANGLERHQIEKYNQYYNDSLPKP
TLFPLYYGNIIDTEEYGTMLVILNLLCAVTIIFISTSAQCLYLTCIIFATSMKALQIRFA
KMLDEDGNILETIKNLINEHQKVIMFVQELNDTVKYLMMMDYLLNAVNIAGVVIII
LEASDGI EVASTLFYAGRLITIVFALGWTSNEIQIQSQALADAICETPWWEQRRTDQ
KLLHMMIVRAQCPLAITIGPFDEMTIRSSLTIMKAAYSYGTIMSQKYR

>CforOR77

MNSIQSLRREYAEDFFYVNRWILRLAGLWCPENKNPYAQFAYNAYAIVVFLFANL
WFTSTEFVSLFYTYKREDAFIKNINFFLTHFMGAVKVIFWYFRGDCLIRIMKTLEDP
DLHYKPFTEYNPGKISKRYKKIGVYTYLSFFALAHATLSSSYIPPIISVTRYMRSDAN
STHLLPEKLPYYSWMPFAYNTEKLYLLAVAYQAGPMFSYAYSIVGIDTLFMNIMN
NIGSNLTIMQGAFKTLRGRATAKIVGQPISSLRLHENAFTDELKQFRKISRHLQTVL
HMSNQLESVYRYVTLQCITATLFICTCLYLVTTPPLGSKQFIAECVYMAAMFFQLF
VYCWFGNEVTLKQCQELSNYIWECEWFATTTSFKKNLIFTMMRTKKPLYFTAGKFL
PLTLPTFMSIIKTSYSIFALIKNTSE

>CforOR78

MKTSPQFFSHVKWFMMSGGIWMLDESKRSLAFVIFYRFYSMAFPVYCASMATSLA
IEIPNLISESSTAVMENVARALVVAIVVTKLVMCKKKRIVDLFEAASKQFAEIAGNA
DPEIKILQQHVEYWKILLVLVVPVIFGYLLLCEMGIENTIRFDWLSKPPNVSLDAP
LPSNFWYPPFDKNAYHHWLLLDQCLRVGGITGMNSVAAMINSLMVFMRLQIKLL
QHHFRNFDKYGGGPEDLRWCDGGGTSKLRLLCRRHQELIAYVEKFNEALKYIILLE
YTSSSIMFAGAIQIVSGEKVVFAFFFMVFNAYAQLMTFSWNCNEILTESAELATALF
ESDWYLSNPETKTLILIMMVRQRPLILTVGPFGSMTLEAGMSRLKIGYSYASVMA
TSSE

>CforOR79

MSSKKG YFA YIRFLMMVVG IWRIEHWGSR SNTGKV VYKAYS VTFQLICWSAMVS
LAVELPELIRTDVAAMDNIGRFILGVIIFKMVMCQSERVLKLLRLALAQDAQILTE
TNAAVKMIYERHVS YDNKFV SLLVTSATCMGVCVSILGDVKCYEFLKRAENRNV
DKPVSSRYWYPFDRDDHYALVMVDQNL RPTLA CLCMGVVSAFVNCVVVFLRLQL
KLLQYDFRHV GKFDEKLKTASAERTVKMLCLKHQRLIEYVGEFNYS LKDIIFLEYM
VTSVSFATLTVQIIAGQQVIFNLTVLTFTIVQLLTFAWNSNEIIAQSLELSFALYESRW
YEQTSATKTLIHIMMRCQKCLCLKIGVLGAMDLSAGISRLKLGYSYTSMLMKTGE

>CforOR80

MIAWQSRRMVDLLGVLLQQNQIQEVSRTELHIRRLYKKYARYNHTLMFLLVTSG
MVIAISIAAVDMNVDNYFTHVRLLMVIGIWKVESPDASVFGKRIYQVYSLSFQLF
CYSAA SLLVEIPSLVKTDVAIAMD NANKFLVYIVIIIK MIAWQSRRMVNLLRVLLE
QNRQLQKASRTELHIRRLYRKHARYNHNMLVLVTS GTVIAISIATVGGVNLYHFV
NSPDNINATEKPLPYRYWYPFDPSKYYLVALVDQ NIRPTFSCFCIGVTSASLNSLAIF
VSVQLKVLQH QFEHFNRQE QEALDCLKLLCEKHQRLIVYTTEFSESFKYIVMLDYT
VCSLTFALLILQIIAGEELVITFTVL TFFTLLQ LMTFSWNCNEIILQHPN

>CforOR81

MSAMDNANRFTVYIVIIIK MIAWQSKRMVDLLGVMLQRNSQIQAA SRVDLAI RRL
YRNHVRYNLKFVFLVSSGVVISLSISMAGFVG VYRFIHS PENGN GSEKPLPLKFW
YPFDSKQH YLLALADQNIRPTLSCFCLGVTSASLNSLAIFVRVQLKVLQH HFKHFRG
GLEAAIDSLRPLCIEHQRLIAYTIEFSESLRYIVMLDYTVCSVTFALLIFQIATGEELL

MNFALLTFTIFQLMTFSWNCNEIIVQSTGLADSLFESDWYNQGGHAKVLIRIMMMR
CQKPLSLRIGWLGVMMLDAGLSRLKLGYSYTSIMKN

>CforOR82

MIGHWEDLDAHFTEKPLPLKFWYFPDSKQHFLALADQNIRPTFSCFCLGVTSASL
NSLAIFVRVQLKVLQHHFKHFRGGLEAAIDSLRLLCIEHQRLIAYTIEFSESLRYIVM
LDYTVCSVTFALLIFQIATGEELLINFILFTIFQLMTFSWNCNEIIVQSTGLADSLFE
SDWYNQGGHAKVLIHVMMMRCQKPLSLRIGWLGVMMLDAGLSRLKLGYSYTSIM
RN

>CforOR83

MDILYHVDPTDPFYITLKYLYQYFWFFPTASIEKRKFWIVSSTFRIFSSACVVTTIAHF
IVSLKNQVHSVIIDDLIVICGGICIIRLDCQYWIHCWDWSALYTRVTSRRPFGEPTY
RTTTRRMNKLSELLWIIFCTAGVCLSVTMTISDRECGRNRKRQGLQEICNMITPTWIP
YNGTLPSPFKHAFLGFQITGYVSYFLTSAVLIIMIWEVAEVILTRVDHLKTVVRSIFD
ENDEPRTRKEIVFAIRYHVELLRSSSEFKVVSXSASHVTCMSGVVIACVATQGLKE
MNASLLYELSGWLISLRFVCHTGQRLRDSMLSIGSALLESKWHQADPTLKMVLM
MLSRTQKPVTLDTIPTGSLDYVLYLGIKASYSYCTWIYSLTETTH

>CforOR84

MKLGEQYFSYIRRLMTVFGIWWIKEELSQSCKKLYAVYRITIQMVCVSSMISYILDV
PALLKSNQTEAFSNIGVIIFFATVIKMMMCQSQPIVKLLRIAVQQDFQAVKDINVEVE
AIYKTETKVNFLITIVMGSMTIVSVGFLVFGDFNCYRYVKQYSNATDKPMLLNY
WYPFDTNKYYALVLIDQNRQILSALCTATVNAFVISIIIFARLQLKLLQYSFKNFHK
LTRDKNSAGGANVLKQLCQKHLDLINYIADLNQAFNVIIIFMEYMILSITFAAETLQII
DGGEKVLFACGVLSNSIIQLLIFSWSSEIIQSKELATALFESNWDYDQKTKVMV
HIMIMRCQNPLSLTIGSFGVMDLDVGLSVNLLVRLKLAYSYTSVMTN

>CforOR85

MTISQSYQNAIVTHKVDACLNSLKRVPKKEIHEVIFQKNTVSVCMKSSGMYFR
YIRWLMIGAGMWKIEEFSAPKKRFYAVYSVIIQLICTSLIFSVALDVPGLMKSDPS
AAVGNIGIMVFFGLTIKTLMCQSKPIIGLLRTALQSEFQVVTSVNANVEAIYEFHTK
LNNCFITLVVTCLLFMGLCVATLGDIESYRYSKRNSNDTEKSLPLNYWYPFDKNKH
YTLVLVDQNRPTLGGLYTAIVNAFVNSIIIFVRLQLKILQYSFRNFDQLEPDNVKNP
TILRILCVKHQELIRYVEGLNHLKFIIFMEYMISSLTFAAQILQITAGIEPFITSILSYT
IIHLLIFAWSCNEIIVQSTELARALFESNWNHDTKVKVMAHIMIMRCQKPLSLMIG
RFGVMDLDVGISRLKLAITYTSVMKSGN

>CforOR86

MLNMDLSAQYFGYMRSMLMIAAGIWRMEIKEFSAMKKQLYGAYSVTAQAICNLLIF
SIGLDVPALLKTHPAAAFGNMGMVIFLGTNTTKTIMCQSKAIKLEIALKPEFQMA
KRVNTEVEAIYKQHTKLNNYFTTVLLVCVLLVGICHSVSGDIECYMHFKQHSNATE
KPVLAYYWYPFDTNKHYTLVLIDQNRPLLTGLCTCIVSAFVNCMTVFVRLQLKLL
QYSFRNFDKLQLHNEPKDPNTLKLCAKHQEIKEYVDELNQSIRAIIFMEYLVSIT
FATQILQIVGGEKPFLTILITYTVIQLLIFAWSSNEIIQSTELAKALFESNWDQDSK
IKTMAHIMIMRCQKPLSLMIGSFGVMDLDVGISRLKLAYSYTSVMTSGG

>CforOR87

MLKPYIAKLFGRAYLKSTTGEIALKGFRTGIYFPNPQVFTEVDYLTEESNNNQLSS
TPDNQDAGPVANQSAPEESVEAQAPEHSLVLPENIQPISTTKTRTSNRVRKATTAKH

RIVNMNEEEAVDADEDVDTMSNVITTEKGPVGMYSIRWFMLVAGIWRVEVDEFST
IKKKIYSIYSVIIQICTSPIVSATLYVPMLFNINRVADAISNIGIVVFFGMVIAKMMMC
QTKPIINLLEVALRTEFRMGLVDAAEVEAIYESHINLDNGFITLLFAWAILMGLCVASF
GDVNCYMYFKQNSNVTEKPVLVNYWYPFDINKHYAVIMIDQNIRPTVASLCVFFV
NSFVNCIIIFVRLQLKLLQHSFRNFDKLCLESGQSEGGNVLMMLCVEHQKLEIYVQD
LNEFSKTITLLEYMVSSVSFAAQIFQITAGVRPYLATIILCYTILQLFIFAWSSNEVIQ
SEELARALFESDWFVQDVRTQALVHIMMLRCQKPLSLKIARFGVMDLDVAISRLKL
AYSASYASLISGS

>CforOR88

MSNVNHESLTQEYFRYVRWLMIVAGIWKIEVDEFSLPKKRLYHVYAILVQMVCSS
PMISYVFNMPDLLKTDKPAIAISTIGIITFFGVTLTKMLICQTKPIVKLLRLALQPEYQH
EGAINAEMKAIYEWHSNDNHVISLLFFGATFMGTFFVDVFGDVNCYMYFKEHRGIN
ITEKPVLLINYWYPFDKNKHVYVFLIDQNIIRAVLGCLVAAVVNAFVNCIIIFVRLQLK
LLQHSFNSFDKLDNIEDSDMLKRLCLKHQQLIRYVEDLNKYFSTIIFLEYMVSSLSL
AAQILQITLGVPRFLAFILLSYTIMQLLVFAWTSNEIIQSSSELAALFESDWFVQDSE
VKVMVHVMLIRCQKPLSLKIGPFGAMDLDVGISRLKLAISYASLMANGE

>CforOR89

MPTLLKTDMPAAISTMGLMTFSVVMLTKMFMCSKSIIVRLLRLALQSEFQVAGDI
NAEIKAIYEWHINCNNVVSILFFGALFVGICVNIFFGDIYCYFYFKQHRGENMTDKP
VPLNYWYPFDNRKHVAVVLLIDQNIIRAILASLLIIVVGAFFVCCIFVRLQLTLLQHS
FRNFDKLNNIQASLLKRLCVKHQKLIGYVDDLKESFKTIILLEYIVSSLSFAAQILQI
TLGARPFPAFLLLTYTAMQLLVFAWTSNEIIQRQKRKNASIIYKPEYR

>CforOR90

MSHARFTQRYFRYVVKWLMIVAGIWRKIEEFSPKPKLYHFYTIILQIMVFSSPLISYI
LNVPIILLKTDMPAAISTLGFITFFGVILTKMFMCSKPIIRLLQLALQSEYQTGGHINT
ETKAIYEHIRFDNYVISILFFGAVLMGLCNDVFGDIDCYMYFQQHRGTNITDKLLP
LNYWYPFDKNKHVAVVLLDQNVRAMLA CLVTAIVNAFVNCIFIYVRLQLTLLQYN
FRSRELNSSEGSKMLKLCVKHQDLIRYVQDLSGSFRTIIFLEYMLSSLSLGSQILQI
TLGIRPFFTFIMLIYTVIQLLIFSWSNEIIQSLELSRALFESDWFVQFNKYTKVDVHVI
MMRCQKPLGLRIGHFGVMDLNVGLSRLKLAISYASLMTSGMVFSPLVSYVFNVP
TLIKTDMPAAMSTMGLITFYGVILTKMFMCSKPIIRLLQLALQSEYQPGRKINREIK
AIYEWHTFRDNHVVVSILFFGGVFGICIDVFGDINCYIYFKQHNGTNLTDKLVPLNY
WYPFDKNKHVAVVLLDQNVRAILGCLVTAIVNAFVNCIFIYVRLQLALLQYNFRNF
GQLDSSEGSNILKRLCAKHQQLIRYVEDLSEFKTIIFLEYMVSSLSLASQILQITLGI
RPFPAIILLIYTVIQLLIFAWTSNEIIQSLELSGALFESDWFVQKHHSKTKVDVHVIMMR
CQKPLGLKVGHFGVMDLNVGLSRLKLAISYASLMTNGD

>CforOR91

MRSRVSSVHILGRVSSQSMSDVPLIWDLLNTEQVFESPIDINLSQTTPLDLPLKWE
NFGIPPRKMKVTNTGHTVILSAKWGQERPYLTDGPLVGKYVFSQLHLHWGTNDM
EGSEHTVDGGHLPGEMHVVTFKSCYLTQESALKEKDGIVILVYMLKLQEKPNVVF
QRLVEALKDVTQAHTSKKIEPFALSYL VREFVVDYFTYCGSVSTDDCIHYVMWLIT
RVPIGVSSSTQVNSLRNMDGEGKLIQRNFRATQPAMDRPVLHVCPSTSKYSTLLPV
PKPDSTTNREDVIKIYSVERFYIQSDVNCYHYFKEHARKNITEKPLNPVTFMPSLQIG
YCEYEPRPAIFQSLKYRSKYCLKPIDVQQLDRYVEDLNEFSKTVIFLEFLVSSISFAS

QIFQITLGVRRPFATIILTYTHIQLLTFAWSTNEIIIQLFDICPIQLYTEKQLPSQLVNLA
NKLQDQTVLNVNDEAVPALKP

>CforOR92

MATIKRGRQFLGFNVAVIKFCMLWTNNFEEKYSAKRFLKDATMIFSLMPCVLSIFA
DFMMQLYDGTESVTSIVENVIALICIIIGMIYMVVCFARNRKNHLLLKINSFKKYG
SFGLEVLEDEKANLFSKLFIFYGILGNFVYMLMPQLSIQKCAKRNMQMINDDVPC
GLVVRSRPFKFDYSPMFEIVFVHQIYTCTVVTVVLVLTMLLCGFLMHVIHQGLHL
KKYIAALKDEHPQEKIYAKLAKCIKYHIQIIEYSQELANSFSSMLLFYITLTSIVLSVL
CFEIMVEAFEDSVRFALHLVGWLIILLSVCYYGQQLIDRSQNIADDVYSIKWVNQT
VEIQKRIHMILRSQTPLTLAAGMGVVSPLAFLKVLSSAYSFFTLKKFKP

>CforOR93

MCTFILAFQAISMILFSTMASIKGIMCQFKYFVRLQKIIIEEAMLLAWNDAQTKKEYIY
TKHTKYSKKLSKFFLLAAGLAASVLVEMGCTNSYKVKMEKRVNVSLEKPLPLKL
WYPWDKNRYHILTIMSQFLDIAVTAIFYVAVAQIFTTTTLLIFLRAKLQIMQHQFRNFD
RNFNNRDIITNGVETVRMLCVKHQNLIELINSVNEALRNIIFVEFSMSSVMFAAGILQ
VIAGQDLLNIEFSISMISFLMLLAWNANEIREQSSKLAMALYESKWYEQKHNTKAI
IHFMIIRCQKPLSINIGPLGPITVDAAMSRIRLAYSYSVMSGK

>CforOR94

MKRRNRRSYVLELQKIVLEHETILLEGKDEDVHKIYTTHVHYSKLSKFFLLAGAL
AASVLFEMGCLDSYKVHKMQKHTNVSLEKPLPLKLWYPWDKNKYHIFLMLSQFV
EIAVSAFYVAVAQIFTTTTLLTFLRAKLKILQHQRNFGHLNHFDEVETIQKLCFKH
QTLIQIISVNDVMRNIIFFEFMSMSSVMFAAGIFQVIAKQDLLFNIEFSVSMISFLMMLL
AWNANEIRTESSQLAMALYESRWYEQTHQTKVIMQFMLMRCQKPLSINIGPLGPIT
VDAAMSFTKKTMIICGIWRLKIKSWSTFQNILYFIYSVIFQITNMMIPTLLAANLPVL
FKTDVSGAFQAISMILFGTMANMKGIMCQSKDFLKLQTMFMEDEAMLLSGNDQE
ANKIYTKHIIYSKLSKFFLLAGGLAASFLIETGCENSYKVHKLGRVNVSLESPLPL
KLWYPWDKNRYHILTLMSQLLDIAVTAIFYVAVVQIFTTTTILIFLRAKLKIMEHQFRN
FGTSYINRDIMTNGVDTVRRLCVKHQRLIERSR

>CforOR95

MAPQTRLLKNVRLLMILLGVGRLEIPNTSKFLPVCYRIYSVIIQIFYATFVINLSVELF
ILFKTDIPTALENMSRFIFVILLIVKVGMCQTEKVVELLRRSQLEEDEIICQKDYQISK
VYKMHALYGFKNLTLVTAVSSAVTLCILGIQASYQFSREHVNTNDTSETIDKPQ
LLPLWYPIIDKNKRHMLVMHQIVQTLTSLFSSLVQFTTNSLLIFLRARLQILQIRFA
NFNSMQVGETSNHGDNIPPMTLKQLCVNHQQLISSIKELNDSLKGILLECSVTSILL
AALLTQILWRRYLAFNVVYFLLVVLQIMALSYNSNEIVVQSSQLSNALYESNWyTH
GRKLQSLLLVMMMRQCQKPLVLTVGPLGPMTTQVGVSVKLAYSYFSVMSS

>CforOR96

MAPNAELFRNARWLMIASGTWRDLIPNVPKSFYKFKIYSTAIHLYSSTPVALLLE
LYSLFKYDKVAGFENISMFYIMVILIVKIRICQSRRVIELLRSLKEETDIHSQSDKNI
LKIKYKSHVSYCTKITFTLTVLVVWSAIYLSGSGIINSWTFPEFVSNETVSKPLPLSLW
YFPDKNKHHNFVLSHQITQIMLTSLFSGSVHTFSNSVMIYLRARLVILQHQFKNFDSI
TACTESPKVDLAGHLRLKALSIKHQRLIRSVHNLNQLLQGIMVLEYSVTSVVLAAVI
FQILEREELIFNCSYFVLVTCQLMALAWNSDQIIVQSFGLSLSTLYSSRWYEQDLTTK
RMTHIMIMRCQKPLCLTIGSFGAMTTDAALSVRLLLLMNSFFICTSLDY

>CforOR97

MGHILVAVLFEFSLVVSVVLNISDFGRIIDSLHLLEQTAFLAKLLIFASSGQQLNL
ERRTDEFCRETFTDRQMDVLRKNLKTFTTVAKVYRTNCVICVSFFSIAPLFASGSKY
VLPLPGYVPYDVSNNITYSVTFFAQVLFFSTAAYLNSNIDIISYKLISIATSFPEILSDK
VGKVTFTSHEVEKQTFKEHIKFHVKLLRFVQDIEHMYTTIIFVQVAASVVICSTTFEI
VIFPIGSGEFIRAFTYLNMLAQVAMYCWFHNLKTLSENVGTACYMSTWYLTDK
YFQRSIIPFMERAKRPVVLTAAKLLPLTLNSLMMILRSSYSFLAVLRHIYGDK

