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(54) GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF

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Related U.S. Application Data

(63) Continuation of application No. PCT/US00/04995, filed on Feb. 25, 2000, which is a continuation-in-part of application No. 09/257,706, filed on Feb. 25, 1999, now abandoned.

Publication Classification

(51) **Int. Cl.**^{7} **C07K 14/705**; C12N 5/06; C12P 21/02; C07H 21/04

(52) **U.S. Cl.** **435/69.1**; 435/320.1; 435/325; 530/350; 536/23.5; 514/12

(57) **ABSTRACT**

This invention provides an isolated nucleic acid molecule encoding an insect odorant receptor. This invention provides a nucleic acid molecule of at least 12 nucleotides capable of specifically hybridizing with the nucleic acid molecule encoding an insect odorant receptor. This invention also provides a purified, insect odorant receptor. This invention provides an antibody capable of specifically binding to an insect odorant receptor. This invention provides a method for identifying cDNA inserts encoding an insect odorant receptors. This invention provides a method of identifying a compound capable of specifically bind to an insect odorant receptor. This invention also provides a method of identifying a compound capable of activating the activity of an insect odorant receptor.

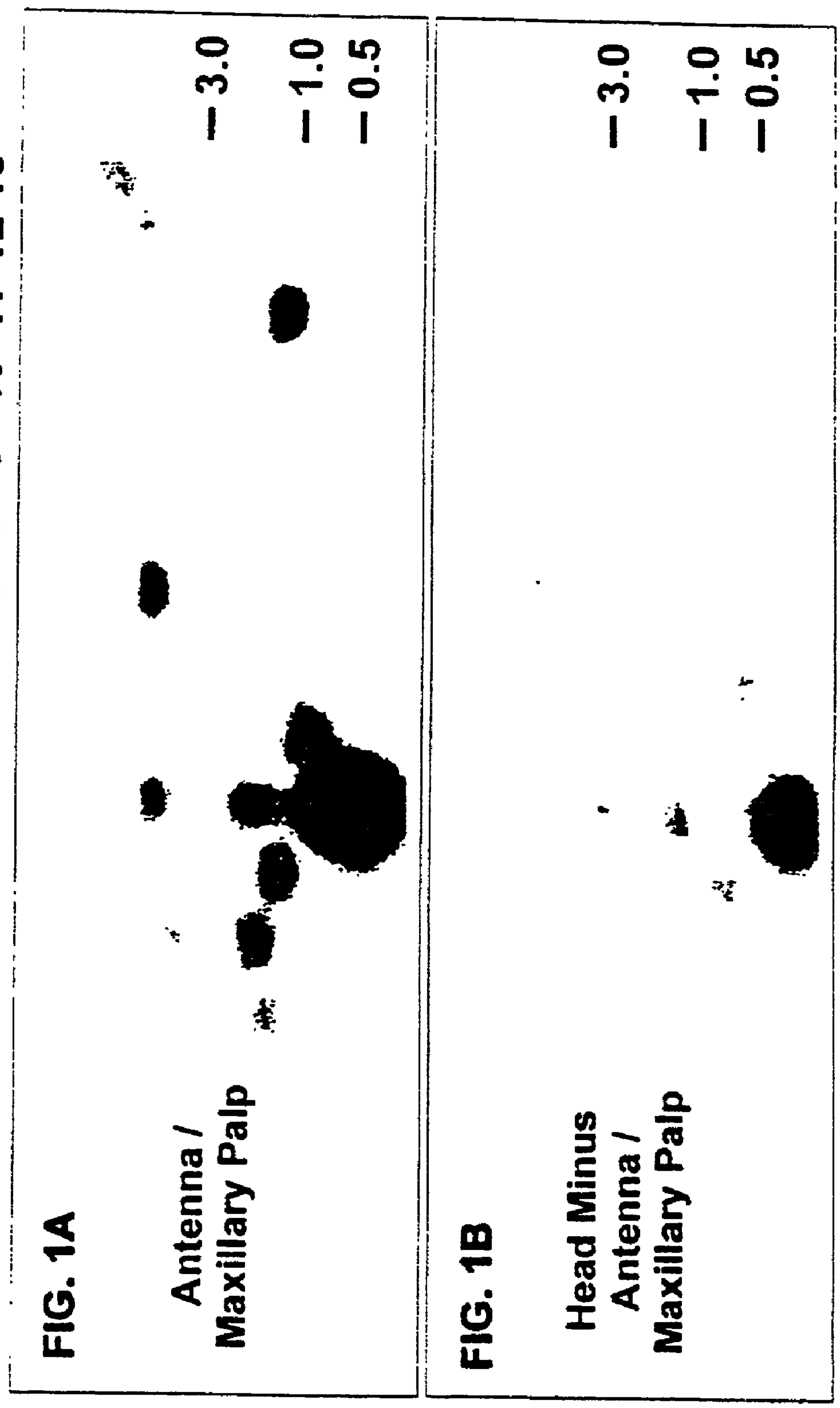

Antenna / Maxillary Palp
1 2 3 4 5 6 7 8 9 10 11 12 13
—3.0
—1.0
—0.5
Head Minus Antenna / Maxillary Palp
—3.0
—1.0
—0.5