>CforOR98

MTIFPRNKHLKVCMYSSSLGIWPFIFEENPTLRQLYQLYSNFMLVYYTFFIGTAYM
KLAELLRADEIRMDDISANLCITLIYTITIRQIMLRGKGVLMIRYIIDTENKIYAAK
DEKVIEAYDRCADLTIKLSKIYLAILFVITMSYFIHPLLEGGYFLQKGNETMLRALP
LSSWFPFDEQKYYWWAYAWHVVDACIGASFVTTYTDILMFSMIVYPTGQLKILDYI
LRNFQFYEANVADGRGDDRASYLAFRECISKHRDIIAYVDDFNGSMQNLMIFFDLQ
SSLQIASILTQVFGNEITLVLLSFVGTFFVGMILRLILYYFANEVLILSVGLAGAIWD
SGWCVQTPRVKYMVMVFMQRAQKSLKLFIPFGVMSLQAFLSVSFAEPSIRVIRFN
FRLRS

>CforOR99

MASNTSNTFQPERDGPFYRSITHFKVAFNWPRSDDPVIRRRHQIYGATLKVISLNFN
VGIVIHMFVSVKEHHYELLIEGLALGSGYLGAMISMTLTVSTERTWSNFLRRLDFK
KFGVPPTLNKIVKRFNFLSNVTYIYSYCGTSLYCFIEITDTAECERVNREEGRTEICG
TVAPIYWPYGLTSTQKIINVIQVVAIMMYSPOCGIFCFPSEAEILNTRVKHASQLFL
ELFDNPDEDLEHLKKRMTFYIEYHIELLSLAEEFNNAFSSLRPCSAGGALVIAFILTO
LLNTYNLGAITHVAGWIIGIFLLCRAGQILQDLSLGAIGEAAVFSKWEYELNNASIKRTI
QLLILRGQKPTYLEAMPVGNHDFDFARLSKTSYTYLTVMNQA

>CforOR100

MPENQIFKVAMYFSSTAGIWPLIFEKHPTLKLCTYMHMILRSEFFVFILRAYFQL
VCLIGEDDLNVQEIFGNLCITLIYTVAILRLRALNRPAVVELFNHVAEENNILSHND
AIVVALYKKAVRKAHILNKLFLFNGWLITLFYFIHPLLTEDRVIVVNNATTYIKLLPL
STWVWPFDAQKHVTVAYVWNVIDGIVGSQFVTNTDILTFTLIYASGRIEILGQKFKN
FSVYVKRLRYEGRVFCAEKAAETALKTLIFEHLQIIRYIDIFNEAMKYIMLDFLQCS
IQMATIILQLLVMEITFVNVIIVGQFFLTMIIRLVIIYYNANEIIIHLSQNWAVDIWWS
DWYDQTINIQRMMAVMILRVQKPLKLLIGPFSAMSLETFAILKATYSYMMMLFNNT
SG

>CforOR101

MVSNRLLILGSVLGLSTFLFWSISPFLESRRTLVTNAWYFPDHRLSPNYELTMLHQD
LAIAYNIIYLVVNTDHFVSNLMMELGKQCEFLGSTLETLDYRFENGALSHEGGKLL
RADSPWFLNRMRSNLVVCIQHYEEVKKLAAVIESFYVSWLLVFLGGTIILCTLLYQ
ATIVSVSSAQFFMLCFFLTSMLEQFLFCWFGTEIRHGVKIIICFCDVYIGITISERADI
QESLPDS

>CforOR102

MTLTSYQAPPQGAFYRTLKHFQAFNWPRNTDLDLKRHNLYNFLFKLVSLFNLS
IMAHFIVNLKDNDFDLVEDLALGSAYVGAMSALILIGLNEKKWSHFFRRLDFRK
FGTPPTYEKMVKRYNLYSIIYVYGYLGTSLYCFIELTDTANCEKLNREGRNEICGT
VAPFYWPRELTTMEKIILNVIQVASILLYSPQSAILIIFPSEAVDLLKTRVKHCAHMFL

VLFDDEPDEDHQTLANRLSFCVEYQIELLNIAEAFNGAFKRCIMHVSITATVVIACILT
QLLTTYNLGAVTHVGGWISGIFLMCRAGQTFRDMLGAVGEAA YFSNWNIDSASI
KKTIEIVILRSQKPVILEAIPCGEHNYDFFVNVSFSSKGRGRNYENIFFQLTKTSYSYL
NLMNL

>CforOR103

MVACPEDVANSVLSIPKYCMILGGIWTLALPTQNRILNAIKVYSMLVKIYLPFTLV
SMYIRFGLTMTTEFSKKNPQDLFKYFGYVVSLSIAVFAAILCQRKVVQFITYVQEE
EQKIGETDDDPDIHQCYSETLKFCRKFNIAVIAFMSNAAVGMTSENLTARFEIDKYNR
QHNESMEKPPFFYELYYFNLDKEKHSLFLLVMNCLFVLINSSVVASTRMLFMTSIIFIS
SALSILQIKFEKSMNQEKALEITKMLVVEHQDVIRATKNLNECIKYLIFMEYLLNS
LTLATLAIPLLTSKRSMSPVLAFGVIFTLIMVLGYSANEIQSSSLADALYECRWY
EQNETTKMLFTMLIRAQKPLGLTIGPFAMTIDSSLKIIKTSYSYVSIMMNSYKE

>CforOR104

MAHAYRKKLEILKVS KCILVIFGAWRNELTEKAYLARCFLYSCFIHLYMTVMIAS
MCGWVGVSLNNKNKSAQEMERLITAITYLSSTFVVMIKIFLCQAGVRRRTISFVLEE
ENKINDTQDEDIFNSHSEQVRFNCNSINLVQAICYLFIYVCFIVENLVARIKVEQYNK
VHNETLIKPLIYDLIYKIDPIKYETFFMFYCYGAAVLLSYGIATNIIISCIIFGSSVIK
ALQIKVRKIAGHGNTFLVSMKEYVKEHQQLIRFVEDLNNSLKYIILIEYITTSLTIAL
VALQFVEDKTSTMRIGRLGYSGSFVYILSLGWSSNEIKIQTMMADALYECRWVE
QSEEAKRILFIMMRTNKPSQLTRGPFAEMTLQSAITVLKAAYSYVSIMIK

>CforOR105

MVGFWPKELIENEMLRKFYHFYSIFIKSLYALVLTSMIAKNFILLTNSENMRDISSKV
LMNLACLVTWIIIQLRVIFYSTTKMRKIISYLEAEQHLLQLDDANYLSCYWQESRY
CSKANVTLCACATTLYLASFYDNTVQSILIEQYNRKNNATLQKPFYDLYYWKMN
VDKYQLFALIVNDFSAIVA VIMGLSAEALILGCISFVIIMIKILQVKIKNFVYPSNDTK
WTIKKIVEEHYNCIRLVKNLNDVLKIPLLVEYILLSFNMAILMLYIRAERFAERGTT
AGYCVGLTIYVFFLWGSASGIKMEGTLSDAIYESPWFEKNSEIAKIMTIMIMRTQKP
LILTIGSFGEMTLNSFLTIMKATYSYATLMMQ

>CforOR106

MRDFPNFLCVPRAESRFLRVPDYREKPLRFLPIEVGNSAGFEITINSRRMAANREIL
NFPKCVMIIFGVWRNHLTSNSILQKFYVFYSVFIHIYMLVFISSMFTWIAVALTGVN
NSAEKNDKIGLNITYLITMLTVMLKVVLCCQTKNIRRTIAFVQEEKKIASKDPEILH
THLEQVRFCTSVNITLTVCHLVLFVFAVIENVVTRLSIERHNNIYNETLIKPVYELY
YHSMUPIKYETILVLFDDIGGTIVISLSVSTNIILSCVIFVSSMLKVLQIKLKKMIIQTD
NIMRDLKQLTKEHQREKSYLMRIGRSFYCGFLVIYILALGWSSNEIKMQSVAIGDAI
YESSWYEHNKKAQEMLLVMMMRTQRPLTMTKGPFDLQSSLMVLKAAITYY
TIMTQKQV

>CforOR107

MAPNREILNFPKCMVVVGWWRNHLTSNSILRKL YFFYSLCIHIYMLVFISSMFTWV
AVGLTGVNNSAEKDKISLNITYLITIFTIMLKVVLCQTKNIRRIITFVQEEKKINAS
EDPEILETHLEQVKFCTNVNVIHFICHLILFVFAVVENIVTRLSIERHNKAYNETLIKPV
VIYELYYHNVDPVKYETLLAFDDIGGTFLNTISVSTNIILSCVIFMSSMLKVLQTKF
RKMVMQGEDVMSKLLAKEHRQLSIFVEDLNESIKYLIMIEYTTISLNIALVTLRII
KEKSYLMRIGRLFYCSFLVYIILALGWSSNEIKMQSIAIGDAIYESSWYEHDKPAQK

MLLVMMMRSQKPLTMTKGPFDENTLQSSLMVLKAAITYVTIMTQKQI

>CforOR108

MKNLVRQHRQLIWFVENLNSVKYMILLEYITISINAALSAFQILKTDSFLERFGILC
YFSYFISYVFLVGLYSANEVRKQSEAIAYAIYESPWYDQSQKVKTALLIMMARAQKP
LLITRGPFGEMSIQSSLTVLKATYTYVTLMTQKYHIK

>CforOR109

MMKNNSINSK KKLQILKFKPKIVMVVFGIWRNQITSNAIIAKLYQFYSVFIHIFILLTT
SMCIWVGISLSHKTKAQEEIEKMITAFSYLMNMFVILLKVTLVQTRGVRNAFAFVE
DEEEKMNKSKDRDILDAHLEQVNFNCNSVNTILALFYLLLYVCFALIENTLARINVK
QYNDMYNETLIKPLIYEVYLYKVDPIKYETIIMLYEYIGAFILLAFSLSTNAILSCIMF
ALSMIKALQIKLRKMAHKDQEAVSILKKNAKEHQFIRFLENLNELLKYLILIEYSTI
SLNIALVALRFLQDDTPTMRIGRVFFSGAFVVYILALGWSSNEIKLQSMASDAMYD
TSWYDQSEEAKRILLIMMRTRKPLRMTKGPFDENTLES AVTVSTNWSLSLNDDE
ICIRQLKTLAILIK

>CforOR110

MLKVTFQCQTKGVRNAFAYVEEEEEKMMKSEDQDILKAHASKQVNFNTVTTILATF
YLLLYVCFALIENTLARLKIKQYNEMHNETLIKPLIYEVYLYKVNPIKYETIIMLYEY
FGGVILLAFSLSTNAMLSCIMFALSMIKVLQIKIRRM TDKDQDAIILKNN AQEHQRF
IRFLENLNELLKYLILIEYSTISLNIALVALRFLQDDTPTMRIGRIFFSGAFIVYILALG
WSSNEIKLQSMADAIYDTPWCDQSEEAKRILLIMMRTRKPLRMTKGPFDMMT
LES AVTVLKGAYTYVTIMA

>CforOR111

MRIGSLFYSGSFAIYILALGWSSNEIRLQSMADAIYDSNWYNQDEEAKRILFMM
MMRAKKPLHMTRGPFDENTLQSAVTVIKGAYTYVSIMIQLHILTEATSNHTYLKK
LDYCRVGLIEREKTAPYITFCVSWLVSEFTSLPSTVLHQSGLT TETLVPFVNNSNRPG
ERELVYTF LSTLQTPTY

>CforOR112

MTAITYLINMFVIMLKVILCETKGIRRTLEFVQEEKKINQSESEDILDTHLENVKFC
NRVNSVLAVSYIVLYVCFALIENTFARIKTGQYNKIHNETLTKPLIYDVYLYKINPIR
YETIIMLYEYVAAAIFLAFNLSNNVILSCHIIFASSMIKSA

>CforOR113

MIAACMWNLDLPPFSKFTKLMYQTYSVVLPALVFLVPVLMIANFPSLLL TDPNSAI
EVTPKMLYCAVLVIKTFYQSSRCRYLLTAAMEEESRLYFINDDEVVRIYEEHIRYC
RIFFKFFCISTMLPVSTECEIAIISYKFSQNLDAVGDKPMPLVSWYPFDKNRHHIWV
MAHQFISIIVTGCYVLSVYVYYSIMIYVRSRLILQHYFRNYDQYQLDGESTTLET
LKVLC AKHQDLININDVNRSVKMTVFLEYSVISILLATILYQLVEGQDMSFNLIFA
FVVSQAQLMFLAWTTDEITTESVNLATALYESKWYEQSQACKILIAIMMMGCRKPLS
ISIGPFGPMTMVSAMSRLKIAYSYMSVMTS

>CforOR114

MDTRKSYFYIYKFLMMIVGIWGLSDHNSSRIKKK FYATYSVLFQLVYLSAMVLSA
DLPSLLKTN SPIAMENMGRFIFCLVTMIKMVMCRSKGVLDLIEDALRQDRELFVQD
DTEIGNIYRWHVNFNKNISLIVTSAALVSLSIAVIGDANAMRRFKKGNATESPLPLH
YWYPFNTDKYFTFVIDQNV RPTLVLFCLGVVSAFVNCLIIFMRAQLMALQFNFRHF
HQYRSHRSPEDILKLLCIKHQGLIKCIGQFNASLKNILLEYTIVSITFGTVILQITAKN

QIVVNSLALIFTTIQLLAFSWSNEIIVQSSELAVALFESNWCDQNKQTKKLIQIMM
MRCQRPLCLRIGQLGLMDLNAGMSVRKE

>CforOR115

MNVLKLLLSTDPLAVDDPLWFIERLWSLAVNNTVWL VIGTLTLVCSISEVCGVLGY
MAYKPNFQTAINFAPMFFTSYHTSLCLTPILLQRNAFQTARKYANEKFWKISTASSE
ALREISVDIIIAKVAWVTNFILNSCSPFFYPYNGVDFDNTLHPMIAILPQLRLPLTVN
YMIVFFNHILVFWKVYYIVLYMLNLTYL VVQYKLVQVTLKWKIVNITEGLGKNVEL
GSMRDDANCQREIHERLKVYVQHYWYLVKYVYQMVTESLKISLLFHVFSGIALMSTS
LLYLSLLRDESADTA AFIL ELVSALYIAFFYVFWAEAFCDQTNVLYDAISLSHWNCF
DRSNSVTILILYDNLKRKLF LTGGGIFIMSFRLLVWNRIYQFIAILTMLGGSLEFGLG
LMFVVRYSDFDMFANFATMFFTA FHTNLALVPFLLQRKTFAEVRRAQLYFWKIQ
EIEPEAVKELKRGIRTGKMVLIVSLMLCCPTPILLPYRGVDYNSTEHTVIMVLPYL
KLPILQHVLA AFYHMLLFGYGYFIFLYLLNWTY MILTYKLEV IILKWKIINITKELE
RKLTFDIIGNTECQIVIKQRLKTWVKDHIQLRV

>CforOR116

MSRRNDFPSMLIFCRRNMTYAGIWRFNISKIPMLQGIYTIYSIFVYVYFPIFLTSLTLQ
FVIMMCDDEEFKNAPQNI FR TITL MITLWTVVEVKAKLSQTRMITRIISYIVDEEEKIR
ECLDNDVLWCYNRQAMFCRKS NFILFSVTMTVA VAMILGNVIQRRQIDIHNAIHND
SMTKHFTYELYAGLDQILSENLEIMNDVSVLIAAALVSSTQLIFISCIIFSTSLKIKI
MQVKFRKMKS YGDYIITL TELITEHQNVISFV GKLNDAMKHIILLEYLLHSLNVASV
SLQFIKSEHNISMAFPVCYFGLLVVQT FLLGWNANEVKVQSLAMADAFWESQWYE
PNYKAKQLMLVLLMRMQRPLVLTIGPPDAMTIQSSLTIMKASYSYVTVMI

>CforOR117

MSADRD MFKVAKILMITGGIWKLKMTKSNLLQFIYAVYSGVVQVLYASGSVSLIS
LFYLFQTDIAKAIENISRLIVVSLQVLKILLCQSEGVVRLFSRAVREQVDVYRHRDG
VVRKVYQDHVKYCKWTTAPVA VFLICGLSQSGIGIWTNFNFELQQRQSNETLELP
LAVPFWYFPDKNKHLLALLFQVFQSQFTSFYCAGTQAYYNSIFIVRAQLKILQY
NFRNFDDRSEANRQISEDFTLTALKKLC EKHQELIRSVEELNDSLKSIMLLEYSVASI
LLAALLFQVMANIGVEFNIVFFILSCQLMAMAWNCNEIIIQSTGLASALYESRWY
QHSQQVKVIVHMLVRCQKPLNLTIGPPGPM TANDGVSRLKLA YSFVSVMS

>CforOR118

MQNLPRSRKLLQVDDNACCRFVPPVGDVSLGNRNRDYLQVRAIAASKQRNLELPL
TVPFWYFPDQNEHHLAALLFQVFQSQFTALYCAVTQAYYNSIFIVRAQLKILQHN
FRNFDDRCEASGQISENFTLTALKKCLKHQNLIRSVEELNDSLKSIMLLEYSVTSIL
LAALLFQIMAQIGVAFNIVFFILSCQLMAMAWNCNEIIIQSTGLASALYESRWYEH
SQQVKRIVQVMVLRQCMPNLNTIGPPGPM TANDGLSRLKLA YSFVSVMS

>CforOR119

MTETKELFEVTRWAMIASGIWRLEIPKANSMIKKLYFLYSIVTQIIFDTSIIMFNMEFI
KLYGVHTDQAIENLSRMIFVLLLIVKFSICQTTEMKTLLRKALEGERKIFTSNSKTIIN
IYSTHAWYFKMLILAMAVATFMLAVYLSEIGISEAYEFHKTHQDFNGSVEAAFPVA
LWYPFDRNQHFIVLCHQTLEICLTGLYTVSVNAFTNSMMIYLRAELKILQYCFKHF
GNYRIKPDIFDGENVSLYLLKMFGRQHQRLLIWTEDLNSTFQKLIFLEYGVASLLA
AVIFQIFAGIRVIFNSIYFVLVSCQLMALAWNANEILIQSENLASALYNSNWDQNQ
RTKVLVRIIMLRQCPLTISIGPPGAMTTNAVLSRFKLA YSYLSVMSPGSK

>CforOR120

MTGKIELFKFTRYTMILSGIWRLEINASRWVRRLYITYSIATQIIFDISIFMFNMEFAH
LFRVDIEQAIENLSRMIFVLLLIKFSICQTKGMQVLIKQALDGETKIIATDNSKIRSI
YEMHAWYCQVLIVSITVASFVLSAYLSEIGIEESYKFHREPRSLNESREDPPVALW
YPFNRNKYFIVVMCHQTLICLTGFYSTAVNAITNSVLIYMRARLKILQHNLENFAT
HRTENCAKGGDHALYSLKMFSKLHQELIQWTVLNGNFKHLIFLEYGVSSLLAA
VIFQIFAGIKVVFNYIYFGLISCQLMALAWNANEVAIESENLATALYNSKWYHESLQ
TRVILQIMMVRCQRQLTISIGPFGALNTEAVLSRFKLAYSIVSVMSSGSV

>CforOR121

MATTQRVLSQQVNMASKKELFKFTKWLMLASGIWRLKIKIASGFLQONLYKVYSITS
QIIYDSVVMIFIVEFYRLYTVDRAKAVENLSRLIFVLLIVKLTLCQSEK MIDLLSLT
LDEESRISAINDPETQKIYRIHVKYSNSLTAIIAICSFSLAIYLTEMGFESNYKSNRRQ
KFDNDTLETALAVQVWYPFDKNKHFQIVMAHQTV EILLTALYSGSVHAFSNSVMI
YLRQLKILQHFRHFHHPDRFENDLRTRSSFHILRNYCRKHQKLINWIEEFNGSF
KYIMFLEYCVSSLLAAVIFQIFAGIEVLFNTVYLVLIICQLMALAWNADEILVEVEV
ITLAIDEYPVIFQSTKLSLALYESEWYNQDKKVIILHFMMQKCRTPLTNLNIGAFGPM
TVSAALSRFKLAYSIVSVMSSGTA

>CforOR122

MPLDFLLFYAFANNAVGNRHVKHILSYLFKICATVSCTSDRCEMATEKELFKSVKF
LMIAGGIWRLQTATSSSVSSWVYTIYSYSIQVFYSTLVVSLVVEFVVR YRANMEG
AIENLSKTIFGILLMLKLLCQSNKLVNLTRSAIKEEEEEVFKKDDKAIQTIYKSHVRY
SSKITYTVAVYSFLLGGYLIEIGITNSYLFYKAHKGFNVSLEKPLPMLWYPFDRNK
YHVWALVHQIVEVFLTALYSGSVQAFNTAAIIFVRSQKILQYLLANFDAYSVTDE
FLEVDDVGLDTLKVFLRSHHKLIIWMEDLDNSFKELLIEYIVSSLLAAVIMQIFAG
KDAVFHTIYLMFLQLVVLAWNADEVKEQLLLWLRHTSNAMTAEREIFKIVKW
LMIASGTWRLDIDTISKTLKYVYLGYSYSVQFFYYSLIISLGV EFTKLF GKNTDAAIE
NVSKMCFALLLVKITLCQSENILKLMRFAVKEEYDIFNGRDEATKNIYLDHITYCT
RITSATAIYSFGLGIYLSEIGIEKSFRFNKSHDMVNSTL DKPLPMP TWYPFDKNKHH
AWALGYQVVEILLTALYSGSVHAFTNSVMIFIRAQLQILQYHFKNCHKSGAEYESN
MPAANASGLKSLAVKHQQLIGWIEDLNESFKDLLLLEYSISSLLAAVIIQIFSGKDV
GFNIVYFLLIFSQLLALAWNANEIKEQSTELSNALYSSKWYDQVQHV KVLVAIMM
MRSQKPLTLSIGPFGPMTADAALSRLKLTYSYVSLMSGNLYD

>CforOR123

MVSNGLDFGPSIYLMTFVGMWREKITNNCVLVQFLYDLYSILLQIYESAVVLLGV
KFGITLTEDLGAALEILSRLIFVTLIVAKVLRCSQSKIRYLLRLALTKEAFIKASEDQR
VKLIYQKHVKHCRMLMVFIMILMCAVLGYFLETATVKTIQLHKFQGSSNDTLDKPL
PLALWYPFDSNKYYACTWSVSSICVVFTLSQLKILQYHFRNFDVYPVGS GDAYIQIE
DVAQRALKLLAIRHQELIKWQKDLNDCFKNLLLEYSLSFMLAAVLFQIFAKIFQS
TELAQTLYESKWVDQNETVKACMQIMVASTLIASLIVEFIVRYRANMEGAIENLS
KTIFGILLVLKLLCQTNKFNLTSAIKEEEGVFEKKDKAIQTIYKSHVRYCSKITY
TVAVYSFLLGGYLIEIGITNSYLFYKAHKGFNVSLEKPLPMLWYPFDRNKYHVWA
LVYQIVEVFLTALYSGSVQAFNTAAIIFVRSQKILQHHLANFDAYPVTDEFLEVDD
VGLRTLKVFRSHHKLIIWMDDLDNSFKELLIEYIVSSLLAAVIMQIFAGKDAVY
HTIYLILIFLQLVVLAWNADQVKEQSANLANALYNSSWYEHSQQVKVFILVMMMR

CQKPLTLSIGPFGAMTADAALSRAKLAYSIVSLMSGNSQ

>CforOR124

MASQKNIFYSAKIVMIVCGIWRLELPTESIFWKTVYRIYSAASKILLSTTVLALLAKF
PELLEKDALAAMEIASLAVASGVVLAKMMACQSRGNLQLIQATARQEEDQLYIQAN
KISQRVYSRHVDYCQKLALIIAIVFFPTTFSLVAQGIQKNYA YTKTDQNNTVERPLIF
LCWYPPFRTENYHSYVLVDQAIRVLNAGTCNLSTTIFIETVLLFLRAQLIILQEQRFTF
YKGTDEAPNAITDHTNQHVVKGLCVSHQKLIYYLASFNESLKFIMLLEYVASSLVI
ALSILEALGGHNVLFNAGFVISNFGGLMFLSWNCNEIIVQSAELATALYESEWYEQ
DKHSNALLQIMMIRSQKPLAITIGSFGPMTVDAGMSRMLAYS YTTVLGGNF

>CforOR125

MADTRTVLGVGKTSWFRKRFRKFFHAVWSAIVACDFTSPVELPGKDSVATYVE
TIANTFWTIAIVILVMSHSNSEQLAKFLRRLERITLKNREHKFVNCPSAWHLPAVLT
CSLDMLFQGVTFDRRNWRYLACRTFLHCSYWTNVRFMYGFAWNLVRNFVWLK
KLETECRLVMLRLRGIRKEHFELCDVLETFNEIYGFAIFATVLSSTMIILCGSTQLVE
YALVEHHRAYAVLVRSVVLTLCTTHWSNAG

>CforOR126

MASRKNMFYAAKIVMIVSGIWRLELPTESIFWKT FYRMYS AASKILLSTTVFALLA
KFPELLEKDALAAMEIASLALACGVVLVKTMACQSPRNLLLIRTARQEEDQLYIHT
NKISEGVYSRHIDYCRKLALIIAIVFLATTFALIAQGVKKNYALVKTHQNITVERPLIF
LCWYPPFRTENYHSYVLVDQAIRVLNAGTCNLSVNIFIETVLLFLRAQLIILQEQRFTF
HKGIDETPIVNAGQVNHQVIKRLCISHQKLIYYLASFNDSLKFIMLLEYVASSLIIASS
ILEVFGGHNVLFNAGFVMTNFGGLMFLSWNCNEIMVQSAELATALYESKWHEQD
KQSNALLQIMLIRSQKPLAITIGPFGPMTVDAGMSRVR LAYS YTTVLGGNF

>CforOR127

MASRKDMFYAAKIVMIVSGIWRMELPTESNFWITAYRTYSTVAKILLSTTVFALGA
KFPALLEKDALAAMENASLTIASGVVLKAMACQSRKNIQLVRTARQEEDQLYTHP
NKISQGVYSRHVDYCQKLALSIAIVFFATTLALIAQGAQKNYALAKTSHNNTVEKP
HILLCWYPPFRTENYHFYILVDQAIRVLNTGTNLSVNIFIETVLLFLRAQLIILQEQR
SFHKGANEAPIANTDQVNHQGLKCLCISHRCLI

>CforOR128

MIFGGCWRELPNTSSLWRHFYSVYSILAYVMIGTSAFSLSANVPSLLEMNVLTAE
CGAQLFCVAVLVAKMIACQSKGNIQLIRSARCQEMQLLTQEATILTRIYNQHIKYC
YKLTISISVVSISTSVAVVEHGIENFLFNHKNNTTLEGPHTMYFWYPFETKNYHT
WVLIDESVRAFFIGICNVSVNVFINSVMIFLRAQLVVLQQEFRNFCDKSGKRKVAGS
KLLRVLCLKHQKLIKYYENFNDSLKFLVLEYYMSSLITASTIIEISGQNVTFSIGLF
LTNFGGLMIIAWNSNEIILQSAALATALYESGWYYQDHETQVLLHLM MIRCQKPLT
ISIGPFGSMTVDAGMSRLRLAYS YTTVMGRKM

>CforOR129

MLTIVFLLTVKMAVFQKKGMRNLLNQTMDEIEISSHGDSKTKKIILYTRYSNRLNII
ITVYSFSVGIHLLIMGIFEYQQFQQIHPNCTEICYKPLQVLYWYPPFDTDKYYGIVIFY
QAFSVLFSDLYNSATQALFNTIMIALTAQLKSLQHHSNSERNVSVGNEQLSKNAT
KRLIISIQKHQSLISFTEELNISMKSILLVEYIISLMIASIVIQVFQGKR VFFNIHYGLA
LSYQMFALAWNANEIREESQNL SNAVYESQWYNRSETFKKLVLT VILRAQKPLSL
KIGPFGSMTADVALSRMKVA YTYVSLMSG EKIGS

>CforOR130

MPKPKGNILRISKYLLSCVGFWKFEDESKQNYVIRSIYLFYSMAIKFYFTVVVVVSIFIQ
FIITIANNSSNSNTETFRQLSHLISLLTAHYIMLVQTSAKFDKILSHMTILERSMLESE
DKEVSDSHLNEIRYSNHVSYSFSILTLCGTSFFLLENYKNNVSVAKLNKKNQTLER
PLLVELYYYKINKDKHANTLFIANEITILNTFIIISTKIIIFTCIVFASSVLKKLQIMFRK
YAVYNDIPMNLKCLVSDHCSVIRYVKNLNDVVKYPILLEIYILNSMSVAAVSVEVI
MEEHNNLMFRPAFYLCLLVVQVFTMGLISNEVIIQSIMLTDALYESPWYDQNKYIQ
KLLLTVIIRCQRPLVLTIGPFQPMTLGSALAICKASYSYVSLMIRNYQ

>CforOR131

MKTQIKVSKAKPILGYSRICLILGGIWPLPLQSQNRVLQRAYSIYSGLMRFYLPFMLI
SLLIKFAISVDERTERNLEKIFFKLNIIILLITCFMMLCQRKEVKEILGYIMEDDNE
IICSKDEDMIQCHLAQVRLCSRSCAIMILTFGSGISMCFENYWRREIDRNNIRYNE
SVEKPFVFEIYFNLDANKHDTALVVVNDVCTAINSLCTSTKMLLFSSIIHSASILK
RLQIKFEKLYGYRGRVLIVLRDLVQEHQNVIGFAEKLNNWLKYLIFWEFLDSDINIA
AVSMQLITSEGKLLISPILFFCVLCSQTFILGWCTNEVKYQIMKGSYSYISIMMND

>CforOR132

MKTQSAIQILKTKPILEYSRYCLILSGIWPQLSTENRIQKVYTIYSGIVKLYLPSCLIS
LSIEFILSTFYESTEKNEKIFSQNLNYIIILLITCFAIMLCQRKEIEEIIITYMMQDNKD
SSKDEDIQCHLAQSRVCSRSCLLIVILTFGSGMSICLENIWRRYEIGQYNKYQNGTV
QKPLSFELYYYKLDACKYGTSLICWKIEQLDKLEKNMLISPILFFCVLCTQTFILG
WSANEIKCQSLMLADALYCSPWCDQSLAAKSVLLTMLVQAQRPLVLTIGPLDAMT
TQSALTIMKGSYSYVSIMLNNYN

>CforOR133

MKMNQRQTVIKELKAKPILNYTRYSLIMAGIWPLRLATQNRLQRMYSIYSGLIKVY
FPSFLLSLSVQFILSTIDENTDENPENIFSQNLNYIIGLLIVGVAAVIYQDKNVKEILNYI
TQDDKEVVCSDKDKDIVLCHLKQARVSSRSCLLMILTFWVGSMCLENFYRRLEID
HYNKHYNESVEKPFYVLYYYNLDPEKHATSVLVANDIFVVLNCLLFASTKMLFFS
CIIYSTSILKRLQIKFVKLDLDCGKSVSQVLRDLVQQHQNVIEFVAKLNKWKYLVLL
EFLNLSLNIAATVSIQFITFEKNMLASPILFFCVLFTQTFVLGWTANEIKCQSLVLADIL
YCCPWYDQSEKIKSTLLMILRAQKPLVLTIGPLDAMTIQSALAILKASYSYPLLLFD
EGVVNVTNGNKILPAKRLERSHLQRDYHLSYAKPKTLVTIYDLNLPYTYLKNWHP
H

>CforOR134

MTDQKSRESVLSFSKYCMILGGIWRLELPWHNVVLTAYRIYSKFVRRFFPLILFSM
FAQFILMVTYENAHKDQETIFKQLGYITCLVMVQVGAILCQQPRLIQIISYAMLEEK
KIMHCSDDEDILLSHTKQLRFRCTCNVVLFAVTTGAGVAILLENFWIRHEISKHNREC
NASLEKPFVYELYYYKLDKENHEGLLLMVNALADFGVCLLMSTKIIFSSCIIFGSS
LLRRTQIRLRKLSSYGLKRLVLEHQLVIRFVQNLNHSVKYMILMEYFLNLSLNIAAVS
VQVMSFQDINMLASPFLSFGILFVETFLGWTANEIKVQSLALSDALYDSPWYEQN
KRIKKAILTMLVRAQKPLQMTIGPFDAMSTQSALTIKASYSYITLMAN

>CforOR135

MKKMISHRPAQRILYYAKFCMIFAGMWRLELPTKCVFLKRLYVVYSAVLQVYFPIF
WISICIQCGIMASNDNSTKSSEELSQNFSFVIAILISEIASILWQQSKGRKLIAYVIKQE
KTILESNDPAILQCHYDHVQFCKLSNLVLIIFAAGIGASITLENYWRRADIRRYNAEK

NASVEKPFAMELYYYKLDKEKHATALLVINHVSSALSAMLVTSTKLICFSCVIFVSS
AIKRLQIIFRKISNHGNDASSTLHLLVLEHQDLIRFVKNLNDLMKYVILLDYFLNSLN
VATVSIIRMSFEAKLISPLFFLSFLFIQIFVLGWGANEIKVQSLALADALYDSTWYEQ
NDTAKKALLTMIARTQRPLFLTIGPFDAMTMESALKIHKASYSYITLMKTN

>CforOR136

MPFAYDLYYYKLNKVEHASILLINDASVVVCGLLAASKIFFFSCIIFPSSILKRLQI
RFRMAVSEERALVVMKEFVLQHQRVIRFIGKLNASKMYVIFLEFLLNSLNIAIVSF
QFISFEPSMLTSPILFFAFLFTQTFVLGWSANEIKIQSLALANAVYSSPWYQCKTIK
GMLLIMMVRAQRPLVLTIGPFDAMTTQSALAIMKASYSYISVMMNNYN

>CforOR137

MQRWKRNRQGILNFPKYCMIAMGMWRLNLPTRNRILTCLYTLYSCLIQIYYPVFWIS
LFIKFVIVLLDKNSNKSLEEWFKDLSYVVGLFIIVIAAQFWQKRNVRSIYYVIEEEK
VLLECRDEELLKCHFELAQFSRLTNYVLFSAFCIGMSVMSETFLRRAKIEKYNQRY
NATLEKPFADLFFVINFDKEKFCILLIVDGVSCFLSDLIGVSSKIMFISCIIFACSTLQ
RLQLKFRKMARYGTDFLITLYHLIEEHQKIIRFVHNFNRSMKYLILVEYLLTSLNIAA
VSIQMILFNSTRASATFFLSYLFSQLFILGWSANEIKMQSLAISDAIYDSPWYQNGN
AKKAVLLIIMRAQRPLQLTIGPFDAMSTETA VTVVKGSYSYVTLMWTKYV

>CforOR138

MLFNSTKASALFFLSYLFSQLILGWSANEIKMQSLGIADAIYDSPWYDQSDAVKKT
VLFIMRAQRPLQLTIGPFNGMTTETA VTFKSTRASAMFFLSYLFSQLFILGWSASEIK
MQSLGIADAIYDGGWYDQNDAVKKT VLFIVMRSHRPLQLTIGPFDAMSTETALTIL
KASYSYITLMRTKYI

>CforOR139

MSLKNQEILKIPKLAMIVLGIYRNNFTESIALRRIYLIYSLIVHVVFIFMTSMTFWVA
MVLAEKDRSEELTEKLISNLAYLASIYVALIKVIFYETKSLQQMITTVENKEKEIQQS
QEQEQLETYAAQARFCTKYNLFALATHIFIYGFAMYGNIAPRIKIGRWNKLYNKT
EKPLIYEVVYYPKMDPIRHETFIMLFSNLGVTIMIWLFSFSTCMLLGFIVFVPSAKALQ
NALRNMSHLKADLSALKVAAVQHQQFVRFVTDMNDSVKYLLMEYITVSFNVAL
TAFTVLKEKSFLQLGILLYSGSIVAYVLILGWSCSEIKFQSMEIASAVYESPWYQHS
KEAKSILFIMVRAQRPLIVTKGPFGEMLSSVAVTYTNISRLVSMQKVNVLISIRVI
KEVLILSDCEAHKPRPQS

>CforOR140

MKSAKNQEILRIPKIAMIALGIYRKNFTNRIALRRVYVIYSIVVHVFAVIFTTSM
SLWVATVFTEKNRSKELTDRLSNSAYLVSIIYVALIKVLFYESKNLQQTITTVENKEKEI
QNSGDQELETYTEQIRFYKKNIFALITHIFVYGFALFENMLTRFKIGRRNKLYNN
TLEKPLIYEVVYFNMDPIKYQTCIMLYSDLGVTVMIWLSFCTCMLLGFIFVPSMAK
ALQKTLKTMPLKTDLNALKVAAAQHQQLVRFVENLNDSVKYLVLLEYITVSFNV
ALTAFTILKEESFIMRLGILSYSSSIVVYVVLVGLGWSCSEIKVQSTQIASAIYDSPWYEH
SKEAKSILFIMVRAQRPLIVTKGPFQMSLESSLAVRIAHNTVYL

>CforOR141

MSSILKLSRYSMVLVGIWRFPISENQLIQTTYFTYSIFMQIFFLLLLTSMISQFVTMTK
ADKNAGISPEQLFTTFAFIINCSIIQIKVILCQTKRLKALISYILVTEKELLRLKDTEIVQ
NHMQLSHFCQISNLAIAFYFTFGVALSIIILVVFISCIIFASSILKSLQIKFRKMSAARTNL
LQFLRKLILEHQDVIAFVGKLNYSVKYLILLEFLLNSVNMASVCVQLITRNMFLAF

IFYCVLFTLTFMGLGWSANEVKVQSLDLTDAVYGSPWYEENVMRKMLVLLIMMR
TNRPLTLTVGPFNAMTTQSALTIMKASYSYITLVARSY

>CforOR142

MYEYNYLKSFSQSDLTIPKYFAFWSVDGRNEWPPYKYFFLFAHAAIMLCVNSLQVV
NLILHFGNLKRMAELGYIMLICMMGESLSVQSFFSRQSFKDLIHMLSEQLFQPKNAI
ELAIVEKIFKFSMRIKNSMLFVSGLCMVACCGTASLYRSQRKLPLAAYYFPDVTVSP
YYDIVYAHQSLAIFYAFNNVFGFAISSMFAHFLGLQC DLLCQRVTRIGKNGSDIRQ
EFLECI RHRLILK

>CforOR143

MIPAPLSYLSILFVQVFVFAWSANEVKVQSLLLADALYDSQWYKYNEAAKKMVL
TMMVRAQKPLLLTIGPFGALTTESALAIIRASYSYVTLMNQYKHNG

>CforOR144

MTSDLA VHTIVYCHNVFFNLEIVDTFKSLFGRQLLIKLLYDFGSL LITALYLYSDRE
GLPYLPDTHLATVTRISSCAFIVMTLWMQFAVMFCCDLVIRESEKLLVTCIDLQRRF
PLGTTEHRELRSFADTIRNRKISFTAADFYE VNRSTMVSLFETMLTYFILLVQFIDK
PNT

>CforOR145

MYPIKKAALYYVLTMFNCLSYYPTEKEKKAKFKFYAVSSCIRILTA VMWVGSIV
HFCVSLKNGVYALIVEDLIFVTGVSTSMITCLLFWINH DNWSNVFLDVTNCQNF GK
PSGFDDRIKALNSMSLYGFIYCCSGIFVYMTFKLTDEECENLNQKQGLSEICNLVAP
LWL PSSVTITRVKKFVIIGVQILCSLYIPTSATISFMIWVTSEILHIRILHLKELIKVTF
DGDEATAKRRLRFCVRYHVEIIRICYNFQRS MYATVGHVASSSGLVLACLGNQLLK
THNFGILILMVGWMVGLFILCYIGQDIKILT SIGDAFLESNWFKGDTKDKKILQIAL
MRTQKPILVKTFLSGVYGYELYFMIVKASYSYLT LIYRST

>CforOR146

FESGFIPSPFLCLVYLFVQTFVLGWSANEIQVQSLALGDALYDSPWHEQNDQAKRLI
LSMIMRSQRPLALTIGPFD TMTTASALRIMKASYSYVSLMIN

>CforOR147

MTFAVSRVETPPITLPQLPNLILGFWGYLGLVLNLVNGHLMILAYPKAKTLM DLHV
RGEVLYKKIESAAKKT ELLIHTLHMALFTYLFLTLPWFTDET NVCYFMPTVDEKLS
RTGAI VFRVVLVYFSVYLCVYVVG TQPLFAFYCLLCLTFQMYLLNDRILEL VENN LG
FGWSLELKYDVNYQRHVAKMLRESARHHVSIKCFKAEVEKVLYYFLLVYYMAY
ILLAVIIFCVTLSPSEN YRGILICFTSLTFNAILTG YAHNLTAQGDYWYELICSTPWYL
WNATNKKALLQVMVHSQESMTFSASTFVKIDTQFLLSYVRNIYGLATALFTISGRE
DKSLHSG

>CforOR148

MGRFIFCLVTMIKMMCRSKGVNLIEDALRQDRELFVQDDPEIRNIYRWHVNF D
NKLISLLITSAIIVGLSVAVIGDANALKQFTKGNITKSRFPVHYWYFPD THEHFTFVII
DQNIRPTLVLFCLGVVSAFINCLIIFLRAQLMELQINFRNFDKCRSHRST EHV LKLLC
VKHQGLIE

>CforOR149

MQTHSTLLLATFYGWFVGLVLICYAGHRLMEKSVALGDEIYLKSTWDDLDKGAQI
DFAFVLLRSQKPLVLRGGPLAIMSLNVIIQVLKAAMSYITLLRETQEV

>CforOR150

MLMHGKRSILFIKPIVIYCNIFGVIPLYNFEKREVSINNWYYSWVALHWMFMLVML
IYEYFVKVELKAKNSEYVFLIFETITLLGTLTIFMMLFNGHCKTKQWEELFRRISF
MENIVNLNTEHMKETNFFKCPFLHFICINFIFFILNITRVDSKYFPVNRQITFYYSFL
YLLIQSNFTSSILYKYEDINRNLLKLRKANVLQSTTALRRIKKCRKMYHEMGKIIGIL
NDLFGFPLFSIYGFCGCQILYLCTDVYVIVAIPTHMAAYSWPLNSALVTVLVVLT
WITSIHYDMVSSQSNKLVTTTCYAIQKNLNICERRQELVDFCDQIEMRKVKFSAARF
FTINRSVIFTHVSVAAASYFIVIVQFLNADKKDRELS