FIG. 1A

FIG. 1B

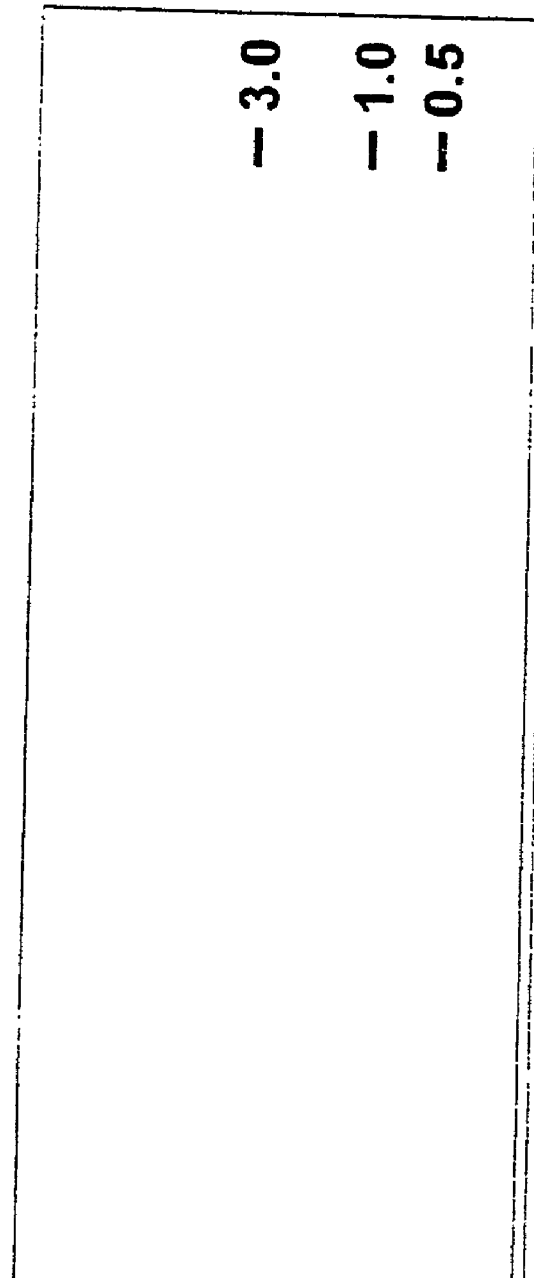


FIG. 1C

Virgin
Female Body

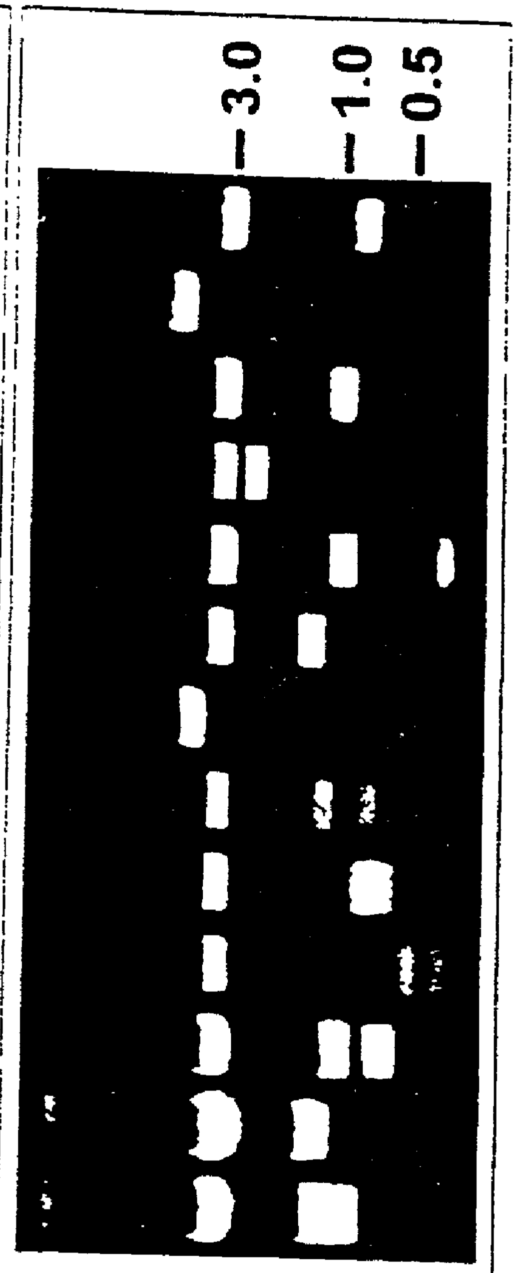


FIG. 1D

DOR 104

FIG. 2A

DOR104 - LacZ

FIG. 2B

FIG. 2C

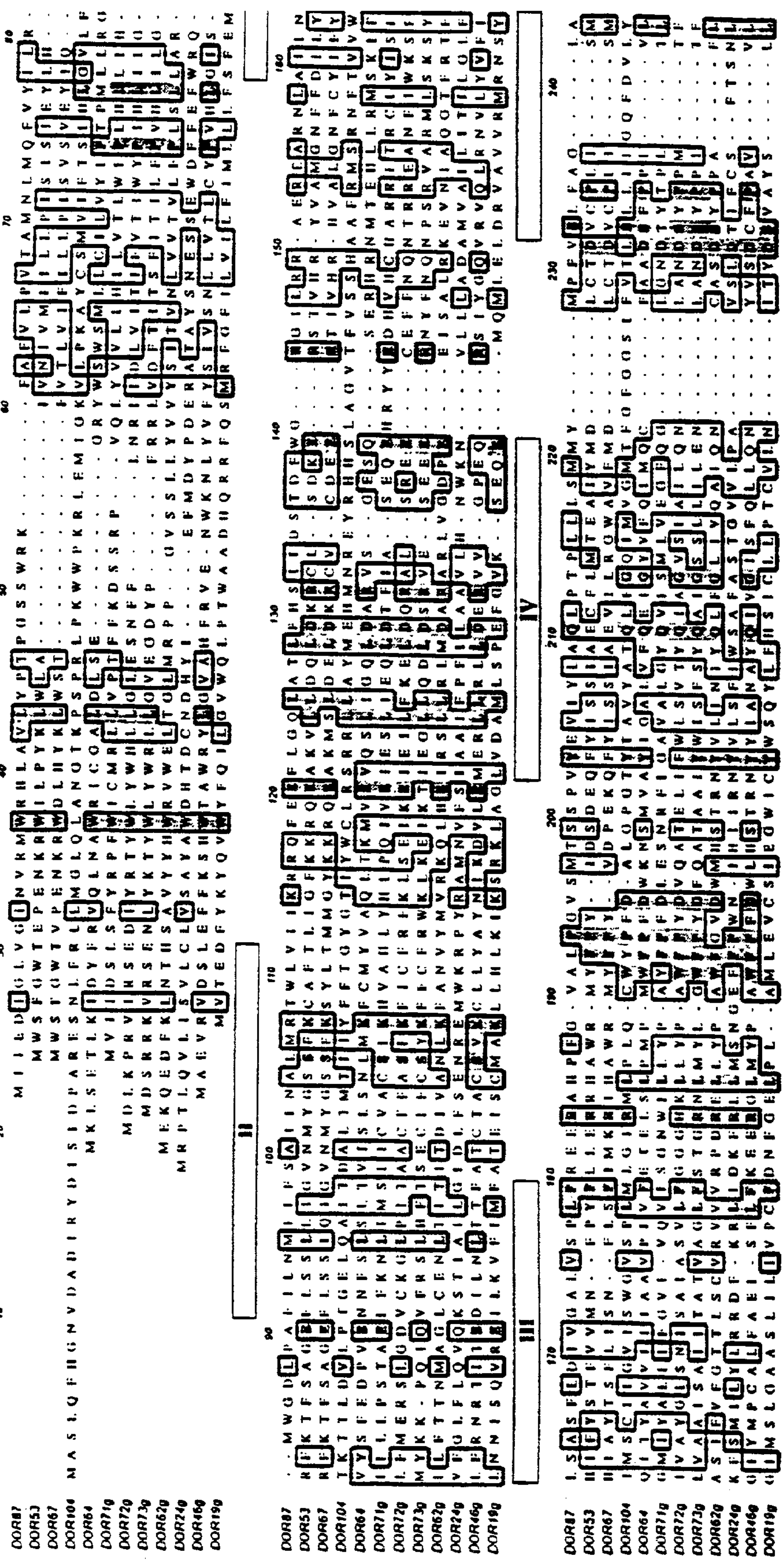
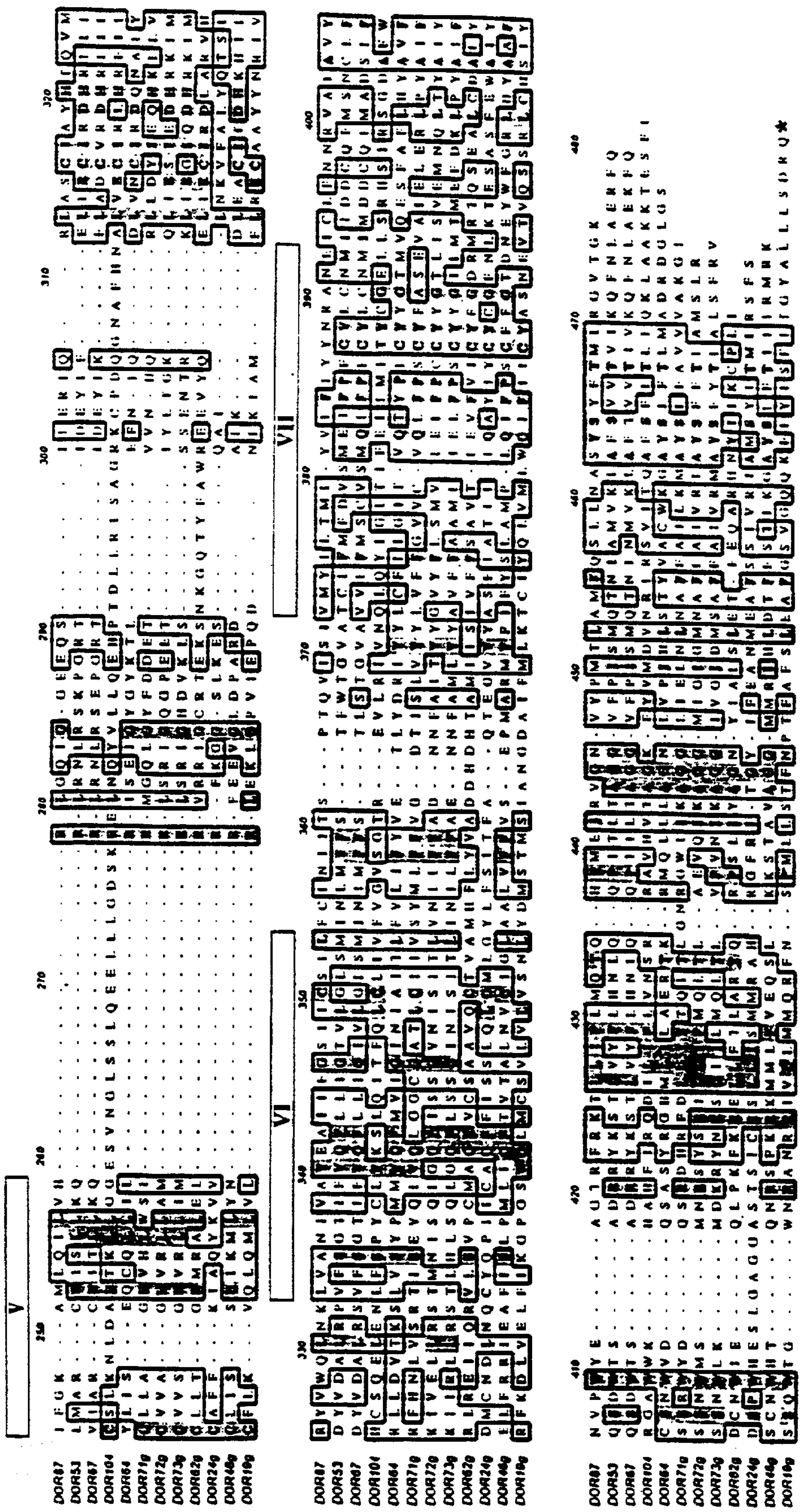