>CforOR151

MNSSGKYFRYIRWLMIAAGMWKIEEEFPAPKKRLYSFYSSIMIQLICTSPIISIALEVPA
LLQSDPAAAVGNIGLLVFLGTVITKMLMCQSKPVIELLRTALQSEFHLAASASTDV
GAIYRFHTKLNNYFITLLITCILFMGVCVATFGDLNCKYFKRYNNATEKPVILNY
WYPFDKNKYVVLVDQNIPTLGGLYAAIVNAFVNSIIVFVRLQLKLLQYSFRNF
DKLEPNEHNGNPILRILCVRHQELIRYVCKLNEHLSIIIFMEYMVSSVTFAAQILQIT
RGIEPFISSVILTYTHIQLLIFAWNCNEIIQSAELAKALFESNWDYDAKITVIAHIMM
VRCQKPLSLMIGRFGVMDLDVGISRLKLAYSASYASVMTSGNK

>CforOR152

MRGCKGANRLTILKTVKTKYLYGSMFTMVENFNSLFGSLLYLMGLHCSTQILQW
GVSLVHIIDVLRSEDDYNRVYLAVVYIMLMLLWLGITMFCDDTVVEESEELMAICY
HIQEDYAVFSDEYRALKILINFINNFKIRFTSKEFYEINRSTMFSIISTTSTYFVVIQFY
DGK

>CforOR153

MGTGTRYFRYIRFLMMTVGIWRIQGEEVSTIYKHLQTYSVVFQLICSSAVISFAAEI
PTLFRKDTAAVMDNVGRLMIYFVIIKISMWQSKQMLHLLQTALRQDNEISSKNDE
KIQQIYEWYHINYDNKIISVIIVLAILIGICVAILGDIECYFFKRSAQNNLTEKPLPLNL
WYPFDRNKYYAELKTTLDPYSIWTDAMSKNISYTPKFVSTAGPNIDGIGCTGNN
YYMAGSFILYPLPVNLFNPLKLNKQLNISNNPTDDLVTGVLNGLDNLELLDMSDN
LWFGINATALSNLKLRWLYLDNNFLSLTVFPQFDYKTLADELVSLEYIGISDNRW
QCDELYDMLTYFKSKNISYTPKFI

>CforORco

MMNFKFVVGVLVADLMPNIRLIQSGHFMFNYYADNSSGMHSLRLGYSCNLVLIL
VQFGCMFVGNLVAEKDNVNDLAANTITMLFFTHCITKFIYFALRSKLFYRTLISWNQ
PNSHPFVSNRYHALALKKMRTLLYCVMAFTILSASAWVGITFVGVHVIQDP
DNENETISEEIPRLPVRAWYFPNAMSGMPYIALIYQVYYYVLFSLLSNLLDSLFC
WLIFACEQLQHLKEIMKPLMELSASLDTYVPKSADLFKAPSSAASDNLIEENEYNN
RNDELNLKGVYSTRQELGGLNFRSGSLQTFGAGGGGLGNGLTKKQELMVRSAIK
YWVERHKKHVRLVTAIGDAYGVALLHMLTATIMLTLAYEATKINGVNVYAAT
TLGYLGYSLLQVFHFCIFGNRLIESSSVMEAAYSCHWYDGSSEAKTFVQIVCQC
QKALCISGAKFFTISLDFASVLGAVVTYFMVLVQLK

>AglORco

MMKFKVSGVLVADLMPNIRLIQASGHFMFNYYHADNSGALHALRLGYSCAHLFLCLF
QYGCIFGNLVVEKDDVNYLAANTITVLFTHCITKFIYFALRSKLFYRTLGIWNQS
NSHPFVSNRYHALALKKMRTLLICVTATTVLSAAAWTGITFVEESVHNIKDPD
NENETITEEIPRLIKSWYPWDAMSGMAYYGLIFQIYYVLFSLAHANLMSDLFC
WLIFACEQLQHLKEIMKPLMELSASLDTYVPKSADLFRAPSAKSQDNYIENDYNAK

NEELNLKGIYNTRQELGGNFRSGALQTFGQGGVGPNGLTCKKQELMVRSAIKYWVE
RHKHVRLVTAIGDAYGVALLHMLTSTVMLTLLAYQATKINGVNTYAATTIGYL
VYSLAQVFHFCIFGNRLIEESSVMEAAYSCHWYDGSSEEAKTFVQIVCQQCQKAM
QISGAKFFTISLDFASVLGAVVTFYFMVLVQLK

>DponORco

MINKFKVVGLVADLMPNIRLIQASGHFMFNYYADNSGSLHILRLGYCCMHLFFVL
VQYGCIFGNLVKEKDNVSHLAANTITILFFTHCLSKFIYFAARSKLFYRTLGIWNQA
NSHIPFLESSNRYHALALKKMRSLLYIILFGTIFSASAWTAITVFGESVHFIKDPDND
NETITEEIPRLLIKSWYPFDAMSGMTYYVALVFQIYYVFFSLFQANLLDNLFCSWLIF
ACEQLQHLKEIMKPLMELSATLDTFVPKSADLFSKSPGATSQDHLIENDFNAKND
LKGVYSTRQELGNLFRSGALQTFGQGGGGVGPNGLTCKKQELMVRSAIKYWVER
HKHVRLVTAIGDAYGVALLHMLTATVMLTLLAYEATKIDGLNTYAATTLGYLL
YSLAQVFHFCIFGNRLIEESSVMEAAYSCHWYDGSSEEAKTFVQIVCQQCQKSLFIS
GAKFFTISLDFASVLGATVTFYFMVLVQLK

>TcasORco

MMKFKVTGLVADLMPNIRLIQASGHFMLNYHADNSGALHTLRLGYCCMHLVFVL
VQYGCNFNVLVLERGDVNDLAANTITVLFTHCVTKFVYFAVRSKLFYRTLGIWN
QPNSHPLFVESNNRYHGIALKKMRLLYIIIIWTSFSAIAWTGITVFGDSVHNIKDPE
NENLTITEPIPRLLVKAWYPWDAMSGMPYYITLVFQIYYVFFSLAHANLLDSLFC
WLIFACEQLQHLKEIMKPLMELSATLDTYVPKSADLFRAPSATSQDQLIENDYNEK
NEDLKGVYSTRQELGGHFRGGALQNFSGGGVGPNGLTCKKQELMVRSAIKYWVER
HKHVRLVTAIGDAYGVALLHMLTSTIMLTLLAYQATKITGVDKYAATVLGYLL
FALAQVFHFCIFGNRLIEESSVMEAAYSCHWYDGSSEEAKTFVQIVCQQCQKAMSI
SGAKFFTISLDFASVLGAVVTFYFMVLVQLK

>TcasOR6

MNSFNWQESIKTNLKAALRLVGLWPKSDFYKFDLYTFCTSLTVVVIVCGHNLSQIVY
ILQVYSDLKALTATIFVASINFLGAVKMYFFIKHIKTVKILFKMLKTYQFKPKNIHQ
QLIKPFLNLWKILYVGYSINVYLIVAMWSLLPVLNGWTWQKKLPFPARYPLDVTKS
PYYELAYVYQFICIWYITVANLNDTIIIALMMYTSCQCDLLCDDLKNTTETRFDDK
KLIECIKHHKAILVFAEKSNSLNMIVLGQIATSTVVLALTMFQLSMVSPLSSEGLNH
LFYIGGIIMQILLYCWFGNEVEAKSSNILYAIYESTWSEASKNSKKNLIIFSIRCQRIK
ATAVKLFALSLRTFITIVRSGWSYFAVLYNVGSE

>TcasOR7

MNKLQKFDWKATIRPNIAFLHLYGIWPEGEEYYKLNFYTLKTILYIIILVISTIVFQVI
NIFFTLDDLTSLTANIYVLLTEILYFIKLCFLVKNMPALKLLMKTLDHKLFQPKANQI
VIIQPLLNFWKLIFLAFVITCSFTVLFWAIFPILDSSEEEKRPLLAWYPYDTKISPNEY
LTYLHQVASIYICYSHLNIDTFITALNTYIQCQFDILCDNLKNIKSDTKNVDTKLAK
CIKHLLILMFANTSNEFFSWIIFQFTSSAAITGMTLFLQTLVVKPFTTEFYNFMAVY
TAEVVQIFMYCWFGNEVQVKSSNIPYAAFSDWTEFSPNKQKSLFLITRSQKSVK
MSAFNVFDLTTDSFILKSAWSYFALLNQVNS

>TcasOR8PAR

MRSFDWKKTIKINIITLQAVGFWPKGDDSFKNLYGLWTAISFTCIIFCHNFFQAVSI
YFILNDLKAVTAVIFLNLSELLGILKSYLIKMPKLLQMLITLNKPLFQPKNERQIK
LIEPNLKFWKQMYNLYWVMSSGALFFWATFPIFDNSIKDHRLPFIAWFPFDTTVSPF

YEIAYVHQVVGIIFVAISTVGVDTLIAALSMYIGAQIDLLCDNLRHLTGPNFNNELL
NCIHHHKITILRFANNSNEFFNWIAFFQFFISATSIGITLFQMTVVTPTSEYFSLISFEL
AIVVEIFMYCWFNGNEIEEKSKNIPYAAFESNWLEASKESKKNMIIFMIRCQ

>TcasOR9

MSNFSWKA AVETNITTLKILGLWPKGDETYKLNFYTYLA VFGVIGLLCAHSFVQIF
NIYFIVDDLEAFTSSIFVTL SCLGTVAKTYLLQNMQMLKELFISINKDIFQPKNNKQ
ILLVEPSIKFWQRFYLIFRVLCYCTTFFWSSYPILDKWTKDHRLPFLAWYPYDSTKS
PFYELTYIHQVVSIIWYLV SASLNIDMLIAALNMFVGAQCDLLCDNLRNIGQNSKEIG
KNLVKCIHHREILRFAVQSNVFFNLIVLLQFFTS AVSVGFTMFLLTIVAPFSSQFYF
ICYGSSIIITEMFIYCWFNGNEVEIKSNAIPYAPFESEWIGVPIEVQKNLIIFTIRAQRPLK
MSALNLFYLSLDTFKAILKTSWSYFTLLNQANSN

>TcasOR10

MEDFSWEATLSQNINFLKVCGLWPPGDEAYKFNL YGIYAGFCVLGFLCVHTGTQT
FNVYFILLDDLEAFTSSIFVTFSCVACVFKTYLLKNMKLLKVLFININKEIFQPKNKE
QQLLIQPSILFWKRFYL VFRILCYNTCFFWCAYPILDKRIKQHKL PFLAWYFPDSSVS
PLYEITYFYQAVAIWYVIISFNIDMLIGALNMFVGAQCDILCDNLRNLGKSDINELN
PDLIKCIQHHKAILS FVSKLNIFFNWIVLLQFFSSAVSVGFTMFELTLVAPFSGQFYF
ICYGSAITTEMFIYCWFNGNEIEIKSSKIPYAAFECNWVGTP LGVQKSLIIFTIRTQRPM
QVSALNLFYLSLDTFKTVLRTSWSYFTVLNQVHS

>TcasOR46

MSKSEKIHTLATYFDSNIAFLKLTAFWIYDDETRRKKYLQHAYNIFWIFLYFVAYQ
PAELLYVYYSFNDLSVFLRALRDIGNHVSLAYKAFNYFIMRRDILKLMETLQHGNY
HYEDCGDFQPKLIVDEEKKEALKWTKYFLNFCNAICLSMFANGVFTFIFLSDKQYV
ERNGQRVYHQEQPVNTVSPFGSGTKLRFVTFIYTMIALTFYAWTIVALDSLITIMS
CISHLKILQGAFKTVRARFIKLCASLSKLLISVSGKLESIYSTQTFVQTFISLGEMCFS
LYLLSETADQNIGNEITYLIATGFELLMYCWFGNRITEASLKISYALYESDWFPSTLS
FKKQIIFTMTRMQKPINVTIGKITPLAFSTFLTIARGAYSFFFLKQRHGINH

>TcasOR64

MMSDEYVKDVFIANRWMLRCAGLWTPSTRSKLVQIPYKIYAIVVFLFVNVYFTSTE
FLSLFYTHKNLYNFIKVNFFLTHFMGAVKVIFWFFKGHVLRDL MRTLESPEFHYE
PCEGFQPLIWRKYRRIGFKYSLGFLALAHMTLSSSYIPLLTKLPYFSWMPFSYSTP
RSYLLALGYQAGPMFSYAYSIVGMDTLFMNIMNFIAAHLVILQGAFASSKMRVLDP
GQMNNEMKRNCRHLQTILRVSEDLERVHRYLTLGQLTATL FILCTSLYLISTPASS
KQFYAELVYVMVAMGFQLYLYCWFGNEVTL MASEIPVNVWKADWYDCDQSFKKS
MIFTMTRMQKPIYMTVGKFAPLTLQTFVYILRTSYSIFAVIKNTSI

>TcasOR65

MTATKSLKEIPPIYLRVHLTVLQILGIDILPVESVPQNLFYTYTALIISTMCLFTIAEFL
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TRGGPEELQIVNDAITMCNRQGYVFYTLVFLIIGARLLYASLANWPYDKHNYFDGN
VTVIVNTKEMPYTTWMPFDYNDSPLYETIFAFQIFSTTVYGFYIGAADAVICG FMM
LIKAQFLIVKRELETLIERAQKAAIAENPDNEDNFGREIERIELLDKRTQDYVAKYA
NECVYHHQELIALCDHAEEDFCYLMLLQFISSLLIVCFQLFQVSTLSPDSVEFFSMV
CYLLLMLFQLLCYCW HGNEVQIVSGELSRYAFGINWIIMRESPKKTLLLLMMRAQ
RPCYFTAGKFSLLSLQTFMTIVRGAGSYFMFLRQMNI

>TcasOR66

MSKNLKEIPPVYLKVHLLTVLQILGIDILPNERIPQTLFYTYSVLLIATMVVFTTAECL
DLVLNYEDIYKLTFLGCCCVTHVLGAAMFLMLYLKRLWGYFTTLENGIFKPNP
CRGGAEFEIVTSAINMCKRQGYVFYVLTGVTGGQGLYAALANLPYDKHNYFD
GNVTVVVNTKQMPYATWTPFDYNDSPLEYEIMFAFQIFSTTLYGFYIGAADAVICGF
LMLIKAQFLIVKRELETLVERAQRAGNPDRGDFGGGINRIEMLDDGTQVFVEKCAN
ECVYHHQELIALCEHAEDFCYLMQLFISSLLIVCFQLFQLSTLSPGTFFFSMACF
LLFILFQLLCYCWGNEVQFVSGELSRYAFAFINWIIMRESPKKTLLLLMMRAQRPC
YFTAGKFSLLSLQTFMTVVRGAGSYFMFLKQMNT

>TcasOR71PSE

MAELKYFKGIVLILKWSLLYPLVKSWPCKCLYYVWALLYVLSFILTFVQCSMYLY
KTPFNLIEEAMIIMNTADXIFYSLFINFTFLYTKRTKLSRFVKDFNQKCLDQTDNKIE
KITMEKSSKLSDKFVFYWTFNCIASSLMPMIASLLGGNKNLPMVVWYPYDPNKTP
YFHLTYIWEIFCISNLGLIYA VLDLVFPCIAIVLGQQFKILASNFKNNVYRALVDSEV
SEKIVQTFSKNLHNSDFNEEIFEIMNSAKFKKNNARYLRKNVKHHQQLLQYCADVS
DILSIFLMGKVSAAIFNTLMAFSLITNADIVGTLYESPWYMC DVHFQRTFHIVQMR
ASKIVNVKAGNYFTMSASSYITFMXNRSGSYIALLLKELTDRGK

>TcasOR72

MAKLEYLTGATFTLKCAVLYPIDSNNPKIKILYAVWAIFFILTFVTGFIQCFVFCI
NPFDLVQEAMIIMSLVFYSTTFFYFIVFYKNWQNMVALVTNINKNFHRATDNVIEKI
SMDQASELSDKLAYVWVTSSSLAVGSVVPVLAIAATGNLEMPMPAWFPYDYNKSPV
FEITYLWQVFCLITLAIYGASDMFFPCITIIIGQQFKILASNFKNNFYTSLIKLGAEESE
VQNFSDIKTHEFRSFYIKYGNIFKILNNAKFQTLNRAFLKRNKHHKLLLRFCEDL
NKILNTFLLIRVSAIVFNLFIFGNIIINADFLWTLYECPWYLC DVTYQKMLLIVQMR
VKRMVSTKAGNFFTMIAPSFIAFQRAVFSYITLLKEVTDLGKD

>TcasOR76

MMESTVTRLKRMYLWPTASVTSRKPFFLITFSCFLLYGSMHLIVNDISMEEVHVI
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SVVL YFFVISVFAWPGIFTQSCEDLNVALNKTEVCGV VSPVWLPFRFDYKPMKQFV
YFWQSFCCLYSNGGAGTISFAMSETIEHLILRVEDLKILFPKIVAERSPEVRRKMLAK
WVDYHLWLLSIGKLMNDTYRYSFSVIVLCAGTLFGCIGYTMKNASTNFNSSFIFF
GWMESVVICVCGQRLMDAFHSVGTTVYNSEWCDDVDFQKGVILITIRAQKPVRI
YAGPFSYVSHLLILTVFQTSYSYINLLNASS

>TcasOR77

MKYILMKKTIAFLSVTGFWPKTKESTKTRAFILFSSSFLLFGSLGYLIVYRKFGSDD
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QYCIFVLSVATGGVFLCPIIFVKNCEMVKQEKNLTKVCGLVSNVWAPFDYSEYPM
KRVSLSWESYCCFINFGCGGIMSFTMIKTMEHLHIRVEQLKDMFPDVVNEKNLAV
RKQKLEKWKYHLLHYDIGELMNNTYRYCLSVIVLCV GILFGCIGISTMQPGSSHN
SLFLFMGWQFQSIICLMVGQRLLDVFLSVGMAYDSAWYEKDVDFQKAVLMIMIR
ARRPVLIYAGPFTNLSHLLILGVLQTSYSYINLLNAK

>TcasOR78

MGHAIMTEILTYLTLMGFWPRSPKSSKASAFILILSTSFLFFGILFYLIVNRQFGSSEID
SIETITSQFGVLYLILFTWKRNDIVEIVELLSDFSKFGKPPFFDQRSTRNLNYRLSCIV

LILIVANIVVAALPVIYIDSCHKANEQLNLTKTCGLIAPVWLPFDYNEYPRKHLVFA
WEVYCCVMNYVGSIGALTMVGTMEHVIRIEQLKYIFPKILDQPNPRIREQMLKN
WVRYHLALFEIGRLMNDAYKWSLSVIVLCVGFALFACIGISMLQSTASQINSICLFFG
WFPSIAFLCMWGQRLLDSSLSVGTAVYSSRWYDMDVAFQKSVLMILIRSQKPIRIS
VGPFTHLSMLLLLGVFQSAYSINLLNATS

>TcasOR79

MGHVIMNEILTYVTLLGLWPRSRKSTKTISYLILSSSFLFFGSLLYLVVHRKFGSNEI
DSIETVTSQFAVLYYMTFFTLKREGTVRIIDQMSDFSKFGKPLFDQHNKRLNYLLS
YFVICLFVAIVGVVALPAIYTGSKHANEQLNLTKTCGLVAPVWLPFDYNGYPLKF
LVFAWEGYCCIIYACSGISSLVVGTMEHLIRIEQLKLMFPEILNEANRHIREQKL
KNWVQYHLALFGIGKLMATYTYCLSVIVLCVGFALFACIGVSTMQSASSNNSVFLF
LGFQSLIVLSVCGQRLIDTCLSVGIAVYNSRWYDMDVSFQKSVHMILIRSQKPILI
YTGPFYSYLSHLLILSVLQTAYSYINLLSARG

>TcasOR80

MGHVIMNEILTYLTFGLWPRSRKSTKTVAYLIISSSFLFFGSFLYLIHRKFGSNEI
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YFVFLVMVAIGGVVALPVVYIDSCHKANERLNLTKTCGLIAPVWLPFDYNEYPRK
NFVFAWEVYCCIMTYACCGIAALVLVGTMEHLIRFEQLKLMFPEILDEPDRHTRQ
QKLNWIEYHLTFDIGKLMTSNYTYCLSVIVLCVGFALFACIGVSTMQSASSHNSVF
LFFGWFQSIGVLCIWGQRLDCLSVGIAVYSSRWYDMDVSFQKSVLMILIRSQKPI
LIYAGPFSYLSHLLILSVFQTAYSYINLLGAKG

>TcasOR105

MKPALKLANVLGLDPLRNDNYTQLKKMFCALCIVSLFVSAYLEFFSNFTTFETYET
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YVYASLVAAACVLFVAVTLIFKPGKPIFLCYGGLHGLESPEFEIYLVVDLIGIVIISVT
VPAFDGLFFYFALYIYTEFKLLKIAFKTMSGQELREAVKHDFLLKYIKKLNVSYP
IFLYQFFCNLLAICFCLFMLSRSRGIPPEMVSFSKYFLCLLAFLVQSYTFCSIGDLITELS
EDVSNAIIFYTDWLDDEAYENKTARLIIMSRAQNPVMLTIGKFANMNLRTFILIVRN
AYSFLAFVNHALN

>TcasOR106

MESALKLIDIHGLHPLKSDKYSTMRTISFLSLVILISAQLEFLSHLSVFEVYNSGPH
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YIYIALLTATCVQLAVLTLIFRRGKPIFLCYGGLYGLES PHYEYISILDAIGIGVISIAV
SGYDAMFFFFALDIYTEFKMIKSAFKRHSQTVSSYNKQFIEAVKHDFLLQYINQ
VNDIFSPMFLFQFFSGLLGICFSLFMISRSGLDINTLSIYSAGLLGFTAQSYTFCLVG
EVISELSEDISNEIFYTDWLDDEVYRNKTAILIVMNRAQESPCLTIGKFADMNLRTFI
MIVRNAYSFLAFINNALD

>TcasOR107

MENPLKLLHIIGLDPRQSDKYSTIKKVISFLIVLAVLLSALIEFFLHHNESQVYDTAPQ
STVPNLQALLKMFALIYKELIDLFTKGNHFWKLDKFGDCHKQKLTCLHXYVDLF
FYVYAVIITGAFLQLALLLIFEPGKPIFLCYGGLYGLESQFEFYAVLDFLAIGVIAIS
VTAYDSIFFYFALYIYTEFKMIKIAFKRENCAQFIEAVKHDFLLQYISKVNEVFSVI
FLTQFFSGLLGICFNLMISTQGTRDMKSFSTYFVGLVGYTAQSFTFCLIGELISELSE
DISNEIFYTDWLDDEVYRNNTARLIVMNRAQESPCLTIGKFADMNLRTFIILRNAYS

FLAFINEVLD

>TcasOR108

MGSILLLNSVLKKMEKALKLVNIGLDPRKNDTFSKFRSIFCFTILISASFSSHLEFFL
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KNLHSTYPIFQIFFYVYVILFLTCAMFALVNWIFDTGKPIISLCYGESEGLETPWVEF
YIVLQSVSEVTIIFLGITGYDMVFLYYAGSVCIQFQMLKMAFAERKMNERQFLKAVK
HHEFLLQYVEQLGDIYSMWFLQYFSSFLGICFGLFLISKEGLPTEPERLSKYFPYIFS
FTMQSFTFCMTGTMLSDWSSEISDEIFHSDWSDDQVYKNKTARLIVMNRAQRPAKI
SIGKFLDLNLRSFILLMRSVFSFLAFVNNILNRIN

>TcasOR109

MGKVKFTEPLEFLNVVGLNPENCSNFSLFRRVISLGFLLVVITLGLLELLHFEGLT
CSRASEAMIVQYQLFIKIAVLLKHRKNLVVLMQKTRKFWPLDKFGQDAKIERPHKL
LKAFFFAAYKLIMLMALQYILRKVSKNGKPLAIAFGESKGLSPKVDHLYFVLHSTS
TFVVLHAVTGFDRLFFFLIGHVLTCLKLVKKSRYLTQNRREKFLQVQHHAFALEF
VRKLNRIYSQVLLNQHLSCFLGICFGLFLVSKDGIPLDGHVTKYVPYVISFITQFTT
FCFIGSLLITWSLQVPAIFYNDWGKNQAYKYKTDKIIAMIRGQRAAKLTLGGFGD
LDLESFNLVVKNAFSFFTFVNAMNQK

>TcasOR110

MDKVEFSDPLFFLNVIGMHPFKADKFSKFRALAFSIAVYFAVIFSGVLELIVNSQGLT
YARASDTLIPQCQLVCKIFVLAKYKKQIARLLNGSQRFWDLGQFGARYGNSFGKT
HKYLKSFLLYKVMLTFTCLQFLAVKIIFKPKPIAISFGETKGLEPLYDHLVYLHA
MITLVTINLVNGFDGLFFYFIGHVLTCLKLVKVAFGDSPIETNWSEEKRFKFAVRH
HRFVLDIEQFNIVYCTMLLVQHLTCLFGICFGVFLMTKDGVPDLDRAKYLPIYV
TFIFQTFFCFAGNLLSWSLEIPNEIFYHDWAKKTTYENKLAKIISMKRQRAARL
TLGGFANLDDLSFRMVLNALSFFTFVNAMMNKKAVTSV

>TcasOR167

MAKTGDIFPVRDPVKRCLFIPKLLLESTNFWPEKRNFLTKFANWVMLIICVLIESQI
AFVNVNIKDITKIASAMSTVSTTFQAITKLTVLIIYNDKLRILKSVWYEFWPSYTA
GREINTKLETYNKIVIVSFLTILISGICFAFGFLSSPLISGERILPFETVYPPFDWTKSPYY
EIIYVTEWMTNIAFILIGICGHDFLMGLCSNVVGQFTLLRELFYLGTKNVAQIIKK
LGHDTNIEPNRQLLRICIIHHVRVTEICKEIAEIFSFCFIQLLSSVTALCVGALIMTFA
DIDAALFTVSSAYIVGHLLQLFLYATLGNEVIYYASRLPNAIFHSHWYNIDLEVKKD
ILFVLQRAQKEVKISAMGVSVDYQTFIQVLRLSFSFYTMLSKVTDH

>TcasOR168PSE

AATKLIVLYIYNDKLRILKSVWYEFWPSYTAGREINTKLETYNKIVIVSFLTILISGI
CFAFGFLSSPLISGERILPFETVYPPFDWTKSPYYEIIYVTEWMTNIAFILIGICGHDFLF
MGLCSNVVGQFTLLRELFYLGTKNVAQIIKKLGHDTNIESNRQLLRICIIHHVRVT
EICKKIAEIFSFCFIQLLSSVTALCVGALIMTFADIDAALFTVSSAYIIGHLLQLFLYA
TLGNEVIYYASRLPNAIFXSHWYNIDLEVKKDILFVLQRAQKEVKISAMGVSVDY
QTFIVLRLSFSFYTMLSKVTDH

>TcasOR169PSE

AVTKLAVLYIYNDKLRILKSVCYKFPSTAGREINTKLETYNKIVIVSFLTILISGIC
FAFGFLSSPLISGERILPFETVYPPFDWTKSPYYEIIYVTEWMTNIAFILIGICGHDFLM
GLCSNVVGQFTLLRELFYLGTKNVAQIIKKLGHDTKIEPNRQLLRICIIHHVRVTEI

CKEIAEIFSFCFIQLLSSVTALCVGALIMTFADIDAALFTVSSAYIIGHLLQLFLYATL
GNEVIYYASRLPNAIFHSHWYNIDLEVKKDILFVLQRAQKDVKISAMGVSVLDYQT
FIQVLRLSFSFYTMLS KVTDH

>TcasOR170PSE

TVTKLAVLYIYNDKLRILKSVWYEFWPSYTAGREINTKLETYNKIVIVSFLTILISGI
CFAFGFLSSPLISGERILPFETVYPFDWTKSPYYKIIYVTEITNIAFILIGICGHDFLMG
FCSNAVDQFTLLREHFGYLGTKNVDQIIKKGHDNIEPNRQLLRIFIIHHVVRVTEIC
KEIAEIFSFCFVQLLSSVTALSVDALIMTFXADIDAALFTVSSAYIFGHLLQLLXHS
HWYNIDLEVKKDIXFVLRAQKDVEILAMGVSVLDYQTFIQVLRLSFSFYTMLS KVT
DH

>TcasOR276

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KFEINVITVFLVNYLLALVASFFYMSFYGDEEIFYLIRFLEDHCPNHKRVLIKLYK
ISFVLLGYVMVVHACQVLYATQHVRFQLILCAHFMANVTKQAKNIKDEHLPDDNN
YQNMIRERLKFCIIRHQEIRRFYFDKLEEMGNLIGGFALLGCFLGISFAMHMLTSEFL
RYHFARTVSSIIAGVTTFATVIAAGQSVETEVDISTRVVKVWKWYTFNESNKRSYM
LMLLSMQTYKIKFSENYSINYELGLSIVRGVFSIVSVVVQLDY

>TcasOR277

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AKEFTFYGPVFFGCFYGM LAIYIILFEKNFIANLSGELKMWSFRSAGAEITRQIRFES
RVVTIYAIIINFVMVVIASCLHITPLESDYETFYMRFFEDKIPDYANVCKTSYRSTFLV
MGYVMMVHVYQIIYATQHKGKQIMLYLEYVKRVTQFNEKIGEKCLFYNESFQKM
VARKLKNCVIRHNEFLKYHRKNTREMSHWIVAFSLCGCLLGISVFFYILSGVIYREQ
YFRVAVLLTTAASTFVAFIVAGQSLESRDNGYSVVSRIEWYNFSETNKKTYFLLL
VMLMQPWKIKFSDKYSINYELGLSIVRGIYSIISVMVNIRFDS

>TcasOR278

MNQPQESFLKNDYLKVLKLISSDVFEPRLVRAILFVVFAVQLTASIITVRALLIKELT
AKEFVLYGPVFFGCFYGM LAIYIIIFQSSFITNMSQELEMWSYSSGGEEINRRVKFQS
RVITIYALVNFLLAIVASYLYFSPLDSDNETFYMVRFIEEKIPDYAKICKIAYRTFLA
MGYVMIVHSYQVIYASQHVRFQIIFFTEYVKKVVEFDEKISEECLFYNERFQTIVGK
RLQNCVIRHIQFLKFDRIKIKEMSNLIAAFSLCGCLLGISISFYVLSGIFYREHFLRVAL
ISVTA VSTFFALILAGQSMESKANSAHIMNNIKWYNFNQSNKKAYLLLLMMSMKQ
YKIKFSENYSINYELGLTIVRGIYSIISVMANMHFDN

>TcasOR280PSE

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KFENKIIKIFVFN CIVTFIGSYLYFLPLDSDNETFYAVRFIEENYPDHRNLLHGLYRS
TFLIFGYAMTVHVYQVIYNSQHLRYQIIIFTEYVASIGNPDKRKENELFYDKGFQKV
VYERLKF CIMRHQEFLVISNKKVGD MRV FIVGYS LCGCLLGISLTFYIFSGKFYREH
FPRVAVACVGAVATFWAVITAGQAI ESEYDSALSTLLGKIEWYFND SNKKNYL V
MLINLMQPWKIKFSEEYAVNYELGLGIVRAIYSIVSVVASMHF EV

>AglOR2

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IYITNNRKNVQEITAALYVTGTFTIDFIQMIFTYKNMNLKILMKEMNRTLQVVKCR
EHYRIAENTKRTYNVLFKSCLYLALLTAVFVMIVPLVGKERATSIKGFYDWTGP
LYFALTYIFQNLVFIWNLICSNFATFTSALLMQVGLQCDLLCCTLDSLDDFYTEDD
VLYEISLENKKLRKDEERFSEAMTKNLVVCIEHHRQIMRVTKNIEQICGTSIFILFIG
GTLILCSSLFQLSVVKGVSVESVMLLLYLICMIVDQLCYSWFGNEVICKSSLILQSAY
KTPWVDCNIKFRKILLQFMTQTCQPISILTGGLFTMSVQVFSIMRTAYSFYFTLLKNI
Q

>AglOR3

MQQNYDFSSYFRPSIIMLKLFGFWRPDRNMKFKGIYNCYTCLCSSIWVAFLLSQIYI
INNNDVQEITAALSVTVTFTVDLIVMMFTYKNNMNLKILIKEMNRPLFQVKCQKH
YHIAKNTERMYKLMFKSCLYLATLTDVFMVPLMGKEKMSSVKGWFPYDYTKP
LYFILSYIFQKL VFIWNTFISFNIGMIILALLIQVGLQCDLLCCTLDSLDDFYTEGNVL
YEISLEDKLLTKDREIFSKEMIKNLVICIKHHRQILRVVKDVERISGTGLFILFVGGG
LILCSSLPPLSIVEIGSIEFIMLLFYLICMLVEQFCYCWFGNEIIFKSSLILQSAFNTPWI
GCNVKFQKILLVFMNTPKMSILTGGLFTMSVPVFSILRTAYSFYFTLLQNIQ

>AglOR4

MQQNYDFSSYFRPSIIMLKIFGFWRPERNMKFKGIYNCYTALCSLIWMAFLLSQIYI
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YHIAKNTERMYKLMFKSCLYLSVLTVDLVTVPPLMGKEKKSSIKGFYDYPDYTKPL
YFILTIFQNLVFIWNTFVNLSIFMIILALLIQVGLQCDLLCCTLDSLDDFCTKDNVL
YEIGLEDKLLKDRERFSEEMTKNLVICVELHRQVIRVIKDVERINGTGIFILFVGG
GLILCSSLFVS SVVKGISLEFIMLLFYLICMLIEQFFYCWFGNEIIFKSSLILQSAFNTP
WVSCNVKFQKILLVFMNTPKMSILTGGLFTMSVPVFSILRTAYSFYFTLLQNIQ

>AglOR5INT

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HIAKNTERMYKLMFKSCLYLAILTDALVTVPPLMGKEKKSSIKGFYDYPDYTKPLY
FILTYIFQNLVFIWNTFICLNTAMTIIGLLTQFGLQCDLLCCTLDSLDDFYTEGNVLY
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VPVFSVTLRTAYSFYFTLLQNIQ

>AglOR6

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CQKHIEIAEETNRNQRLLYNICLFLGVSTDIFAALFPLFSKEKVILAKAWFPYDWTK
PFNYFMTYIFQNAVLIWHTFVCYSIDIFTFILLVQIGIQCDILCYTLNHLDDFYFKDGI
LHEISLRDKLELRKMEKFSKAMVKNLVVCVQHREIKLAKDIQRIKEIGIFVLFAS
GALVLTCLFQLSMVQFGSVESMMLLFFSICMLTEQFLYCWFGSDVIYKGSLLQA
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SIQ

>AglOR30

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VLPYYSWMPFKYNTDDSFLLALGYQAIPMFSYAYSIVGMDTLFMNINLSIGFNLEM
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VHKYLTLAQMTATLFIKCSCLYLVSSTPIASKQFYAEIVYVMVAMGFQLTYCWFNG
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VSIKGSYSFFTVLKSTNE

>AglOR31CTE

MDSYAEDNFFHVRWILRCAGLWPPATKNKAQALYRAYAVFIFLVNRYFTATEL
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PERLPYYSWVPPGFDTGPSYLIAGYQAGPMFSYGYSSIGMDALCYGLMLCIAGNL
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KDLEHLQKYVILAQVSTIQMIICSCLYLSTVPINSKQFYAEIVYLVAMGIQPFLLCL
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TTFVS

>AglOR32

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GFQGLMVREAKRKSFKVSVLVFSLYTLAGVLAFAAWTSIIVKVKGQQFEVNITC
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VGEALLTIRLRTRLKIDFPFGYAGLRDDDCPELERSLYSELNGCIKHLTSLQARDEL
EGIFTYIILAQTICSILIISSCLFVAAMVPISSTFFSQGEYFLCILLQLWLICNFGNEITF
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FSYFAVFRSM

>AglOR33

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GTFQGLMLSKAKRLTSFVSVMFILYNFVGMASQISSITLNEVVKDDHLPGNLT
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LEIVQCAFRTIRERCEKRLDLPENYKIFVDESNTLEKTLYDELTHCTKHLNILLQVR
DDIENVFTYVTLAQTASLIIFASCLYVASTVSMTSPEFFAQVEYFLCVLVQLSVICF
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VAVCRGSFSYFTLFKSVQ

>AglOR35

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EFKPSLIFLKEKRFKVISISVLCTFTLVGVSAHASAVRVIRKEINGTIFEGDYNCQDF
VPYFLIPFEVDTTTKCEYVLFMDISVCAFAWLVCYDGFIAALLNCVKTHLVILK
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KASFSYTVFRRVED

>AglOR38

MEDNIHMKFAKILMILGIWPVKLTGWKLILYNAFYASYVYYIMYDISQGAIIFVA
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DHVQSSMLAMKYVYVSLGSLYFIPIVRNLVEEDDHKYLIFTSWFPFSDKH
AVAYLIQFFGGFYGYAYIVYCGSFFFCMLKYCVGQIKILQHIFRNLRQYTVKYSRN
NDLDEKCSSEIFVKLCIREHQYIISLVKRLDDCIKTLMLLEFQISSFQLSLVVYQILQS
SGWTIERTAVLSYLVTLCSQLFIFYWNAHEIIIESTELAQAVFENEWYTFDRNIQNLL
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>AglOR39NTE

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>AglOR40

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VQLVLLMEDQVNYTEVVNNLCILFIYFNSALRCKSIKGAIRNVIKDVGKSEKKL
WESMDENLKKIYNENVKRNNLFCKIFAGNTLLTNVGYAIWPLFMEKQTVINNTT
MEVKYLPISAWMPFDVQKHYSAYLLLLFNCNYLCTMFFISTEALAFGLMTYPLG
QIHMLNHILRNFRKYKDSLQRSMNLKEEAASETQLRECIVKHQDIKYYVDIFNAEM
KHTYLLDFLQCSLQLTCVLYRFMTQRNLVLILINLQFILVMLIRLFITYWTANEVTL
QSLAVSDELYSMEWLDQKVKKMLFMIMRGRPLILFIGIFKAMSLEVFVTIKVV
TYSYISLRYRHN

>AglOR41NI

DIFAFSLIIFGVGQIKILKLILSNFQEFAMNIKDQLHCSQEEASYITLRECILKHQEIIIEY
IKEYNLVMKNIMVLDLSSVELASGVLTLVVLKATYSYITVIY

>AglOR42

MIFPKNEHLKITIYISAVLGVWPFIFEDNPVLRKIYDVYSKCFYCYLLYVLTAAIQLF
IVTDEVLVDVEIVANLCITLLNFVAILRVNAIKTERVKNIIQNVFKLEEKMMNSGND
EIIIEYNRHARQNQTCNKIFLVNVYLVAILYFIHPLYVEDTIKYYPNRNETVVIKALP
LSTWYPFDQKHYVLTYYIWEQIDAFMATTFIASSDIFAFSLIIFGVGQIKILKLILSNF
QEFAMNIKDQLHCSQEEASYITLRECILKHQEIIIEYINEYNLIMKNIMVLDLSSVE
LASGVLTLVTEMLPNTIYSSQLAFSLFLRVLVYYWYANEIMVHGSEIGMALCNS
NWYEESEVQKMMVIMLMRCNRELYLEIGPFAAMTLRTFLGVLKATY

>AglOR56

MYKAEREEPFYTSNLNLSRMRQIPVSMKKSVMRKFITFLMSKVVGFLFCTAIGPILH
LIISIMRNSGTNVTEDISIIFGASGGGIVSLLFTLKYKNWSNFFKDLVDTRQYTRPRNL
QARATRLNHLGKICFFCAWWVTITYAIAAWFSSKGCQDTNDPGKFGEICPTFIPIWL
PFGTNDVAAGTVVFLVLTFFVGLIAQSFLAECFVMYESTEIFICHISELKSQKQKTEL
DAPFSVETRDKLRCLVDYHVYILNLGYRLSSLIKYTAGHMSLLSALVCGCVANQM
LNTKPMGSLFFLAAWLFCFCHSGQRIKDKTLSIADAIWNTKWKYKADVKTLDK
VQFILLRCQKPICFEALPMGVTDYAFYFMMIKTGYSFFALFRQSL

>AglOR57CTE

MYKIEKNGAFNSNLNLYKMTYQIPVSMKSYLKKFVAIYLLSKVVSFFFTTIGPLLF
LIVIIVTHSETDISEAASIIIAGTAAFLVNVLFTLKYKHWSNIFKDLEDLKKFGKPASY
QKTVNFLNRLGHISIFGSSMVIFIYGLVAWYNTKFNKEFKEDFNQISPVVVPIWLPFG
ANNLTAGTIIFTMQFIFSGILTCQTYLIQSFIYESTEILICYISHLNDFKETFAGSSRV
EMRNRLRFCIGYHVHILKGYRLRSLVKYTVGHVSLLSALVCGCMANQMLTTKPI
GSFILLIAWLIAVFSYCHAGQRIKDKSMSIGNALYESKWYNADNETMKDVQFILMR
CQKPCYEAIPLGIIDYPPYFM

>AglOR58

MYKIEKNGAFSISLNYLKMTYQIPLSMDKSYLKKFVAIYLLSKVVSFFFTIIGPLLFL
IVIIGTHSETDISEATSIALGGTAAFLVNVLFTLKYKQWSDFFKDLEDLKKFGKPASY
QKTVNFLNRFYISIFGSMVIIIYGLTAWYNTKLIKEINEDFDQISPVLPVPIWLPFGA
NNLTAGTIIFTMQIIFTGLLTGQPLLIQSFIHYESTEILICYINHLNDNFKKTFEASSRVE
MRNRLRFCIGYHVHLLKLGYRLSSLVKYTVGHMSLLSALVCGCMANQMLTTKPIG
SFTFLIAWLIAVFSYCHAGQRIKDKTISIGDALYESKWYNADNETMKDVQFILMRC
RKPICYEAIPLGITDYPFYFMMIKTGYSYFTLLNQST