FIG. 3A

FIG. 3B



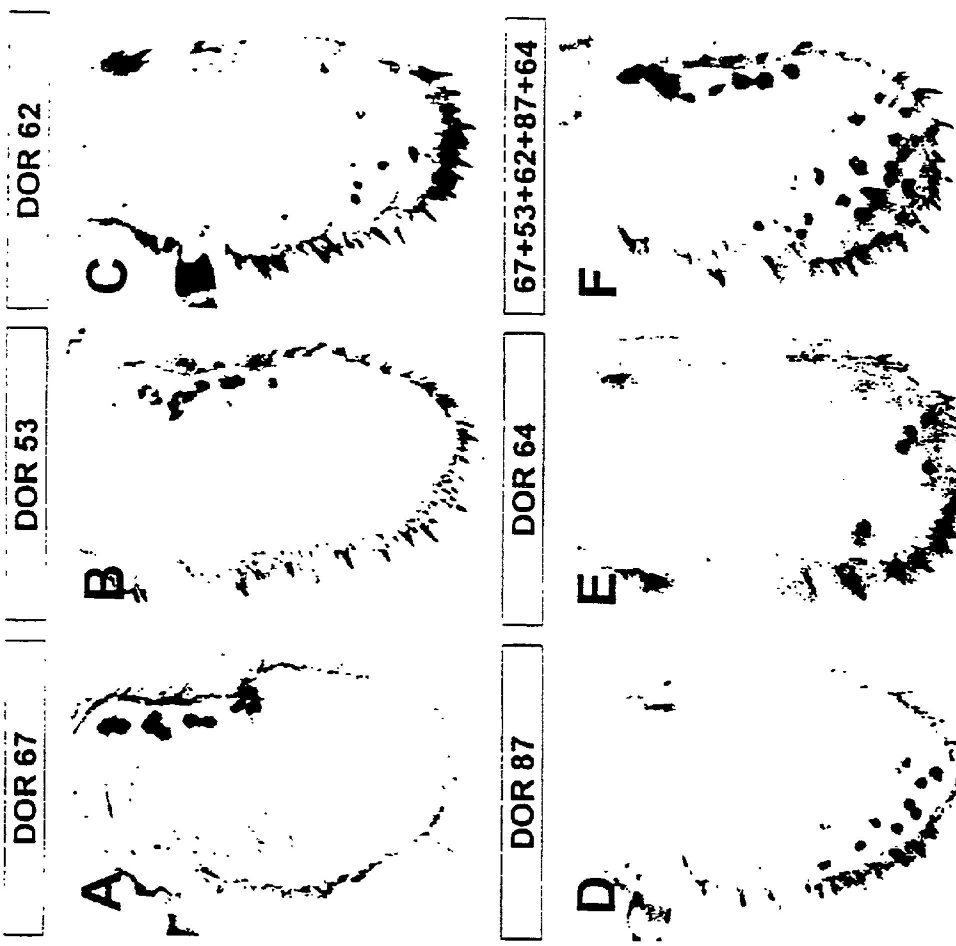


FIG. 4A FIG. 4B FIG. 4C

FIG. 4D FIG. 4E FIG. 4F

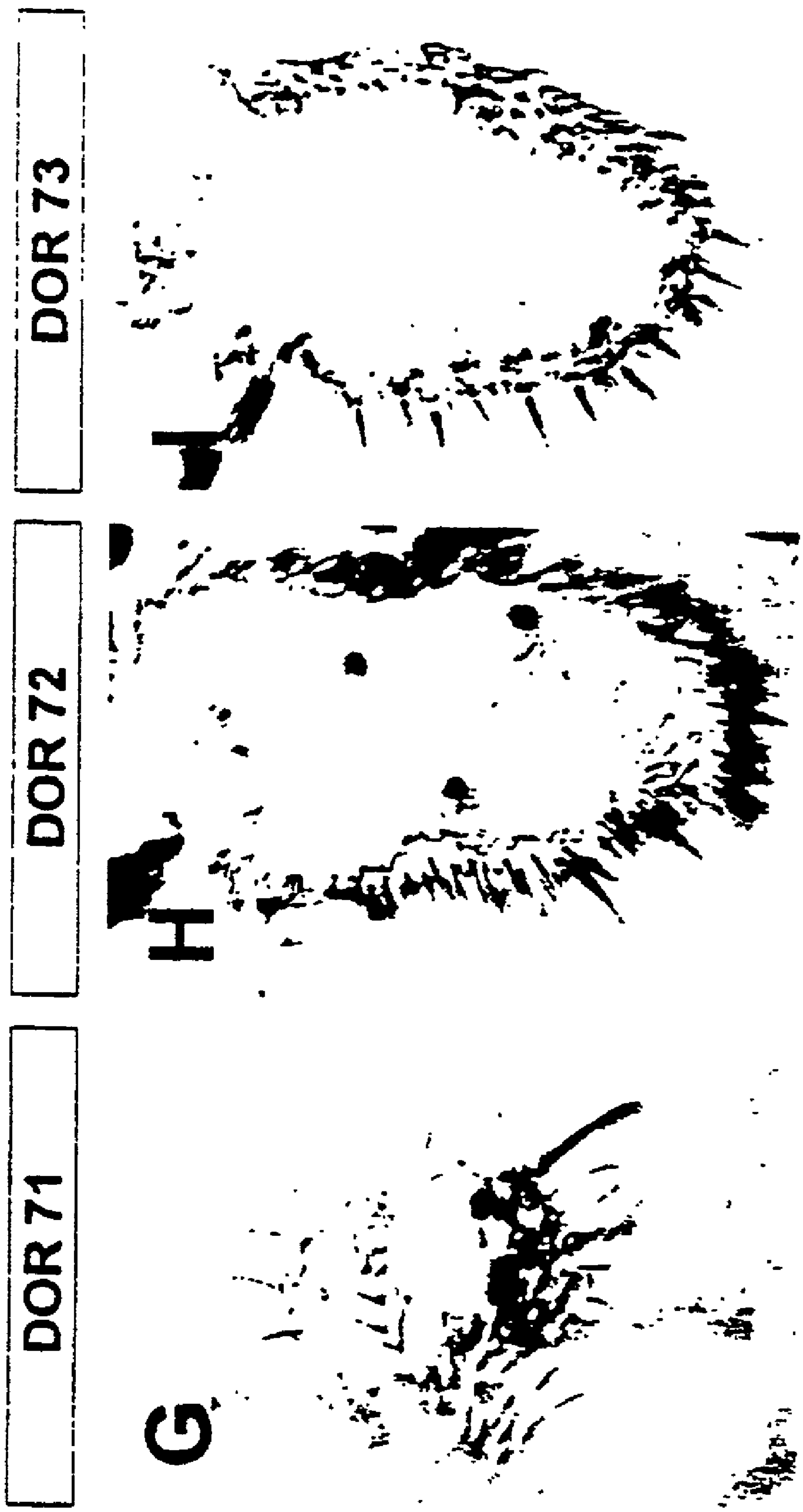


FIG. 4G

FIG. 4H

FIG. 4I

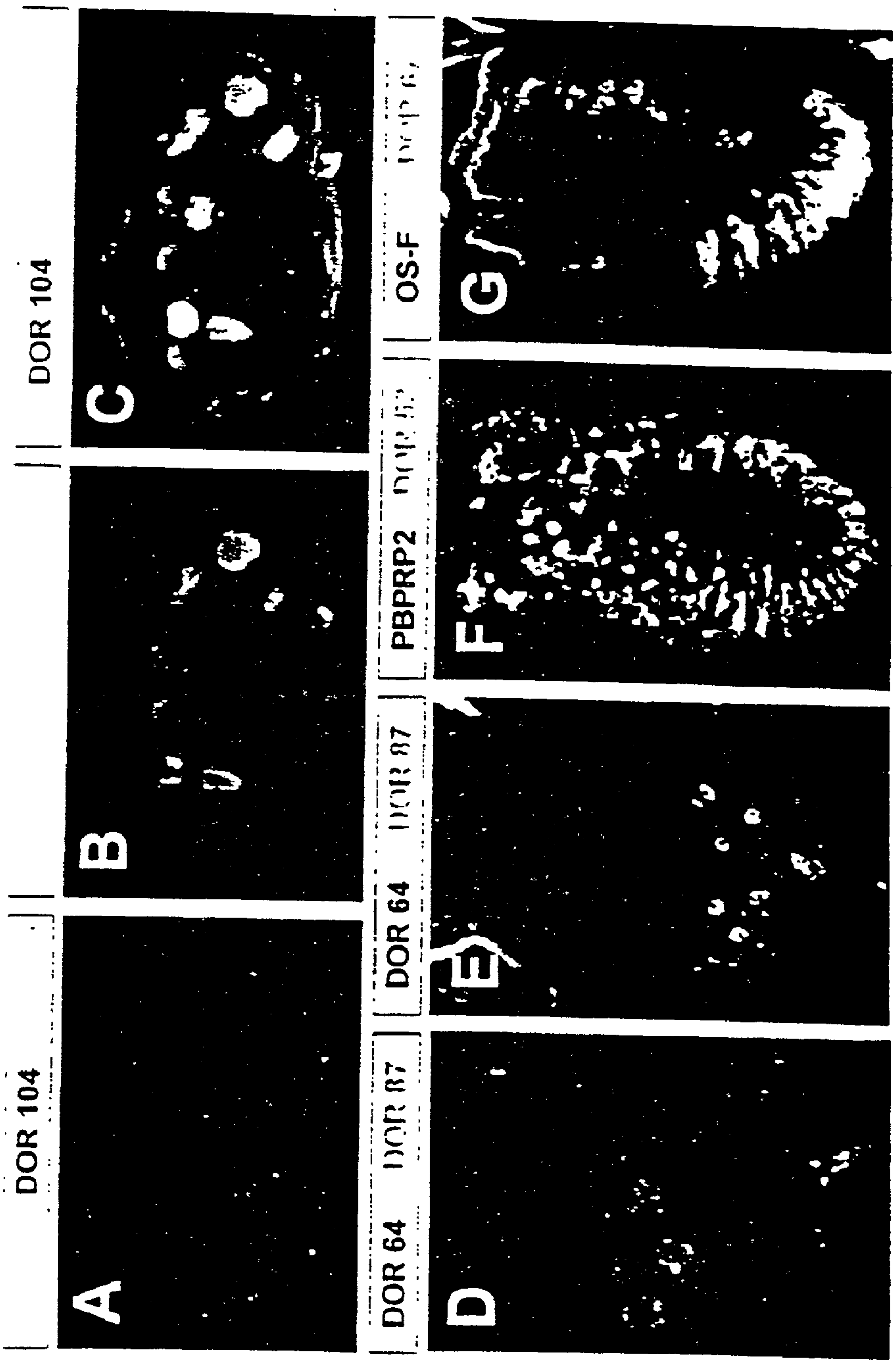


FIG. 5A FIG. 5B FIG. 5C

FIG. 5D FIG. 5E FIG. 5F FIG. 5G

FIG. 6A FIG. 6B FIG. 6C

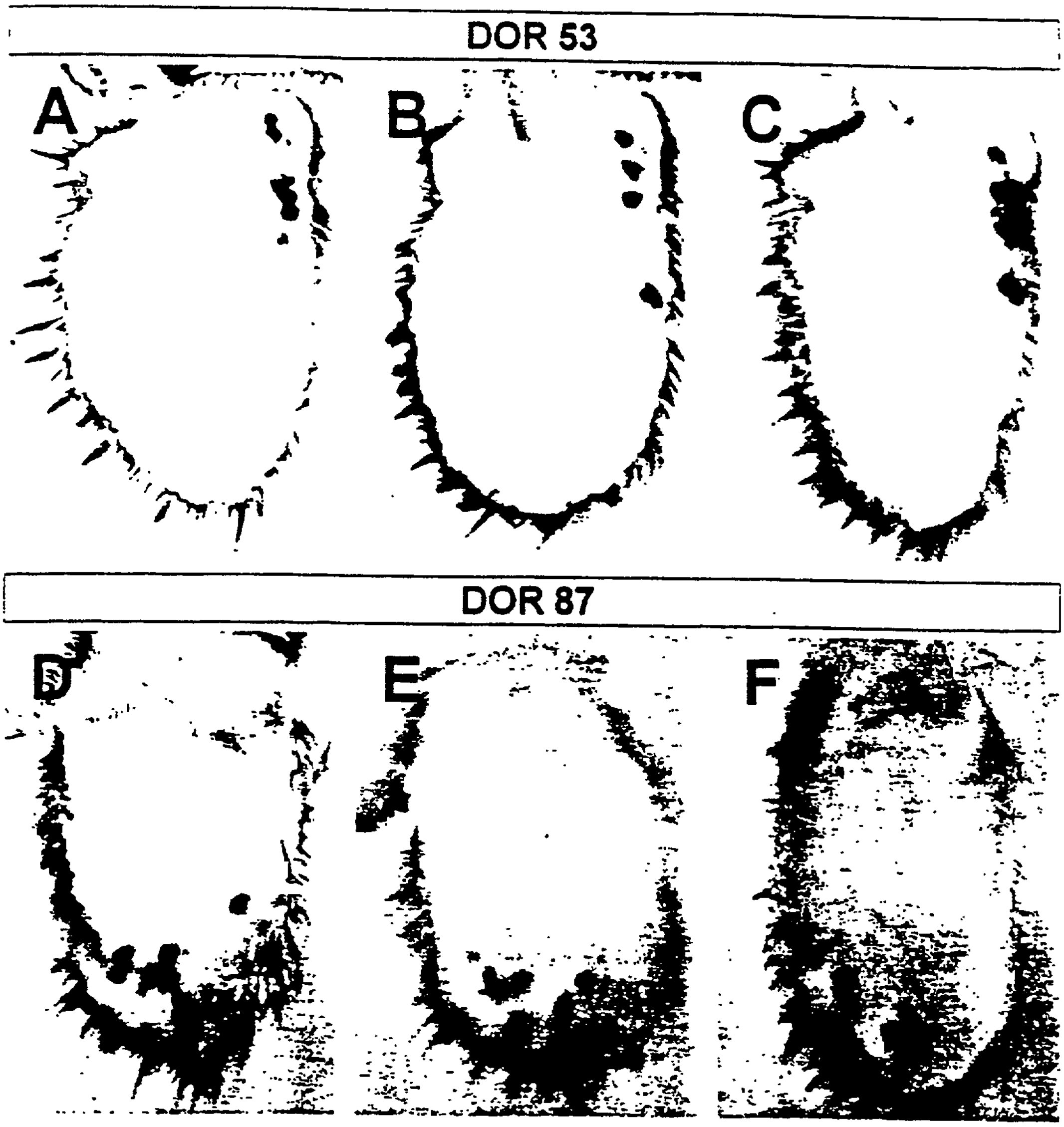


FIG. 6D FIG. 6E FIG. 6F

FIG. 7A

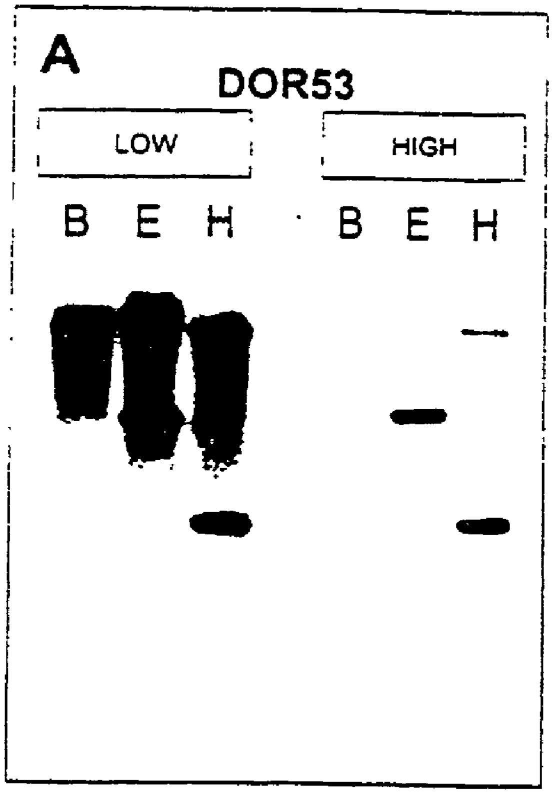
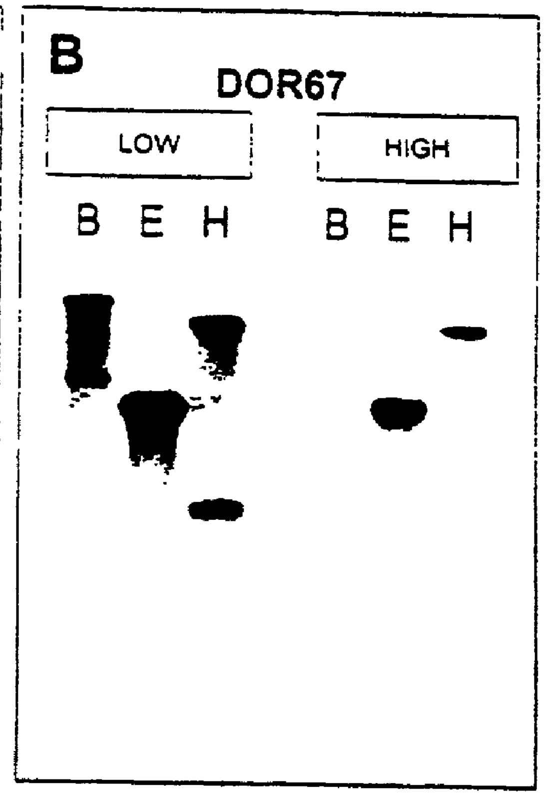


FIG. 7B



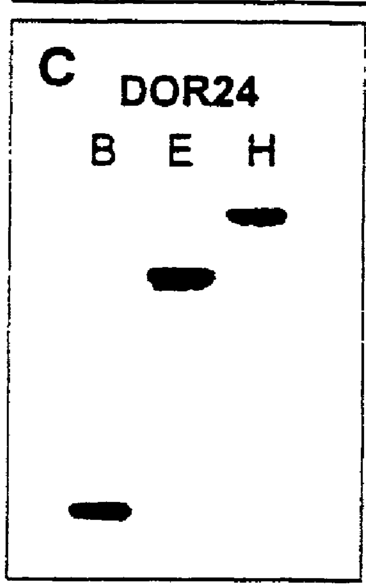


FIG. 7C

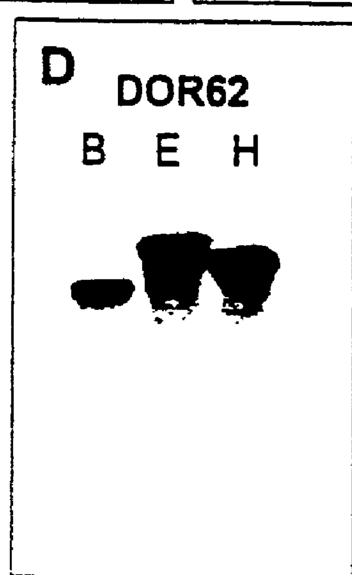


FIG. 7D

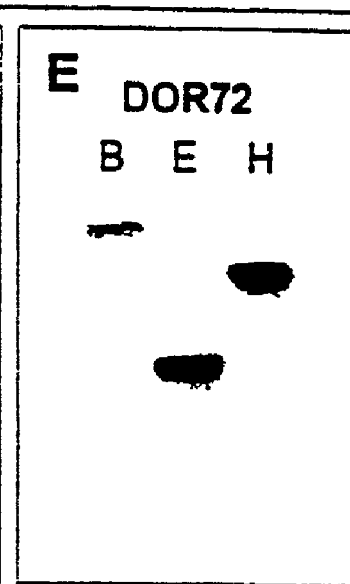


FIG. 7E

FIG. 8A

DOR62 [AF127921]

```
LOCUS       XXXXX          553 bp    mRNA            INV       02-FEB-1999
DEFINITION  Drosophila melanogaster putative odorant receptor DOR62 mRNA,
            partial cds.
ACCESSION   AF127921
KEYWORDS    .
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 553)
  AUTHORS   Leslie B. Vosshall,Hubert Amrein, Pavel S. Morozov, Andrey
            Rzhetsky, and Richard Axel.
  TITLE     A Spatial Map of Olfactory Receptor Expression in the Drosophila
            Antenna
  JOURNAL   Cell (1999) In press
REFERENCE   2  (bases 1 to 553)
  AUTHORS   Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and
            Axel,Richard.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-FEB-1999) Department of Biochemistry and Molecular
            Biophysics, HHMI-Columbia University, 701 West 168th Street, New
            York, NY 10032, USA
FEATURES             Location/Qualifiers
     Comment:       /product='odorant receptor DOR62'
                    /tissue_type='adult antenna'
                    /note='putative seven transmembrane G protein coupled
                    receptor; genomic DNA sequenced by the European Drosophila
                    Genome Project and given accession number 62D9.q'
     source          1..553
                     /organism="Drosophila melanogaster"
                     /strain="Oregon R"
                     /db_xref="taxon:7227"
                     /chromosome="X"
                     /map="2F"
     gene            <1..553
                     /note="Drosophila melanogaster odorant receptor DOR62"
                     /gene="DOR62"
     CDS             <1..459
                     /gene="DOR62"
                     /note="odorant receptor"
                     /codon_start=1
                     /product="DOR62"

/translation="QELIECIRDLARVHRLREIIQRVLSVPCMAQFVCSAAVQCTVAM
HFLYVADDHDHTAMIISIVFFSAVTLEVFVICYFGDRMRTQSEALCDAFYDCNWIEQL
PKFKRELLFTLARTQRPSLIYAGNYIALSLETFEQVMRFTYSVFTLLLRAK"
BASE COUNT       141 a    145 c     132 g     135 t
ORIGIN
        1 caggaactca tcgagtgcat ccgcgatctg gcgcgggtcc atcggctgag ggagatcatt
       61 cagcgggtcc tttcagtgcc ctgcatggcc cagttcgtct gctccgccgc cgtccagtgt
      121 accgtcgcca tgcacttcct gtacgtagcg gatgaccacg accacaccgc catgatcatc
      181 tcgattgtat tttttcggc cgtcaccttg gaggtgtttg taatctgcta ttttggggac
      241 aggatgcgga cacagagcga ggcgctgtgc gatgccttct acgattgcaa ctggatagaa
      301 cagctgccca agttcaagcg cgaactgctc ttcaccctgg ccaggacgca gcggcctctc
      361 cttatttacg caggcaacta catcgcactc tcgctggaga cctttcgagca ggtcatgagg
      421 ttcacatact ctgttttcac actcttgctg agggccaagt aagaacttta taatctcttt
      481 ttggggagaa aaattttaaa gcacaatagc agaaaatat atcagataat ataacaaaaa
      541 aaaaaaaaaa aaa
```