>AglOR59

MYQVQRNKPFWYTIKALHIVMAIPVSFEKSYLRRFYIKNVVVRFGAFACLAILPSC
HLISSIKEHNGADISEDISMILGGVGTVTNTLLAFKYDLWSTFFMDLENCGLHFG
PSTLKKRKKELNIYSLTYTIYTYFGQFVYGLEAALKWSDCKKLNEEKGLKEICGAF
FPLKLPLDVTSPGSAIFALQFSFTIFSIPSGGVICFMVLEVTEVVICYYKELKSNFE
RVFDVPDEEKRKERLRF CIRYHKHMLGLTRRLQKMVKYTAGHLSLISAIVFGTLGN
QAFKSKPLGAMIFLVGYIIFSLCRAGQRLMDETQAVSDAAYNKWKYDADPKIM
KNIVLIARAQEPMLDALPLGSFCYPLFLLIVKTSYTYLTLQQT

>AglOR60

MYEISKEKSFYSSLTILRYTYAIPSATEKSGLTWFRFIFIVIRLASLLNFVILPCLHLIST
VRAKTGVDISEDLSMFGAFGFITNAVTFLLIYEKWSQFFIDVEDCNRFEPGIEER
KKKLNLYSLLYALYAICGVLIYGVIIASSETSCKRMNEEHGLSETCGMFTPIVLPFD
GSNVYIRSIIFGIQMLLGMFTLPSTALISFLLYEGVETLILHITQLKKSFIEVFDVASNA
ERKKRLRFCVYYHINILSLCQRLSTLGKYTSGLFCMACALVFGCIGNLILKSKPIAGI
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VMIGALPLGCMNYALFLMIMKTSYSYLTLLTQNT

>AglOR71

MFKGISKKVLNTSDSIKICVWFPKLLLNSVCMWPGQINDILQGFAFWSIMAVCTFV
EYGLYNFIANNFENFNESFTAISFFSTTLQVIVKGSVFYYYLNTAKRISDVILYKFWP
SNLLGKEVESSLKRYQILLIGMMSIYFNGSFFSIVFILTPFKETRQTPYKTVYPFEY
SDGPKFEIMYLVQSFTNFYVVLGVVIGVDTLMAVCCNITAQYRLLKNAFLKLGTD
EVKELNSKSLSTLCAESDTSERNTTEEKKFLIRCIKHHQTIEDVETVYSVIGFFQLGFSI
VSICLSSFVLTTKNLEFSQLVNITIFLSGNIVQLFCYCSVATEVNFEMDNLSQYIFSSY
WYQADFVNFKRDILFVIKKSQEVQKITALKLFPLNYNTFIQVLRVSFSFYTLSSNITV
K

>AglOR72

MFEGIPKRILNTSDCAKICLWFPKLLLNLVWLWPDQMNDILQGFAFWSVMGICTFT
EYGLYSFISNNFNFNESFTAITSFSTLMQVIVKESIFYYLKTAKRILDVILYKFWPS
NLVGREVESSLNRYHILLIGMISIYFHGSIFSIIYILIPFKETRETPYKTVYPFEYSS
PKFEIMYLVQSFTNFYVVLGVVIGVDTLMAACYNIIAQFRLLKGVVLKLGTDDEVK
EINSKLILSSESDNIGRNVTEEKEFLIRCIKHHQTIEDIETVYSVIGLFLGFSIIAICM
SSFVVTTEEIEYVQLVNISIFISGHIVQLFCYCSVANEIGLEMDNLSQHIFSSYWYQTD
FVNIKQDILVIMKKSQEVKRITALKLVPLNYDTFIQVLRISFSFHTLLSNITVK

>AglOR80CTE

MNSYYNVVLYCTGVHPSYSVGNFRVIANLSVTVCGTILVLMNIYKETKLEGVESLS
LLLIVLIKYLTLVFGRRLLKITYATENFWEVNITDEGIEFFKQHLDREVDFHKLFSF

TGMVAYAAKPLMQNNKSSILGCYVPPAIPYPVFFIFELYFLGFVSSTFISFNILICSLII
SVVIQFRLLSKIRTIINFLGIETKHDMDICFRKCLKHRIKYHQFLIRYVQDLNKLSTP
VAILIVFSVSLVCLNMYNLSVNKSSIVNSYKVMITVSSVIAEFFSVYGFPAQLMMDE
SAATADTIYYECNWYLPKVRPLRKDFLMIIMRSQKNVCIKAGNYHVVSQTILL

>AglOR81CTE

MISNFCNISLYCTGVHPRHPFGIIRILNVLVSCGTVLVLLKIFKENDMQGVESLSIF
FLVITKYLTIFGRRLVQQILKATENFWPIDITDDQTIFFKKHLDRVQNFHLFVMTG
MLTFAVKPFVLTDASSMFGCYVPPQIPYPLFYIFEFYLLSFLSLGFVSFNVMICTLIM
SVVTQFRFLNYKIKAINFSDIENDHDLETCFSKLDKDRVRYHQYLIGYVQELNKLST
SLALMMIFSVSLMCMMDMYILSVHKGTVVDHCKVILTSSAVISEFFSVYGLPAQLMM
DESAATADTIYYECNWYLPKVRPLQKDFLMVIMRSQKSVSIRAGNYVVSNQTIL

M

>AglOR82CTE

MKDSYFYKHFMLGIHPDKQFNKCRFIFDVITTCIFILALIKLFQDKNLINVELVSSV
FLAAIKYLTLVNWRKMTRQFEYTIIEFWKIVVADNQITFLLRHLKAVETFYRYVFIF
GPFVFMKPLVTQDSSIFNCYVPPVIPPLFYILECYLVFLGSSAFIALNLFACSLIVL
VAVQFRLNLKIKYLNLEDIENSQDFNRFVRELKIVNYQQFLMRYVKDLNKLFCV
PVAFLMIISVILCSNMYILSTNQGTVDVDRSRIMVTSSCVIVEYFLVYGLPAQLLMDE

>AglOR83PSE

MISSYCYKYFLFLGVHPQQPFSKCRVFFNILITTFFFLMACLKCYQDKNLDYVESLN
SFVLASIKYLGVMVLSRIQQILQRMEDFWKVNADDKIMLLMQYLKRIETSFNCLLI
FGIFIFALKPFIVKGSIFNCYTAYDSISFVLYFEFYLLLAISFISFSNFTCALITLVV
VQFRLNLKIGSINLNAENTDGLDEFIRDLDKTIVEYQQFLIRYVKDLNKLSTVPTALL
MVSSVTEMCINMYILSLNGDIIDKTRILVSLCILMEYSLVYGLPAQLLMDELAATA
DMIYHECEWYLPILRPLRNDFLIIARSQKSVRLRAGNYHVINNQTILLMIKTAYSFY
TFLHNIVQRANN

>AglOR84

MISSYCYKYFLFIGVHPQQPFSKCRFIFNITIIFFFLMACVKCYQDKNLYFAEILNSFF
FVTIKYLGVMVLGRNKIQILQSMEHFVKVNVADDKIKYLMQHLKRIERSLSCLHIF
GVLIYAGKPFIAKGSIFNCYVPSIIPPLFYVFEFYLLLASTSYICFSSFTCALIILVV
VQFRLNLRLRSPDLNDVENTDGLEKFIRDLRSIVEYQQFLMRYVEVLNKLSTPIA
LLMVSSVTELCINMYILSLNGEIIINKSRAIIVSFCTLLDYTMVYGLPAQLLMSESAAT
ADMIYHECKWYLPILRPLRNDFLIIARSQKGVRLRAANYHVINNQTILLMVKTAYS
FYTFLQNIGQRPRN

>AglOR85

MENISYFKHFSFLGIHPSQPMDKLRIIFNCSLVSCICLLALLNSYFEKDLGVVDVCNG
LIIVTVKYLGLIFGRAPIKRILEAMRHFVNTDVEDDQVKYVYQYFKTIEKVYKHAIF
FGIILHVAKPFFVRGSSICNCYIPPRIPPIFYAFEIYVIIVGAASAFCFNVFVCSMIVSV
AAQFRLVNLKIEDLNARKIENDHDLRVYKVNLSIIKYQQFLIRFVDDLNKLSTVPI
ALLMVSSVTMICSSLYVRTTHQGSVFEEGRFFIIIFIVTAEFFLIYGLPAQLLMNESEA
TADTLYSECKWYSPQLRSLRKNFLIMMIRSQKSICIRAGHYHVINNRTILLMMKTA
YTFHTFLQEVT

>AglOR110

MCKLDKSANKHKLFAKIFMKGDPLGFLAYPMHFNMRNHITLINMVKALIVLYLQT

FNIIGMVYILKDESGVYLQRYTSVILAQQIGIISLVIHIYYTKDIMLLRDVIEASFLPLN
AVGKELHQNLLRQCSSLIRKLYLLVFILAIPILCNVPLTAGREDVQFTVMFIKKHFG
VWSYLFQGLYYFCLMALGYGLASVCTVCLYLMTHLKFQFRLSSEYLKQISSDCKL
DYEDHYYQEVIKQKLRSFVQAHNKIKATSVFLEIAKWPLLVLTMASILSYTAFGYF
AVSEDIPSKFVRFGLGTVIAAIFTVILITSGQGLQDEAADLYNAACHCDWNHWNQ
NRKTLLMIIINTSIEVKMTSFGILDLGHQILLLLLKVSYSMVLLFVNLLK

>AglOR111PSE

MSAKEENARERNLLGDTFMKDDPLFFLIYPVLFNMRNHIFLINMIKGFIVLYLEVFN
VIGIVYIWKDEIETYMQRYISVLLAQQIDILVPRVFIKEHFSVWPNFFQGIYYFCLLA
LGYGIASSTNSCLYLMTHLKFQLHLLSEYLKRISGFTPDCEDAIYQEVIKERLRSIV
QAHNNINRTAAVFLTVGKWSLIISAMSTMSYTAFGYIAVSEDIPSKYYRCGLGVM
TAGIISFIIIRSGQQLQDASANLSSAGYQCEWVHWNVQNRKTLLMIITNTSKKVMT
SFGL

>AglOR112INT

MDDTCKISKTHKCICKMFMKEDPLHFLIKPLYFGMKKHIFVINVIKSLIILYLQIFNAI
CVVYICSDVTYLRRYISGILIQQVGISSYALMIYYARDILHLSDAVGTSLPFNATGT
KIHQELLRQCALTRNFFPLTFILLTAVHCGLLPVVSDFAHYQFAVTFLEHLGVWS
YFFLGLYYLCVLSAGYSIGCICCVSLYLGLHLKFQFQLLVSYLKQISLDTDANIEDGF
YQDLICKRLTSFIVAHVKIKRLSFMFLEIGKWSVLVTTVSCSFLYTSLVHFIAMSSNL
YSAACECDWADWNVQNRILLMIIINTSKTVKMTSFGLLDLGNVIMLRMLKLTYS
LVLLFINVNK

>AglOR113

MDAKEVRDTRFLLDERPMKDDPLFFLYPLYFNMRDRILLINTAKCLNILYLQTFN
VIGLFYIFKDETG VYWKYLSVIFIQQIGISSYLWQIYYARHFLYFSELTGKYFLPFD
ATGTKVYQRILGQCALTKKLLLAMFTGLIGTISILLPIIGNEEDIEFTVMFIKTHFN
WSKFFLVLYLVCVSLGHSIACSTSMILYLAMHLKFQFYLLVEYLTQISCIENIDD
VFHQDALHKRLRSFVRAHGKIKTTAAIFLELSKLSVLVSVILLSLLSGLAYLVMMD
VSPSIYFKCILALSISATVGYMITKGCQDLRDESTNLVNVACQCKWFLWNVQNRKT
LLMIIANSSKEVKVADYANLDLGYEIIIAIWKITYSIVLLCLNLNK

>AglOR114INT

MDAKEVRKTRFLLDERPMKDDPLFFMLYPLYFNMRDRILLINIAKCLILYLQTFN
IGLFYIFKDKTG VYWKYLSVIFIQQIGISNYLWQIYYARHFLYFSELTGKFFLPF
TGTKSASLYNVACQCKWFLWNVQNRKTLLMIIANSSKEVKASGFGNVDLGYEIIIA
ILKITYSTVLLCLNLNK

>AglOR115CTE

MDAKEVRKTRFLLDERPMKDDPLFFMLYPLYFNMRDRILLINTAKCLILYLQTFN
VIGLFYIFKDKTG VYWKYLSVIFIQQIGISNYLWQIYYARHFLYFSELTGKFFLPF
ATGTKVYQRILGQCALTKKLLAIFTGLIGTISILLPIIGNEEDIEFTVMFIKTHFN
SKFFLVLYLCIASLGYSIACSSSMIYLTMHLKFQFYLLVEYLTQISCLAPNDDVL
QQDALHKRLRSFVHAHGKIKTTAAIFLELSKLSVLASVILLALLSGLAYLVMMDV
TPSTYFRSILGLGTSLSVGSIITKGGQDLRDE

>DponOR1

MCLINFLSYPRKILLIGATWPKYHSSLGYKIRRTVTLANILSLLCLSYNASFHM
GDFVQFSESLYMLISVVNAFLKIVLLTLNGKVFLKLIGMLETSPFKRFETLYKKIVKDFL

TVKAVEFFYWIEVSGTVLFLSLFPIFESEALPMDFPHFNNGTFHYPFYIFEAFSLFVSA
YDNMAVDLLTVGHIISIAAVQLRILNQKLVDTDKNIKNMPNYSVGNVERLTIGYLTE
CCIHYSDIEKYVKSILEVFSVIIFVQLGTSVVAICNAGMMILSVKLASIEALSFFYIV
TMFAQLGMYCWFGNFVYVESLEVTTSCYLSHWDERRSAVRKTLFMLMERAKKPL
AIRAVKFATLSFDTFIAIKWSYSYFALLNNSMKN

>DponOR2a

MNLSKFIEFPRKTLVLTGSWPQQHSSWPYLSRRIIVMTSIALLLLALVYNASFHFDD
PIKLSSESLFILISVVNVFLKLIIMVVNEKVFLNLIARLETSTFIKGGILYQPIYVKFMEI
VRPVYVTYFILVCGCVTFRSSFPFDNKKFPLDFPHFDGYPHYVFYFFQVFSLSSV
AYDNMAIDLVLVGVVIAAVQLQVLNSKLRDTKQNVQFLPNYSISNHETLTVGYL
KDCCIHYSIDIEEYIKCLLDMFSIILVQLGSSIVVICSSGMVLLSLKPLSIEAISLYFYLI
TMFTELGMYCWFNGFVYVESLEVINSYLSHWEERGPAVRKTLFMLMERAKRPLE
IKAVRFFTLSDTFIVILKWSYSYFALLRNWMAD

>DponOR2b

MALVGFIAPRKVLLLTASYPQKDSWSYKTRGFASLTISVLLLLTLVYNASFHIDN
FVALSESLFICMSVINVLLKAIMLSVNQKTLWALVGMLETSTFTRNKVMYQSIISNF
LQIVRVVDFGYFTVVFGLLFRNLFPAFETGSLPMEFPHFNDGYFHYPFYFFQSFSL
LVALNMMALDVLVGVVIAAVQLQVLNSKLRDTKKNVHVLPNYSMEDEEALTIG
YLKECCIIYSDIEGYIKCLLDMFSIILVQLGSSIVVICSSGMVLLSLKPLSIEAISLYFY
LITMTELGMYCWFNGFVYVESLEVINSYLSHWEERGPAVRKTLFMLMERAKRP
LEIKAVRFFTLSDTFIVILKWSYSYFALLRNWMAD

>DponOR3

MSVLGETTQIKKKWRSSIAITEKVLVITEIWPNDTSLYRTMKVVFITIVCIVFNLTVI
DELKMLAIRQDYKTLSMHLSTFGLYIGFSVKIILFQFTKHGPLKNMLDSMDSPIFHA
YPPEMQKHQDNCIRVSNLIGKFFVYLVGGTILFYLNKPFYSSYPLPITFSHPLTTTTF
YLLLTLQCVCFSYLIMIGICFDMLVMGLANVATAQLDMLIEEITFTPTSJETLEKEE
HRFIKCAERHNAIISYVNSIEDVFTYIFLAQCQVSVTCICNGLFQLTHVAPVFSIHFY
YNCIFTFNVLFIEIGCCWFATLMTNKGNDVADACYNYNWLHSSSATRKLLLIMLCR
SQKPLFITVGKIIQLSIGSFLSVLKTAYSYYALMQHLYDKTSQ

>DponOR4

MNFEELFKVPKLILNSFGLWPQTNRSPLAKIRRFSLIFLGVMTSILLFECYILNNIDS
TFELITVSIPPSTLLKQLAFCLNGDHFLAELIFLREPALTSVPRHLENQMKRHLNLA
KYFGDRYLLMCLASAVGYNLLPLITDKPLPIPTLLHASLYQPGIYLLIICYLLNGTA
NNCCLDYALNCMCVIRGQICVLNGKLRARVICKEEKDLNVELVRYISACVEQH
AKIIELEVELTEKFSEIVLIQYLTSIAAICIIGFRMVTVDLVSFPFLMAAFLLCMFCQ
LGIYCWFGNEIILQSLLTREACYEFDWINADLQVKNMLLIIMERSKRPLHLTAGKFSI
LSLDSFTSVINSAYTFFAVIQTKYSQSSSHNL

>DponOR8

MIKQPSYEVYATDFFSVNRWILKCAGLWPPSTPNRVVRRLYQLYTIGVFLFVNLWF
TGTEFVSLFYTYKSQYELIKNVNFFLTHFMGAVKVVILWYFYGHLLRDIMNALESPO
LHYEGYADFSPHRISHLHRAIGRRYSLLFLCLAHATLISSYIPPLIAVAEYLNQPQGG
LQKLP SRLPYFCWMPFSYDTPGKYLLAVAYQAGPMFSYAYSVVGMDALFMNILN
CIAENMVLIQGAFKTVRERSTLHYCVGALAPPCHAIREHPLVLRQMDLETKKIKHL
QITLRACKHLEGIYHIITLSQVTATLFICTSLYLISTASPFKQFFAELVYMMAMLFE

LFLYCWFGNEVTLKYEQLPMHIWESQWLATDDCFKKQMIFTMLRTNRPVYFTAG
KLARLTLPTFMSILKTSYSIFALIKNFSK

>DponOR9

MDTLGPALTKVRLRPLSLDIPDSKGTDPKLNLYSAIDRISFLCGQAKLSKNRSWILR
FAYSLYSYTLIIAIMFIIEIITFRKSLTELTTVLSEIGMMFTHLVGMVKFWILHKRD
EIEQVKNKLRDVQFEYVGGIDDFQPGLKMRKEKLFIIIISTFIFALYNFVGISAHISAAS
MMYKYTANGNFLGNTTCETFVPYFYFPYFDVSSPSSCHYLLFYMDLSLDIYASYIA
TFDSVVFILLNLLATQLNILGDALRTIRKRCVKRLQMKVDSSSLYDADNPLENEM
YNELTHCTKHL YLLLEVGNDESIFTFLTLLQTIASLLIFASCLFVAARVKPTPIFYS
QLEYFSAVLSQLTVYCWFGNEITLASSAIPYSIYSSDWFSSSERFKKSMLLTMARLQ
RPLYV SIGFTPLALTTLLSVIKGSFSYFTLFQSAGTD

>DponOR10NTE

KCVHMKFVRRMTMLLLGIWPIKAQGFTKRFYETYFWITFAYYIAFNISGLTMAMLT
WSHNYLITANSMAIVIEYVSNAYKVLKLSQTFKDLLHEIADSERNIFDSNDRDFTD
IYAKNTEKNRKIVLFYTIMGTTGISLYFITPLVSNAVTPPLGFNNDTGVVNHHFIIFSW
FPFDPDRHYSAA YLIQFTGCLFGYSYIVHCGAFYLSILT FIAAKLKILQHLFVHFSKY
SRQMENAYELNEEQAQFVLLRLLIQEHSKIIDFVKRTNNCIKLYTLINFLVSSFQLSL
VAYQIFKL PPLQQVTVFSYFITLITQLILNYQAAHAISIESQNLAGSIFKGDWHSYSPK
ILRILQLVCMRAQKPLAMTLHSFANVQVNLLIKIFKALYSYICLILKT