FIG. 8B-1

DOR104[AF127922]

```
LOCUS       XXXXX        1493 bp    mRNA            INV       02-FEB-1999
DEFINITION  Drosophila melanogaster odorant receptor DOR104 mRNA, complete
cds.
ACCESSION   AF127922
KEYWORDS    .
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1493)
  AUTHORS   Leslie B. Vosshall, Hubert Amrein, Pavel S. Morozov, Andrey
            Rzhetsky and Richard Axel.
  TITLE     A Spatial Map of Olfactory Receptor Expression in the Drosophila
            Antenna
  JOURNAL   Cell (1999) In press
REFERENCE   2  (bases 1 to 1493)
  AUTHORS   Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and Axel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-FEB-1999) Department of Biochemistry and Molecular
            Biophysics, HHMI-Columbia University, 701 W. 168th Street, New
            York, NY 10025, USA
FEATURES             Location/Qualifiers
     Comment:      /tissue_type='adult maxillary palp'
                   /note='putative seven transmembrane G protein coupled
                   receptor'
     source          1..1493
                     /organism="Drosophila melanogaster"
                     /strain="Oregon R"
                     /db_xref="taxon:7227"
                     /chromosome="III"
                     /map="85B"
     gene            1..1493
                     /note="odorant receptor"
                     /gene="DOR104"
     CDS             21..1421
                     /gene="DOR104"
                     /note="odorant receptor"
                     /codon_start=1
                     /product="DOR104"

/translation="MASLQFHGNVDADIRYDISLDPARESNLFRLLMGLQLANGTKPS
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VWIMSCLLGVISWGVSPLMLGIRMLPLQCWYPFDALGPGTYTAVYATQLFGQIMVGMT
FGFGGSLFVTLSLLLLGQFDVLYCSLKNLDAHTKLLGGESVNGLSSLQEELLLGDSKR
ELNQYVLLQEHPTDLLRLSAGRKCPDQGNAFHNALVECIRLHRFILHCSQELENLFSP
YCLVKSLQITFQLCLLVFVGVSGTREVLRIVNQLQYLGLTIFELLMFTYCGELLSRHS
IRSGDAFWRGAWWKHAHFIRQDILIFLVNSRRAVHVTAGKFYVMDVNRLRSVITQAFS
FLTLLQKLAAKKTESEL"
BASE COUNT      332 a    373 c    407 g    381 t
```

FIG. 8B-2

ORIGIN

```
   1 ggcacgagca gtcgatggcc agtcttcagt tccacggcaa cgtcgatgcg gacatcaggt
  61 atgatattag cctggatccg gctagggaat cgaatctctt ccgtctgcta atgggactcc
 121 agttggcgaa tggcacgaag ccatcgccgc ggttacccaa atggtggcca aagcggctgg
 181 aaatgattgg taaagtgctg cccaaagcct attgttccat ggtgattttc acctcccctgc
 241 atttgggtgt cctgttcacg aaaaccacac tggatgtcct gccgacgggg gagctgcagg
 301 ccataacgga tgccctcacc atgaccataa tatacttttt cacgggctac ggcaccatct
 361 actggtgcct gcgctcccgg cgcctcttgg cctacatgga .gcacatgaac cgggagtatc
 421 gccatcattc gctggccggg gtgacctttg tgagtagcca tgcggccttt aggatgtcca
 481 gaaacttcac ggtggtgtgg ataatgtcct gcctgctggg cgtgatttcc tggggcgttt
 541 cgccactgat gctgggcatc cggatgctgc cgctccaatg ttggtatccc ttcgacgccc
 601 tgggtcccgg cacatatacg gcggtctatg ctacacaact tttcggtcag atcatggtgg
 661 gcatgacctt tggattcggg ggatcactgt ttgtcacccct gagcctgcta ctcctgggac
 721 aattcgatgt gctctactgc agcctgaaga acctggatgc ccataccaag ttgctgggcg
 781 gggagtctgt aaatggcctg agttcgctgc aagaggagtt gctgctgggg gactcgaaga
 841 gggaattaaa tcagtacgtt ttgctccagg agcatccgac ggatctgctg agattgtcgg
 901 caggacgaaa atgtcctgac caaggaaatg cgtttcacaa cgccttggtg gaatgcattc
 961 gcttgcatcg cttcattctg cactgctcac aggagttgga gaatctattc agtccatatt
1021 gtctggtcaa gtcactgcag atcacctttc agctttgcct gctggtcttt gtgggcgttt
1081 cgggtactcg agaggtcctg cggattgtca accagctaca gtacttggga ctgaccatct
1141 tcgagctcct aatgttcacc tattgtggcg aactcctcag tcggcatagt attcgatctg
1201 gcgacgcctt ttggaggggt gcgtggtgga agcacgccca tttcatccgc caggacatcc
1261 tcatctttct ggtcaatagt agacgtgcag ttcacgtgac tgccggcaag ttttatgtga
1321 tggatgtgaa tcgtctaaga tcggttataa cgcaggcgtt cagcttcttg actttgctgc
1381 aaaagttggc tgccaagaag acggaatcgg agctctaaac tggtaccacg catcgatatt
1441 tatttagcgc attaaaaaaa agtcgagtaa aagcaaaaaa aaaaaaaaaa aaa
```

FIG. 8C-1

DOR87 [AF127926]

```
LOCUS        XXXXX         1556 bp    mRNA            INV       02-FEB-1999
DEFINITION   Drosophila melanogaster odorant receptor DOR87 mRNA, complete
cds.
ACCESSION    AF127926
KEYWORDS     .
SOURCE       fruit fly.
  ORGANISM   Drosophila melanogaster
             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
             Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
             Drosophilidae; Drosophila.
REFERENCE    1  (bases 1 to 1556)
  AUTHORS    Leslie B. Vosshall, Hubert Amrein, Pavel S. Morozov, Andrey
             Rzhetsky and Richard Axel.
  TITLE      A Spatial Map of Olfactory Receptor Expression in the Drosophila
             Antenna
  JOURNAL    Cell (1999) In press
REFERENCE    2  (bases 1 to 1556)
  AUTHORS    Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and Axel,R.
  TITLE      Direct Submission
  JOURNAL    Submitted (02-FEB-1999) Department of Biochemistry and Molecular
             Biophysics, HHMI-Columbia University, 701 West 168th Street, New
             York, NY 10032, USA
FEATURES              Location/Qualifiers
     Comment:       /tissue='adult antenna'
                    /note='putative seven transmembrane G protein coupled
                    receptor'
     source           1..1556
                      /organism="Drosophila melanogaster"



                     /strain="Oregon R"
                     /db_xref="taxon:7227"
                     /chromosome="II"
                     /map="43B1-2"
     gene            1..1556
                     /note="odorant receptor"
                     /gene="DOR87"
     CDS             30..1157
                     /gene="DOR87"
                     /note="odorant receptor"
                     /codon_start=1
                     /product="DOR87"

/translation="MTIEDIGLVGINVRMWRHLAVLYPTPGSSWRKFAFVLPVTAMNL
MQFVYLLRMWGDLPAFILNMFFFSAIFNALMRTWLVIIKRRQFEEFLGQLATLFHSIL
DSTDEWGRGILRRAEREARNLAILNLSASFLDIVGALVSPLFREERAHPFGVALPGVS
MTSSPVYEVIYLAQLPTPLLLSMMYMPFVSLFAGLAIFGKAMLQILVHRLGQIGGEEQ
SEEERFQRLASCIAYHTQVMRYVWQLNKLVANIVAVEAIIFGSIICSLLFCLNIITSP
TQVISIVMYILTMLYVLFTYYNRANEICLENNRVAEAVYNVPWYEAGTRFRKTLLIFL
MQTQHPMEIRVGNVYPMTLAMFQSLLNASYSYFTMLRGVTGK"
BASE COUNT       329 a     413 c     408 g     406 t
```