>DponOR11NTE

NPPAVYHLSFARKMLLMLGIWPLNRGDWLEKLYELYFLTTFIYYIAFNISGAALAIL
TWSENYLTTASSMGIVIEYMSNAYKVAIFKSATMRGLIREINEKEQQIFESDNQKVK
RLYMKNANENRKVVLSYTVMGTVGISLYFLTPLVGNALIPLAFNNETGIQAHYFIV
FSWFPPDPNQYYWAA YLLQFIGCLIGYSYIVYCGVL YISILNFIKVRFQIIQHYFINLS
DYGEEYEQLYTVDQEMAQFLLLKVLVKEHLQIIDFVKRLNDTMQFFTLNFLISSF
QLSLLAYQILQLPLIQQLPVLSYFTTLNTQLILTYQAAHMIVVESSNMADSLFMGN
WHTYSPRTLRTLQMICIRAQKPLAMTIGPIAQVKVTALIQIYKALYSYMCIMMKI

>DponOR12NJ

LIPRGNHLAFVATVCMCAGLYPANLLSANHSTAIA YRMYNNFLKLLMVLCFISSYT
QLYILLSAQELRYEEIVKNISISLLLILMLLRQMFI RYSPDVARLLSMVGS AERLYGE
TEDFAVWRIAEKERLFFKRHFFAYVA VLCAICVEYMVMPFYYQEAGA QDATGISK
PFLLSLWFPDQHVYYWETFCLSSFFIGLLVLSQVTTDALFFCLIRHPVVQLQMLQH
YFQHFEHYSKRLEE QEEVEESVSYIRMF EKCIQMHW RVIEFLDLTNKNFSGMMLM
DFVQSSFRITSICCVMGMSKSVDFMVLVFTLSLLTLTFVRECYIYFSGSQVIFLSCGL
GD LAFETDWYRQSRHFKFMLQFFIQRSQKPLKLGIGPLADLSLGALLSILRATYTYL
TIVTGFDG

>DponOR13

MYNRNQFFVARICKLAGLYPVQLLPADENLRKLYTVYYHVLVVLFFICLMSFFAE
LFRLLHAETVIVDDILKSFSLATPLVVTSFRQGIIRSPDVRKMLKNAGIVEQRVYEE
NDPEVVKLFEKAGQVSMLYLYLVVATAFLSLISILEPMYDKHRVFSGNATVSPGK
TPLPLWFPYDVQAHYWETFFLTILLVWAVVLFQVGM DVLFFYFIRSPVIQLEILHHY
LKHFNYYTARISVEPGNVASNIMMKKCIEMHQKVIKVDIFNENFSNIMVLDVQSS
LRLASICVVITMTESVTVSSFGFTLIYLVISIIREYYIYHSGNEIIFLSSELVHSVYETD
WHEENRQFKYMVAMFMVRAGKPLNIKIGPFGSLGLPAFLSILRASFSYFSLVTGTQ

QL

>DponOR14

MYNRNQRFVVARICKLAGLYPVQLLPEDENLRKLYTIYYHVLVVLFVICLMSFFAA
VFRLLHAETVIVDEILKSFSLATPLVLTFRQGIIRSPDVRKMLKNAGIVEQRVYEE
NDPEVVRLFEEKAGQVSLLYLYYAVSIVFLGLVCMLEPMLDNEQVFSGNATTSFR
KMAIPLWFPFDMQAHYRETIFLTILVFCILAGFQVSMDFVFFYFMRSPAQLLEILHHY
LKRFDYYTGRMSVEPGNVASNIMMRKCIDMHRKVIKFDIFNENFRNIMVLDVQ
SSVRIASLSAVIIMNESDSVISFGFSLIHFWMALVREYIYYAGNEITFLSSELVFSVY
ETDWYKENRQFKFMVVMVRAGKPLNINIGPFGNLGFP AFLSILQGSFSYFSLVT
GIQKS

>DponOR15

MFIRNQRAFVARTCKLAGLYPVQLLPEDENLRKLYTIYYQALIMLYFICLISFCTELF
HLLRAEKATVDDILKSISMTTLFAMTALRQWVIRSSPDVQKILRKAGNVEQRVYEE
NDPEVVNIFERAGHVALLYIYYAVGTVFLCLGCILEPLYDNQKVFSGNATAFSRK
LPLPLWFPYDIQAHYWETFCVTILLICLLVVFQVAVDVVFFYFIRSPVIQLEILHHFFK
RFNDYTGRISVEPGNVASNVMMRKCIDMHRKVIKFDIFNENFSNIIVLDVQSSFR
LASISAAIIMTESFTVTSFVFTLIFLWITLVREYIYYHAGNEIIFLSSGLVHSVYETDW
YIENRQFKYMKMFMVRAGKPLDIKIGRFGSLGFPALLSILQASYSYVTLVRGIQKS

>DponOR61

MYQPKKTDIFYYSLLFMRYLHYPSRANESSWKIYRIISLFIKILNSFVWIECVLHFS
MAVKDNVPVDISEDIVGFTGLANSMLFCIMFELNVKEWSRVFFHITDTSKFGMPPK
MSQVIDKCNRFSWIYFLYCCTGIIYGIINIVDPGPCERWNAEHNHDCRTLTPLW
WPEDDIEPGLKTIIVICQLISCISYVPPSATLTYIIWEAGELIIAKIHHLKQLFESALDN
DKLEIRRARLRFCIQYHQDIISTIEELNGAARKVCGQLSFVASIVFSCIGTQMLKEYSI
HPMLHLIGYAMAVFLVCQNGQKIRDQTYDIQDAVYKARWYDNITSTTKDSQLIML
RCQKPLCMDAIPFGIFNFSLLLVIKTSYSYLTLINKTS

>DponOR62

MYFPNQNEPFYTLRFLQYSSYPWPNQAEKWYNSTSLVRVFTSFVSIECALHCT
MALKDGIPVGISEDIVGLTGVANCMFVSAMFQLQAKRWSSCVLDIIDTKKFGLPK
MPQMVKKTERIAIWYSIYCTVGILTYTFYSAIKATSCHEQNLKKGTHEICGMITPFW
WPYKDNPIVKLLFNLYQLVSVLLILPPSALVTFASWAASQIIKTKIHHLKGLFADV
SDKDSKRQKARLKCCIYHQHIFKISKELNGITRLLLGQSSFSAILSCIGSQILKEYS
VGAFLHLMGYTAAVFLLCETGQTILDEFNVRHAVYASDWHLADSSLAKDIQFVL
LRSQKPILMDSYLFSGFSYSLIVIVKTAYSYLTLMNKSSI

>DponOR63

MYPIRKDLPHYASLRMLESIGFYSENTNGFKRSIVRTLIFCILCWSIILLSAVLLIYEN
LNDKNYASVFFNIAVAVASTSTYCTLLFVKYQEKWSDILTALVNYEKFGKPRRY
NQLKERGDRVAMACWGGILTGVFLYMLFAILHENDCELEKTGGGVCGLIPTWLP
APYDNSLLARLVLLYDIPNAAA VSSFVLVTHLNIQVNEFNARIDHLSLLFNDIEFC
KDPQAQLNKMKHCIEYHQDIIRVSLQFKNLSKRTMGHMTLTFTIVTASMGCLLQT
SKNFYQENAFFEIIYVINMFIMCYCGQRLEYKMKTVGDFLYSTHWYNLNPQLQSL
IPLVILNSQKTIRMDAVPIGYLNYELFVTLTKTTFYSYFVLTQLT

>DponOR64

MLYPVRKGLPFYHNLLVLKLAGYYPKSSNYNKKLFFYCLVCWMSLWTGTLWNLI

LLYLSIQNKSSHGITEAMGYLIGNSSLALICLHFALKHQDWSHLM DALIDFQKYGKP
PKFNTVQTNASKVGITFFKVLFC AAVMYCVLQVLL EEECEKCLTFGKTSCGMLLPT
WFPASHAESKLAKRLLLLIYQLLACWAIAPFTVIVSLVLQANEFIA YRIDHLKSLLRK
VGSNENPDLQLHHFLAYVQYHHHIIRLCRKLN YVAKYTTGHVALTFVTVVACFGH
HSIQEKSLSLTYQATYVISM CILCYAGQNMQDQMRSIGDALYSSTWYNCSLKVQ
KMIPLVLLRTQQPIGLDAVPLGVFN YMLMVMVLKTTYSYMSFLSRTI

>DponOR65

MEGPKRVKCKVSLNFLRIARILPAAGMENS RQYLA AIAGIFSLVTLTLLVISYVF
VGLNNHFPMVFIQFPVIVCLVSIWGV MWINGFCVKNRHLLLQLEEALADCSTFGKPP
AFKIFQEKMNLLAKLHLSYVTGGALL YFIFFAPMHKKNCEALNIQRNFSEICALLPI
HIPLVPYAALEKFPFLQLINAAEFLMLMYIYV VCGTVVWLNVEVIEYICLRIRHLKT
VLLEALACP NRATRRGLFGRAVQYHEEILRMGR LADEFFGTELVLHVVLTGAILGV
SAFVMLESATLETLMIFVGWLNAIIMGCAAG QRLINESATISDVLHEVDWFEFDNG
LKKDLLFFLVR SRKSMYIRAGNKLS ELIEFFQILRTSYSYVTF LNSIDGN

>DponOR70NTE

DVLEQMFAAFNVCKNPVLLKLFKTIMALN VLIITIQAACIIKNFSFNMIYHGWEL
ALNLMGTSFMALFLYKQDIFLPLVNFKERHC WNSEAMGRKILKEIKDNAKGKLA V
FTISSFTVLSTNMLACVFYKEALQKQYLIL QMITSYWRVHLVYPLWV ALTMANTM
GGLTAYYFFYFVHFLKYQIRLFKAFITYTSG KLDSSSFSGKIYQQEVKKMLR IIIKRHI
ILKTWGLMMLKPGQIILLMSMFFGGFLTICN CMAVLFIPDTRLLFATLIFFTATYIHM
VARFGQRFEDIFNELYVTTLLSFPWHKWD SSNRSLYLVMIQNMQRPVKLEVP LLVS
LNYANEVRKVDSRYSTAKKLIFNY

>DponOR71NTE

NLLPDVYQFIMLSRSTRHLIKLTMLVSACI IIVETYYFTKKFNADLLQYAERYSLSLY
ACIITSLYPRMMKALMINLKTLSLFYVSLE DVDAQTKQNIFSARTRCSIVFKMLCM
ASILCFSVCNYYWLQNKDSLLAIEVLH KYVSKDSILTKVAYCLIFIITEVLFIPSVASP
MYFVYVHFHMEVKLMMLTYVTTIDTMNSAEIAT QSTNHEYYRNMMTKLAIVE
KHSVIKRYNNAFAKQLQLLYMLYICSGVIFGLS AVCTLVSRPFKLIKSLSTWIA YVV
FSMSLTHVSQCFEDASANLSDAVLNLKWYN WNKPCQLSYLILITNCLKGMPVSVL
LLFDANYSFYKKVTRFLYTMGGFLYSIRK

>DponOR72NTE

TLLPEICSFLMISDRMILLNCIFAIYDIIA VSVD SYYFTTVFSWTFKQYGGSYFAHCY
GLLLNVLHPVVIKMFAGQLRMFERLFIVDTS NISDQTAGLLVYIKHKINAMFVAMI
VASLATTGVNVYFWCQDRDQIMLTSKLLTD YFSPGSIIVKLFNFIE TFADIIACIPTVT
IPAYFIYLFYHVEVQLLLTDYVRSLHNEHER TFTNKMGLSTENYHSISNSVKKIVK
WHLEIKQYNYEIFAINQMVHFLYICTGLLVS IFSLSLFSPNGNALQIGITLISFALFA
YIPCDTAEDYEEFSMHLSEAIYDL DWYNWDVKCQKLYLMLITHTTKGIQVTIFMLF
GINKELLK KIIAKLLYPVMNLLYSASKSN

>DponOR73NTE

VLLPLLYRFIMITQYASIRKLIYFLV FVAGSLVLTQTYLFLKIFE AQIWIKYTCFYFLTI
YITGCMPLAIKMYEIWMPRLKRIRKCILSDL TRLGPTFYATIQS QARMRTFIFAIHVS
LIVGLAVANVFLFSLKKTQLSII SVLFEDNLPSAASEITQWILCVLALISVCILFLPAY
YILYGIFYMKLQFIILHFLKHIHEILKRNEQ VNRFDTTYQQNVKRNLTFIIKRHQEILI
FSREISEACSTTNFIYVLNGILILLYAI FAVYVPAFTWVQPLGGFITFYGIFFYMCYHG

QHYEDINLEFLASVETLEWYHWNRENVSILLLIHV MAGTQVKMPLTTFISLNYTLF
KQVIKLTYSVVNILSSIRK

>DponOR74NTE

TLLPILYRFLMLTQLKFTRRLIYFLV FVSGSLVLIQTYQFLK VFDVQIWIKYASFYFA
TTYMVGSMPLAIVMYEIVMPRLKLIRKCVHTDLTRLGPTFYRTIKYQAKLRTIIFVI
HVILIAGLILVNVILFSFDKTEFFIISLLFEENLPTAVSETLHWIMCVLALITVVILFLPA
YYILYGIFYMELQFVVLINIIKHIREILQMSEEINMSDKTYQEHVKRNLIIFIKRHQEIL
IFSKEMADVSTINFIYFLNGILTLLYAIFAAYAPAYIWVQPVGGFTTFFGIFFYACYH
GQHYEDINMEFLANLENMEWHHWNRDNRMLMLIQIMAGTQVKLPLTTFISINYE
LFKQVVKLTYSVANILSSTKK

>DponOR75PSE

MVINSYITIALYDIWTSKLLIVRRCAFTDLKLLGS AFKAQITHDANNKSFSFVYVYTL
ATCFMVTHIISLNSNRRNTLIISLLMDEHLSPTLSEL SHWIICGISCVSYGILCLPAYI
YVLFYLQFHFIDILLKYLQEINDYLFKFDHQTNRA VESHQRNVKNSWIHYQTPPRNID
VQFVQQLSSYYVPHSLYTMSAMFILMYAIFSVFVPMYTWVQSVTAAVTFASGFY
LCYQGQIENINEKFVS*LENLEWFAWNKDNISIYLILHHTARPKLKINVISFISLNFEL
FKQMVKFAYSVTNILRSTRH

>DponOR82

MSDSSDYFDLNYKISTWFLIPPKFTLKIIYWIIATPHFILACGS AFLEISKLFIGGSG
EFSANILNLGVSALHFMAVNRVSRWLFKKGEFDIILERIRKLSMDYSLFEYQSNCLE
SNENQPNQPVQPTIRR VFVAEAEINPIVEYKLEKMEKSKIHCLRITIVFLIYVVLNLSI
SYAFNYMGPTYEKWNPARNKTFVYRDYPYPLWYPFDTSISDGYLLGFFYQPYAF
FFIMAAFLSIEDLSVAIIHLTTHIKILGYAFGYVDHNINPMLEHHEIIEELKQQRIIKLI
NDLKEIYKCAEILNSYLSQQLLIQEFLMSIVICCSVYRVTVVTSSSTEMSYLSTMAVII
GADMFIVSWYNQGFTLEV FELQHRIYELEWIDYQPKLRKLLLFLMCRVQKPFHFT
MGFGFPLDARVFLSMIKMSYSFYTLITRSSQKLTANT

>DponOR83

MDYFDLNYRISAFFLLIPPKISILKIIYWIVA VPHFFLICGS AFLEIGKLFMGGSGEFSS
NILNLGISALHLCATNRVSRWFLIKNEFEVILANLRKINTDFSLFDYQSHQSGFKMD
ANEPENAIKIKYKTTKLETKRYCLGIFLFLINVALNISISYAINYGNPLYEKWNPLL
NKTSVYRDYPYPLLYPFDTSVSDGHYLLGFFYQPYAFFCLMCAFFCIEYLCVGTIHH
LTTHVNILGYAFSYVDENIDPMLDYSKVIMLKEKRIIKLSGELKEIYNCAKELNAVF
SGQLMQEFLMSTVMCCC VYRVTTNISTAEIGYLS TMVAVCVAEMFTVSWFNQCF
TLELFKIQQRIYELEWIDYPPKLRVLLFLMCRVQKPFNFTMGFGFPLDVNVFLSMI
KTSYSFYTLITRSGSKFSNEDV

odorant binding proteins

>DponOBP28

LKITLPELQEYVDDLHKLCLEKGGLTENDHQTYNINDKNEKMMCYMKCLMLES
KWMKSGGEIDYDFIETQAYPEVRDLLLSALNKCR TIEEGADLCEKSYNFKCMYE
ADPVNWWFFV

>DponOBP27

RLTEKQVAAA VKLVRNMCMGKSKVNPEDIDKMHQGNWDVDYEAQCYMWCGFN
MYKMLDKENHFDDKKSALQQMEQLPTDLQDYVIKCMGQCENAVTNFDDKCVVAF
EYSKCLYFCDPEKYFLP

>DponOBP26

LSDEMKELAQMLHNTCVAETGVNEDFIRKVNAEKIFADDENLKCYIKCLMAQMA
CIDDNGIIDEDEATIAILPEEYQALAAPVIRACGTKHGANPCENAWLSHRCYAEMEPS
AYMLI

>DponOBP25

HPPRGPPGPPFLGHPDPESANECRTEVGLTSEDRETKKNGELTEKELCFIRCLGQK
NGALSDAGALNIETIKNDLPDHLEDSEAVIACLKKVGTVTTCQHIKKVAKCYPEPK
EPMVRT

>DponOBP24

MSDEMQLANQLHTTCIGETGAAEDAITNARNGDFSEADSFKCYIKCLLSQMAIID
DNDGTIDVDAMVAVLPEEIQEATEPIIRKCGSIIGANPCDSAWLTHKCYKKEGPEHY
FLI

>DponOBP23

AMTEAQMKAALKLIRNVCQPKNKATDAQIAAMHNGDWNQDKNGMCMYMCVNLN
YYKLQLPDNSFDWETGLKVVESQAPPSMAGFIMETTTGCKDAVKTRDDKCKAAVE
ITKCLYDQNPEKYFLP

>DponOBP22

ELDQTSLLPETKELMAALHKNCIEQIGVSEADVDQLRAANFEEDAKLKCYTRCLM
AESGVMDENGAIDVEAFAEILPEAVRGNIQTIFRRCSLTNKDIEDQCVKAYEMVKC
WHKEDPESYFMI

>DponOBP3

LKITLPELQEYVDDLHKLCLEKGGTENDHQTYDINHKNEMMCMYMKCLMLES
KWMKSGGEIDYDFIETQAYPEVKDLLLNALNKCRITIEEGADLCEKSYNFKCLYD
ADPVNWWFFV

>DponOBP21

LSDEMKELAQMLHNTCVAETGVNEDFIQKVNAEKIFADDENLKCYIKCLMAQMA
CIDDDGIIDEDEATIAVLPEEYQALAAPVIRACGTKHGANPCENAWLSHRCYAEMEP
SAYMLI

>DponOBP20

KKNKSNDEEKAKSYKKVFKECQKDETRVDASIIRKLKHKQVDLPANFGEHKLC
VFTGIGLLKADNTVDEDKLLKIASAKPQKDIVDNIVMDCTSSKSTLQETALNLDK
CLTYSIEF

>DponOBP19

DLTEEQKQKIVANGKACVAETGADPELIKAARQKGFADDAKLKAFALCMSKSGF
QNEAGEIQSDVVKQKLGLAIGDEAAAKLVEKCLVSKGSGETAIETFKCYENTP
THIAVF

>DponOBP18

DFDFSNYKEFENLAGDQREKAIKLFKECMAETGATHEMMEKSVEGDIPDDIVFKN
HLVCIGKKSFGIDENGMHIKEKLEKLTLLLGNEELVDKILDKCFMEKSGPQDTAF
ELAKCCHREYHN

>DponOBP17-1

ELDQTSLLPEAKELMAALHKNCIEQVGVSEADVDKLRANFEEDANLKCYTRCLM
AESGVMDENGAIDIEAFGEILPEAIRGNIQAIFRCSLTKNDIVDQCVKAYEMVKCW
HKENPESYFMI

>DponOBP16

AMTEAQMKAALKLIRNVCQPKNKATDAQIAAMHNGDWNQDKNGMCMNCVNLN
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ITKLYDQNPEKYFLP

>DponOBP15

YVPNVNDKIRDFCIDDSGVSIEMVENLLANPEKELIDVESCIVHCIFTEMGLLSENG
NVEIENFKSLKASEAPYIDLNCLLEEIKSIDHCNEMMILRACHV

>DponOBP13

QDFTEEQRKKIENRQQCIEETKVNPDIEKADLGDFAEQALKCFKCFYQKAGFV
NDKGEVQKDVVEAKLPPQADKKRALEIVDKCALKGKDACETVYLIHKCYFEHTHP
EAEKTAKDGGKSEEKKA