FIG. 8C-2

ORIGIN

```
   1 ggcacgaggc ttatagaaag tgccgagcaa tgacaatcga ggatatcggc ctggtgggca
  61 tcaacgtgcg gatgtggcga cacttggccg tgctgtaccc cactccgggc tccagctggc
 121 gcaagttcgc cttcgtgctg ccggtgactg cgatgaatct gatgcagttc gtctacctgc
 181 tgcggatgtg gggcgacctg cccgccttca ttctgaacat gttcttcttc tcggccattt
 241 tcaacgccct gatgcgcacg tggctggtca taatcaagcg gcgccagttc gaggagtttc
 301 tcggccaact ggccactctg ttccattcga ttctcgactc caccgacgag tgggggcgtg
 361 gcatcctgcg gagggcggaa cgggaggctc ggaacctggc catccttaat ttgagtgcct
 421 ccttcctgga cattgtcggt gctctggtat cgccgctttt cagggaggag agagctcatc
 481 ccttcggcgt agctctacca ggagtgagca tgaccagttc acccgtctac gaggttatct
 541 acttggccca actgcctacg cccctgctgc tgtccatgat gtacatgcct ttcgtcagcc
 601 tttttgccgg cctggccatc tttgggaagg ccatgctgca gatcctggta cacaggctgg
 661 gccagattgg cggagaagag cagtcggagg aggagcgctt ccaaaggctg gcctcctgca
 721 ttgcgtacca cacgcaggtg atgcgctatg tgtggcagct caacaaactg gtggccaaca
 781 ttgtggcggt ggaagcaatt atttttggct cgataatctg ctcactgctc ttctgtctga
 841 atattataac ctcacccacc caggtgatct cgatagtgat gtacattctg accatgctgt
 901 acgttctctt cacctactac aatcggccaa tgaaatatgc cctcgagaac aaccgggtgg
 961 cggaggctgt ttacaatgtg ccctggtacg aggcaggaac tcggtttcgc aaaaccctcc
1021 tgatcttctt gatgcaaaca caacacccga tggagataag agtcggcaac gtttacccca
1081 tgacattggc catgttccag agtctgttga atgcgtccta ctcctacttt accatgctgc
1141 gtggcgtcac cggcaaatga gctgaaagac cgaaaaaacc ggagtatccc cttccatatt
1201 ccccctgctc ctttatttcc ctttcctttt ccctttccgt ttcccattcc gcttttccag
1261 caatccgggt aatgcaaaaa gttgttgctg gctgtggtcc tggctgcttg tttggcattt
1321 gcatatgctt gtcgtttgaa aggatttaat cggactgctg gcacggagtc ggcatcctgg
1381 ctcctggatc ctggcatgca aatagttggc ttcttagatt gttacacaaa atagattgta
1441 gattgcagct gaatgttgtg cttggaataa agtcaaaagg atgtggagtc ggcccaaggc
1501 tctgcccatt ctgtttgctc gggatgcccg aaagtatgaa aaaaaaaaaa aaaaaa
```

FIG. 8D-1

DOR53 [AF127923]

```
LOCUS       XXXXX        1305 bp    mRNA            INV       06-FEB-1999
DEFINITION  Drosophila melanogaster putative odorant receptor DOR53 mRNA,
            complete cds.
ACCESSION   AF127923
KEYWORDS    .
SOURCE      fruit fly.

  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1305)
  AUTHORS   Leslie B. Vosshall, Hubert Amrein, Pavel S. Morozov, Andrey
            Rzhetsky and Richard Axel.
  TITLE     A Spatial Map of Olfactory Receptor Expression in the Drosophila
            Antenna
  JOURNAL   Cell (1999) In press
REFERENCE   2  (bases 1 to 1305)
  AUTHORS   Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and Axel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-FEB-1999) Department of Biochemistry and Molecular
            Biophysics, HHMI-Columbia University, 701 West 168th Street, New
            York, NY 10032, USA
FEATURES             Location/Qualifiers
     source          1..1305
                     /organism="Drosophila melanogaster"
                     /strain="Oregon R"
                     /db_xref="taxon:7227"
                  /note="_tissue_type='adult antenna'  _note='putative seven
                     transmembrane G protein coupled receptor';"
                     /chromosome="II"
                     /map="22A2-3"
     gene            1..1305
                     /note="odorant receptor"
                     /gene="DOR53"
     CDS             79..1179
                     /gene="DOR53"
                     /note="odorant receptor"
                     /codon_start=1
                     /product="DOR53"

/translation="MWSFGWTEPENKRWILPYKLWLAFVNIVMLILLPISISIEYLHR
FKTFSAGEFLSSLEIGVNMYGSSFKCAFTLIGFKKRQEAKVLLDQLDKRCLSDKERST
VHRYVAMGNFFDILYHIFYSTFVVMNFPYFLLERRHAWRMYFPYIDSDEQFYISSIAE
CFLMTEAIYMDLCTDVCPLISMLMARCHISLLKQRLRNLRSKPGRTEDEYLEELTECI
RDHRLLLDYVDALRPVFSGTIFVQFLLIGTVLGLSMINLMFFSTFWTGVATCLFMFDV
SMETFPFCYLCNMIIDDCQEMSNCLFQSDWTSADRRYKSTLVYFLHNLQQPITLTAGG
VFPISMQTNLAMVKLAFSVVTVIKQFNLAERFQ"
BASE COUNT       331 a     286 c     279 g     409 t
```

FIG. 8D-2

```
ORIGIN
        1 tttttcccc acataaaaga aaagccattg agcgagcggg ttaagtcccg agatgccttc
       61 atttacttgg atcgggtgat gtggtccttt ggctggacag agcctgaaaa caaaaggtgg
      121 atccttcctt ataaactgtg gttagcgttc gtgaacatag taatgctcat cctctgccg
      181 atctcgataa gcatcgagta cctccaccga tttaaaacct tctcggcggg ggagttcctt
      241 agttccctcg agattggagt caacatgtac ggaagctctt ttaagtgcgc cttcaccttg
      301 attggattca agaaaagaca ggaagctaag gttttactgg atcagctgga caagagatgc
      361 cttagcgata aggagaggtc cactgttcat cgctatgtcg ccatgggaaa ctttttcgat
      421 attttgtatc acatttttta ctccaccttc gtggtaatga acttcccgta ttttctgctt
      481 gagagacgcc atgcttggcg catgtacttt ccatatatcg attccgacga acagttttac
      541 atctccagca tcgccgagtg ttttctgatg acggaggcca tctacatgga tctctgtacg
      601 gacgtgtgtc ccttgatctc catgcttatg gctcgatgcc acatcagcct cctgaaacag
      661 cgactgagaa atctccgatc gaagccagga aggaccgaag atgagtactt ggaggagctc
      721 accgagtgca ttcgggatca tcgattgcta ttggactatg ttgacgcatt gcgacccgtc
      781 ttttcgggaa ccatttttgt gcagttcctc ctgatcggta ctgtactggg tctctcaatg
      841 ataaatctaa tgttcttctc gacattttgg actggtgtcg ccacttgcct ttttatgttc
      901 gacgtgtcca tggagacgtt cccctttgc tatttgtgca acatgattat cgatgactgc
      961 caggaaatgt ccaattgcct ctttcaatcg gactggacct ctgccgatcg tcgctacaaa
     1021 tccactttgg tatactttct tcacaatctt cagcaaccca ttactctcac ggctggtgga
     1081 gtgtttccta tttccatgca aacaaatttg gctatggtga agctggcatt ttctgtggtt
     1141 acggtaatta agcaatttaa cttggccgaa aggtttcaat aagttgagag ggacgagctc
     1201 tgctactatt atattatata ttatattata ttatatatat attattttat attatatatt
     1261 gctgtaccct aataaatatt tagtaataaa aaaaaaaaaa aaaaa
```

FIG. 8E-1

DOR67 [AF127924]

```
LOCUS       XXXXX          1321 bp    mRNA             INV       06-FEB-1999
DEFINITION  Drosophila melanogaster putative odorant receptor DOR67 mRNA,
            complete cds.
ACCESSION   AF127924
KEYWORDS    .
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1321)
  AUTHORS   Leslie B. Vosshall, Hubert Amrein, Pavel S. Morozov, Andrey
            Rzhetsky and Richard Axel.
  TITLE     A Spatial Map of Olfactory Receptor Expression in the Drosophila
            Antenna
  JOURNAL   Cell (1999) In press
REFERENCE   2  (bases 1 to 1321)
  AUTHORS   Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and Axel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-FEB-1999) Department of Biochemistry and Molecular
            Biophysics, HHMI-Columbia University, 701 West 168th Street, New
            York, NY 10032, USA
FEATURES             Location/Qualifiers
     Comment:      /tissue_type='adult antenna'
                   /note='putative seven transmembrane G protein coupled
                   receptor'
     source          1..1321
                     /organism="Drosophila melanogaster"
                     /strain="Oregon R"
                     /db_xref="taxon:7227"
                     /chromosome="II"
                     /map="22A3"
     gene            1..1321
                     /note="odorant receptor"
                     /gene="DOR67"
     CDS             102..1202
                     /gene="DOR67"
                     /note="odorant receptor"
                     /codon_start=1
                     /product="DOR67"

/translation="MWSFGWTVPENKRWDLHYKLWSTFVTLVIFILLPISVSVEYIQR
FKTFSAGEFLSSIQIGVNMYGSSFKSYLTMMGYKKRQEAKMSLDELDKRCVCDEERTI
VHRHVALGNFCYIFYHIAYTSFLISNFLSFIMKRIHAWRMYFPYVDPEKQFYISSIAE
VILRGWAVFMDLCTDVCPLISMVIARCHITLLKQRLRNLRSEPGRTEDEYLKELADCV
RDHRLILDYVDALRSVFSGTIFVQFLLIGIVLGLSMINIMFFSTLSTGVAVVLFMSCV
SMQTFPFCYLCNMIMDDCQEMADSLFQSDWTSADRRYKSTLVYFLHNLQQPIILTAGG
VFPISMQTNLNMVKLAFTVVTIVKQFNLAEKFQ"
BASE COUNT       348 a     281 c     294 g     398 t
```