>DponOBP12

GKPNDLFTRITPGDVEVCGKDTGVDRKDFEEAREKGALNHSMLCFLKCAMEKAGF
LKDGHLEIDQAKEASPKMTEPVVECFKAVGPSTCDDIQKVENCLPGS

>DponOBP10

LTDKQKELLTQHYNQCVAISKVDQAVLQKARAGDFANDPNLKTHIKCISEKIGFQG
TDGKFRRDVIEKKLKETLPGDNAKNAKLIETCVVANKDPQLQAFNAFKCLYTNAKI
NLL

>DponOBP9

DQVQDIWDRVHQCCQSPNTHVPQEIFDQLKRGETPILPANFGLHANCMLKKMNL
QDNDGHIISGVKEAAQRHYQSAEKINQIVKDCSATKKTKEETALNLFCLGQNRV
NIG

>DponOBP6

DAEINETAFAKGRDRIMAMSRTCDENPATAVDQKALKKYLQSNPAPANGAAHA
LCITKNLQWQNEGDSVKNPVITEKVKAIFGSVDAKVQYIEECTEAKATPEDTAEQ
LLKCYRKHSPKIE

>DponOBP5

DQREKAVEFQRDCMEAHGLEDLHEIMDGKPIQNEAFYFHFFCVVKKAKLISDN
GIVNTDHFENLKGVIDEENMAHVAALTRRCLIQRDDIFTTIKMAIDCFYSSEHKL

>DponOBP4

LSDEMQLANQLHTTCIGETGAAEDAITNARNGDFSEADSFKCYIKCLLSQMAIIDD
NDGTIDVDAMVAVLPEEIQEATEPIIRKCGSIIGANPCDSAWLTHKCYKKEGPEHYF
LI

>DponOBP2

LECGLSKISSEHFRKIASSECVKDNELNRIWELTSETSMEEDSVSSDEEVPVTKGREA
PNFHDLGSSAHRNMKMSGASRTKRSRKGFNNEPMSNVQKSSPASTTTEHTTTM
QSEENEENAAANNVEESGEVCILQCIFEKLEMTDTNGLPDHKKVASALVKSASGRE
TQDFLQDSVDECFQETEEDGFENSCEYSTKLVTCLAGKGSNCADWPVGDLPF

>DponOBP1

RLTEKQLAAAIKLVNRMCMGSKANPEDIEKMHQGNWDVDYQAQCYMWCGFN
MYKMLDKENHFDKKAALQQMDQLPIDLQEYVVKCMDQCENAVTNFDDKCVVAF
EYSKCLYFCDPEKYFLP

>DponOBP17

LSDEMKELAQMLHNTCVAETGVNEDFIRKVNAEKIFADDENLKCZYKCLMAQMA

CIDDDGIIDEEATIAILPEEYQALAAPVIRACGTKHGANPCENAWLSHRCYAEMEPS
VSG

>DponOBP32

DQTSLPPEKELMAALHKNCIEQIGVSEADVDQLRAANFEEDAKLKCYTRCLMAE
SGVMDENGAIDVEAFAEILPEDIRGNIQTIFRRCSLTNKDIEDQCVKAYEMVKCWH
KEDPESYFMI

>DponOBP7

DLTEEQKQKIVANGKACVADTGADPELIKAARQGKFADDAKLKAFALCMSKIGF
QNEAGEIQSDVVQQKLGSAIGDNEAAKKLVEKCLVSKGSGEETAIQSFKCYENTP
THIAVF

>DponOBP6

KITLPELQEYVDDLHKLCLEKGGTENDHQTYNINDKNEKMMCYMKCLMLESK
WMKSGGEIDYDFIETQAYPEVRDLLLLSALNKCRITIEEGADLCEKSYNFKCMYEA
DPVNWFFV

>DponGOBP83aX2

KITLPELQEYVDDLHKLCLEKGGTENDHQTYNINDKNEKMMCYMKCLMLESK
WMKSGGEIDYDFIETQAYPEVRDLLLLSALNKCRITIEEGADLCEKSYNFKCMYEA
DPVNWFFV

>DponGOBP83aX1

LKITLPELQEYVDDLHKLCLEKGGTENDHQTYNINDKNEKMMCYMKCLMLES
KWMKSGGEIDYDFIETQAYPEVRDLLLLSALNKCRITIEEGADLCEKSYNFKCMYE
ADPVNWFFV

>TcasOBP11

FSHDELDTLSFIKTCNRTSPISMRTMNEVLINKKLGHESSAFKCFHCLFMKYG
WMDSGGFLLHDIKQTLSESDVEIASLEFILYKCTATESNNRCERAFVFTQCFWDK
MAEQQPSDQFFYNIEDKK

>TcasOBP24

EIVVPDDLKDYINELHDHCLKEMGLTEGDHKNYNIHVKDPKMMCYMKCLMTTSK
WMNMDESIQYDFILSSVHPAVKNILLPALDKCRDIPKGTMECEKAYNFMCLFNA
DPENWFFI

>TcasOBP16

GLDPKFLEKLTQEVQAVGTSCGEKEHATADDMIEIMEEKFPPTSHEAKCVVACFYK
HYKMMKEDGTFDKDAAVKAFDEIKAQDAEIHAKILKVIDACDAKKQMSDDHCVS
AASMAGCVKTEAIANGLTKEAFMAS

>TcasOBP26

KVEIPDLEAEIDEYFEQCFEPNGVTMDDIKAYKMGDKDPKIMCFMRCLFVSGKW
MDENENMQDYDIKETIHHAIRHITPELENGKEAQTGDKCEKSFNFFMCMNRAEP
EDWILDYKS

>TcasOBP25

KVDIPDLQAEIDGYYDICYKQIGLTKDDLKAYKIGDRDPKIMCFMKCVFVEAKW
MDENENLQDYDIKNTIHHHSIRHITLPELENGKKAEGDKCEKSFFNFCMNKAEPE
DWVLIQ

>TcasOBP08

ISEEMQELVNQLHSTCVAETGVSEDLINKVNSDKVMIDDEKLCYIKCLLTETGCIS

DDGVVDVEATIALLPEDMKAKTTPVIRSCGAKMGANPCESAWLTHKCYLETSPAD
YVLI

>TcasOBP20

ENEHEILEVRALCMNETGVSEETARNYKPAEDPASEEILCMVKCIFEKIGCLKDDGS
FCVDTMKKKNYIMDVINEENEKIYECLRGVVGKITNCRDMAAVEECFVKNDK

>TcasOBP2

EKESSEALQQIFTELDGPAELRDQCLEKNSMKVTDLKYNTSNDIPEKELCFYKCF
YEGVEFIDANGNLNVNNMKEIPAISELGDEVLNEITACVEKIGKIRCCGDLRKIEQC
YQNTM

>TcasOBP21

ENLDMFDPAGLQACMKKLSVGETELAKALEDKSKDPPEKIMCLFKCALED SGFLQ
DGVVDKSKWPMPECVQDVVKITNCNDMVALKHCFD

>TcasOBP22

LDCGIHINKNDALKATINKCLISNKTLEDLWDMAPMSSESDSSSEVPPVDGKMLQ
NFRIKRASVRLTNTETNETTPEPKAVSSEAQATENCIIQCIFDNLQMTDSTGYPVHT
KILDGLLKNTTNRELRFQDQTTDECFQVMDKEDTMDPCSYSNKLVTCLAEKGRS
NCADWPVGELPFKP

>TcasOBP15

QSLSEDEMRENARKLMTSCKDKVGASDADVEALKMHQMPESREGFCMLECVFDS
AKIMQDGKFSKSGMIEGFKPLIGDDKAKLESLEKLSATCESELGDGEDKCETAKRL
VECVIKNGKTHGFEVPPPRE

>TcasOBP23

QLKAAVKLVNRNMCQPKSKATNEDIEKMHHGDWNIDRTAMCYMHCALNSNKLIT
KENVFNRYAITLAEKNLPTALKTASIEAANLCKDSAKTLDDKCVAAYEISKCLYE
SNPEKYFLP

>TcasOBP09

AMSEAQMKAALKLVNRNVCQPKTKATNEQIEAMHTGNWDLKNGKCYMWCILN
MYKLGKDNSFDWEAGIATLKAQAPESVRDPAIASVNNCKDAVKTTSDKCEAAE
IAHCMYLDNPEKYFLP

>TcasOBPC19

DESVYLSNHEACVKLSGVDETLLETIYEGDVFEDMKFKTYIHCFFKKSQFQDENG
MHFDAIKSSFHKDFSQTENIDKTITECEEKKNLNGESALET AFLHFKCFMGEL

>TcasOBPC08

TRFFNHDEIQKLECFPDIGGGLKAELWPNVSCVFRKGFDDKGEFKIDVLKQKL
SKFQDDKYL VNEIAELCVDKHDFMTAAMKSALCLNKHAPWFSPYQD

>TcasOBPC06

FSLSNREQAIFLSTYSTCLETSKVDSERALRTASGIIDDEPKLKEFLFCINKQNGVQD
DAGNFVKDAVRKRIEHPLLTDKTMEIIVNKCTRKRETGEETAYQFLKCSYFTIMNE
KHQ

>TcasOBPC07

KQDFHKKCLASSGANADTIAKVRNGKFSNDPQTQKYFGMLRSVGVVNQAGQLQ
VAALRKQVPKDMKRDEAMKIYMSCKDKKGANND EYLLYKCFWEASPRHVKI
DGQ

>TcasOBPC03

LTKEQKEKLDKISKECKNQSGVSQELIDKARTGELINDPKLKAQIYCVSKKAGLAT
EAGEINMDNLKTKLKKVAANDDEVNKIIQKCVVKKPTPEETAFAFEVYKCLHANKPN
FSVVD

>TcasOBPC02

LSEQQTEKLNQLSKECRALTGVSQETITNARNGNFEEDPKLKLQVLCIGKKVIGIMN
ESSQIDENVLKAKLRKVSNDDEEVNKIYNKCAVKKPAPEETAFAETIKCVMKNKPKF
SPVE

>TcasOBPC01

LTKEQIDKLEPISKECRELNGISEDILKVRERGEAVNEPKLKNHVLCVSKKTGLASE
TGETNVEVLRRTKLRKVSNDDEVNSIIQKCVVKKSTPEETAFAEIFVCLRKVKPNFSP
AN

>TcasOBPC05

LTDEQKSKLEEYSKECLKESKVDESVLKEAEKGVYLLDDPKLMNHVYCLVKKINSQ
KDKGELEVTQIKEKLMMQINDEKEVDKLIQLCLVQEKSARYSLGKCEVSS

>TcasOBP10

TKQEDDDRQETIRQYRDDCIAETKVPALIDRADNGDFTDDAKLQCFSKCFYQKA
GFVSETGDLDFVIKDKIPKEANREKALAIIDKCKELKGADSCETVYLVHKCYFLHS
YGTDKKTE

>TcasOBPC14

QHLTEEQKNNWRKWSNECKVLIGVSQEAINKIRNNEFDSVDDKIKKHGLCFAKKA
SLADSSGNIINQIKIKLRVIEDDEEVDRIVTKCTIRKNTPEETTFETFRCLRENSSKF
VPV

>TcasOBPC21

LENEGQNPDTANCVLGGQRIKDSEIAKMAHCILTKTNLMTDKGTFNSNLLKERLR
QSVHSDELVDKVVMMCTVEKETPLKSAFSGYKCLRYLVPWFPLD

>TcasOBPC04

LTDEQKEKIKNYHKECSAVSGVSQDVITKARKGEFIEDPKFKEHLFCFSKKAGFQN
EAGDFQEEVIRKKLNAELNDLDATNKLIKCAVKKDSPQQTAFETIKCYENTPTH
VSLA

>TcasOBPC09

FNNPEDELRRSAACLEQSKVSSSEIKNLQIGNFDDDERLKEYLFCVSKNAGYQDPA
GHLQHEMIRLRFKGGRYSDDTINEVLQCGHQKDTQPETAFAFMKCA YQNAFPRN
YK

>TcasOBP4

LDVEKIRNELMADKNFVELRNKCLDKLGLKEEDLRDLKFDGDVSEDLMCFGKCIQ
EEDGLLDSEGNLNEEKLEKKIETMPFLSRVSDDTKNNIMECLKEIGKIETCQDFGKQ
RDCIHKYV

>TcasOBP1

AILEDSELMKVVENCVKKTNANESEFSSPNFLETTSPALCTAKCLESLEIVNSEG
NINMETLKEYAQPFESEAVATCGEEIKSVTTCDDMEKYRKCVEPLIKNS

>TcasOBP05

YFFMSQKFAEVREECLSENSMTMDELHEGWKMENLPESHL CFLKCLLEKREVIDE
NGVPQKEKIDEILTVKQLSDEKREEISTCITNVEKIENCETMSEIMRCFPKRRD

>TcasOBP3

QKKGKYWTTISECLTEHSMGVEDMKKFDLPAEKMSEEMLCFNKCFYDKLLITDEN
GEINTDNLMSIPLVNAIDASKHDDLVTCLKKVKGIEECDGVKKIEQCFVEFI

>TcasOBP6

ISEEMQELANTLHATCVDETVSEDAIESARKGNFAPDDKLCYMKCIMEQMACI
DDEGIIDVEATIAVLPEEYQAKAEPIVRKCGTKIGANACDNAFLTNKCWYEEDPED
YFLV

>TcasOBP07

IEMDDDMKELINNLHNTCTGETGATDDQIENARKGNFAEDDSFKCYFKCVFDQMG
CMTDDGKVDSEAVIAMPELADKIASTVRGCTEVGANPCETAWLANKCYQKSN
PDMYFVP

>TcasOBP19

QDFIDKFVAKVKSIGETCVPETNASKDDISSLLAHKMPDSHEGKCLIFCFHKQFQIQ
NDDGSINREGAIKALEPLKADDAELYEKVISIFKKCESTPVDGDSCLYAASLAECAV
KEGRAMGLDNLIVLEIE

>TcasOBP14

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>TcasOBPC17

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>TcasOBPC16

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>TcasOBP17

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>TcasOBP18

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>TcasOBP13

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>TcasOBP12

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>TcasOBPC15

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DTSQEQ

>TcasOBPC20

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VVGNN

>TcasOBPC18

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KN

>TcasOBPC13

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>TcasOBPC10

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>TcasOBPC12

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>TcasOBPC11

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>TcasOBP99b

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MAEQQPSDQFFYNIEDKK

>CforOBP1

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>CforOBP2

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CGMEEARKAGLHEQFAEF

>CforOBP3

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>CforOBP4

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NLL

>CforOBP5

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>CforOBP6

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KGPA

>CforOBP7

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GDVKMDKSRRTKRSKATKELNTEPSMGNNRKFYSFPTTEESNAAETNSNEDD TDG
DMCALQCILEKLEMTDSNGLPDQQKFVDVLVKRASGKAVSDLFKESTE ECFQMA
EEDSEEACRYSTKLV TCLEKGRSSCDDWPQGS LPW

>CforOBP8

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HIDIGQF

>CforOBP9

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REEHGL

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GDNGD

>CforOBP12

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NHVSVF

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AVQDHVAHHGHVHEHSHAHH

>CforOBP14

ENIEKFNRFHAA YLKCQESPETSIDEDFLCDV VINQEVPAEVPESAPN FLLCLAKLLQ

LQDEDGNLNSALIRERIEHHQKDPNRVAKLMDTCIVQKDTQPQYTTIFMIDCLSREA
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>CforOBP15

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VATEEPAAKEKPNKTE

>CforOBP16

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KCMYFCDPEKYFLP

>CforOBP17

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SREGLKVGHTKVEALLEVL

>CforOBP18

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>CforOBP19

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>CforOBP20

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>CforOBP21

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>CforOBP22

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AYFLI

>CforOBP23

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>CforOBP24

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>CforOBP25

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>CforOBP26

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HCIYDDNPEKYFLP

>CforOBP27

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>CforOBP28

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SKYGNDLGLANQ

>CforOBP29

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>CforOBP30

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>CforOBP31

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CILDYFA

>CforOBP32

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FCLLEYFA

>CforOBP33

PQYTAEYFKVHQECQADSKYLISDMTVFQELEYEKPKPSEVKIPSNFNDHMFMY
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CLLESFA

>CforOBP34

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NFYA

>CforOBP35

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LAVAADKLKTLFVDPNNSAAIVSECAAPTQGLQDPVEVAGIFYFCTLPLYA

>AglOBP17

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>AglOBP2

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GLQKENGELDLETIKSKVALSVTDSKVDRLVQECAIKKKSPEKTAIHLFMCLDKN
GVTYFHEF

>AglaOBP3

SLTEEQIQKLKGYHKDCAAETGVDELVTKARKGEFSEDPKFKDHLFCVAKKIGF
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PTHSIV

>AglaOBP1

VLDESEFTPKLLEQVKALHDTCASQSGADDGLIGKIKKGFVEDPKIKSYMCKGLT
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HDLNPGIFIF

>AglaOBP16

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>AglaOBP15

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QKKDLLDTEGNPKEEFRSFLKESFSSESWLAALQDKVISTCLDEGKNATANRDAS
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>AglaOBP14

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>AglaOBP13

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>AglaOBP12

KLQLPDLQEYADELHDLCIKRTGITEDDHIAFYDIANNPHDEKLQCYIKCLLMEAN
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>AglaOBP11

EMDKEHQECLDETELTEAEVSEFLLGDDAENDAKATKFLMCIFKKKEAVNDEGHF
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SK

>AglaOBP10

RPDENLATINMAHNECQSNPRTYVDEDILDRISGGEKIDNPSVRAHILCVTTKLGVL
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HDHNSHIHYHHQKT

>AglaOBP9

ALPQSEYGPQLEALQKNVRAACISTSGVDETAISNVGNVFTDEPKIKHYLTCVLK
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HQNPDLFVFF

>AglOBP8
 ILKQSDFTPELKKLAANLHVTCVSKTGIDEALIDKVLNGEFVVEPKMKA YMTCLLL
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 YINSDIFIFF

>AglOBP7
 ASEEQHERVKKIHSECQADPKTHADDELLKKYHKGEEVDKSIVGAHMLCMSTKFG
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 LRGHEHIHNR

>AglOBP6
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>AglOBP5
 ASLPASEKKFINQVHANCQSNPKTFVDESLLKNLPANKDNAQVGVHMLCMASKGA
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 PYTPDLN

>AglOBP4
 APSIRDIHGECQSDPATRLDHDEFKAVRTGESFDRTKVGHMLCMNKKFGTQAD
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 GHGHEHHHGHHEHHHDH

>AglOBP18
 ILKQSDFTPELKKLAANLHVTCVSKTGIDEALIDKVLNGEFVVEPKMKA YMTCLLL
 EGTLIDEKGTPNLEFGATLIPENIREESVKNIKHCYAVNNDVTDLEEKIFRVFKCYY
 YINSDIFIFF

Appendix X Comparison of the numbers of detoxification genes and members of the cys-loop ligand-gated ion channel superfamily among species

Detoxification genes	<i>Cylas formicarius</i>	<i>Anoplophora glabripennis</i>	<i>Tribolium castaneum</i>	<i>Dendroctonus ponderosae</i>	<i>Agrilus planipennis</i>	<i>Onthophagus taurus</i>
Cytochrome P450 monooxygenase(P450)	87	126	149	106	76	153
Carboxylesterase(COE)	93	68	85	61	33	74
Glutathione S-transferase(GST)	26	18	41	38	19	47
cuticular protein	90	121	149	132	82	138
Cys-loop ligand-gated ion channels						
Nicotinic acetylcholine receptor subunit(nAChRs)	9	1	12	-	-	-
glutamate-gated chloride channels(GluCl)	1	2	1	2	2	3
histamine-gated chloride channel(HisCl)	2	-	2	-	-	-
GABA-gated chloride channel (Resistance to	1	2	1	3	2	1

dieldrin,

Rdl)(RDL)Ligand-gated

chloride channel

homolog 3 (LCCH3)

GABAA and glycine

receptor-like subunit

1

5

1

4

5

6

cys-loop ligand-gated ion

channel

2

1

4

-

-

-

PH-sensitive chloride

channels

-

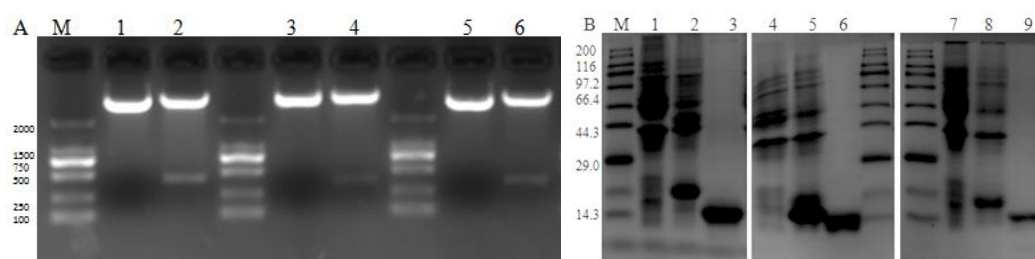
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Appendix Y Prokaryotic expression and purification of CforOBP4-6. A, double restriction enzyme digestion of the pET/CforOBP4-6 prokaryotic expression vector. B, SDS-PAGE analysis of CforOBP4-6 purification. M, protein molecular marker; A 1,3,5, the pET/CforOBP4-6 vector was not digested; A 2,4,6, the pET/CforOBP4-6 vector was digested; B 1,4,7, total protein expression in *E. coli* pET/CforOBP4-6 was not induced by IPTG; B 2,5,8, total protein expression in *E. coli* pET/CforOBP4-6 was induced by IPTG; B 3,6,9, purified pET/CforOBP4-6.