FIG. 8E-2

```
ORIGIN
        1 ggcacgagga aatgttaagc cagttctttc cccacattaa agaaaagcca ttgagcgagc
       61 gggttaagtc ccgagatgcc ttcgtttact tagatcgggt gatgtggtcc tttggctgga
      121 cagtgcctga aaacaaaagg tgggatctac attacaaact gtggtcaact ttcgtgacat
      181 tggtgatatt tatccttctg ccgatatcgg taagcgttga gtatattcag cggttcaaga
      241 ccttctcggc gggtgagttt cttagctcaa tccagattgg cgttaacatg tacggaagca
      301 gctttaaaag ttatttgacc atgatgggat ataagaagag acaggaggct aagatgtcac
      361 tggatgagct ggacaagaga tgcgtttgtg atgaggagag gaccattgta catcgacatg
      421 tcgccctggg aaacttttgc tatattttct atcacattgc gtacactagc tttttgattt
      481 caaacttttt gtcatttata atgaagagaa tccatgcctg gcgcatgtac tttccctacg
      541 tcgaccccga aaagcaattt tacatctcta gcatcgccga agtcattctt agggggtggg
      601 ccgtcttcat ggatctctgc acggatgtgt gtcctttgat ctccatggta atagcacgat
      661 gccacatcac ccttctgaaa cagcgcctgc gaaatctacg atcggaacca ggaaggacgg
      721 aagatgagta cttgaaggag ctcgccgact gcgttcgaga tcaccgcttg atattggact
      781 atgtcgacgc attgcgatcc gtctttttcgg ggacaatttt tgtgcagttc ctcttgatcg
      841 gtattgtact gggtctgtca atgataaata taatgttttt ctcaacactt tcgactggtg
      901 tcgccgttgt cctttttatg tcctgcgtat ctatgcagac gttccccttt tgctatttgt
      961 gtaacatgat tatggatgac tgccaagaga tggccgactc cctttttcaa tcggactgga
     1021 catctgccga tcgtcgctac aaatccactt tggtatactt tcttcacaat cttcagcagc
     1081 ccattattct tacggctggt ggagtctttc ctatttccat gcaaacaaat ttaaatatgg
     1141 tgaagctggc ctttactgtg gttacaatag tgaaacaatt taacttggca gaaaagtttc
     1201 aataagttaa gatatgcaag ctctgctatt ataaacctac actcgagaaa atatttcttc
     1261 acattaataa accttcagta cttactgctt gtggcgcccc cggaaaaaaa aaaaaaaaaa
     1321 a
```

FIG. 8F-1

DOR64 [AF127925]

```
LOCUS       XXXXX         1308 bp    mRNA            INV       06-FEB-1999
DEFINITION  Drosophila melanogaster putative odorant receptor DOR64 mRNA,
            complete cds.
ACCESSION   AF127925
KEYWORDS    .
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1308)
  AUTHORS   Leslie B. Vosshall, Hubert Amrein, Pavel S. Morozov, Andrey
            Rzhetsky and Richard Axel.
  TITLE     A Spatial Map of Olfactory Receptor Expression in the Drosophila
            Antenna
  JOURNAL   Cell (1999) In press
REFERENCE   2  (bases 1 to 1308)
  AUTHORS   Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and Axel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-FEB-1999) Department of Biochemistry and Molecular
            Biophysics, HHMI-Columbia University, 701 West 168th Street, New
            York, NY 10032, USA
FEATURES             Location/Qualifiers
     Comment:      /tissue_type='adult antenna'
                   /note='putative seven transmembrane G protein coupled
                   receptor'
     source          1..1308
                     /organism="Drosophila melanogaster"
                     /strain="Oregon R"
                     /db_xref="taxon:7227"
                     /chromosome="II"
                     /map="23A1-2"
     gene            1..1308
                     /note="odorant receptor"
                     /gene="DOR64"
     CDS             22..1158
                     /gene="DOR64"
                     /note="odorant receptor"
                     /codon_start=1
                     /product="DOR64"

/translation="MKLSETLKIDYFRVQLNAWRICGALDLSEGRYWSWSMLLCILVY
LPTPMLLRGVYSFEDPVENNFSLSLTVTSLSNLMKFCMYVAQLTKMVEVQSLIGQLDA
RVSGESQSERHRNMTEHLLRMSKLFQITYAVVFIIAAVPFVFETELSLPMPMWFPFDW
KNSMVAYIGALVFQEIGYVFQIMQCFAADSFPPLVLYLISEQCQLLILRISEIGYGYK
TLEENEQDLVNCIRDQNALYRLLDVTKSLVSYPMMVQFMVIGINIAITLFVLIFYVET
LYDRIYYLCFLLGITVQTYPLCYYGTMVQESFAELHYAVFCSNWVDQSASYRGHMLIL
AERTKRMQLLLAGNLVPIHLSTYVACWKGAYSFFTLMADRDGLGS"
BASE COUNT       331 a     314 c     305 g     358 t
```

FIG. 8F-2

```
ORIGIN
        1 ggcacgagcc aagaattcaa aatgaaactc agcgaaaccc taaaaatcga ctattttcga
       61 gtccagttga atgcctggcg aatttgtggt gccttggatc tcagcgaggg taggtactgg
      121 agttggtcga tgctattgtg catcttggtg tacctgccga cacccatgct actgagagga
      181 gtatacagtt tcgaggatcc ggtggaaaat aatttcagct tgagcctgac ggtcacatcg
      241 ctgtccaatc tcatgaagtt ctgcatgtac gtggcccaac taacaaagat ggtcgaggtc
      301 cagagtctta ttggtcagct ggatgcccgg gtttctggcg agagccagtc tgagcgtcat
      361 agaaatatga ccgagcacct gctaaggatg tccaagctgt tccagatcac ctacgctgta
      421 gtcttcatca ttgctgcagt tcccttcgtt ttcgaaactg agctaagctt acccatgccc
      481 atgtggtttc ccttcgactg gaagaactcg atggtggcct acatcggagc tctggttttc
      541 caggagattg gctatgtctt tcaaattatg caatgctttg cagctgactc gtttcccccg
      601 ctcgtactgt acctgatctc cgagcaatgt caattgctga tcctgagaat ctctgaaatc
      661 ggatatggtt acaagactct ggaggagaac gaacaggatc tggtcaactg catcagggat
      721 caaaacgcgc tgtatagatt actcgatgtg accaagagtc tcgtttcgta tcccatgatg
      781 gtgcagttta tggttattgg catcaacatc gccatcaccc tatttgtcct gatattttac
      841 gtggagacct tgtacgatcg catctattat ctttgctttc tcttgggcat caccgtgcag
      901 acatatccat tgtgctacta tggaaccatg gtgcaggaga gttttgctga gcttcactat
      961 gcggtattct gcagcaactg ggtggatcaa agtgccagct atcgtgggca catgctcatc
     1021 ctggcggagc gcactaagcg gatgcagctt ctcctcgccg gcaacctggt gcccatccac
     1081 ctgagcacct acgtggcctg ttggaaggga gcctactcct tcttcaccct gatggccgat
     1141 cgagatggcc tgggttctta gtagcccagt catttcactc acattctaca tcaagtagta
     1201 ctaccactga acacgaacac gaatatttca aaagtaaaca cataatattc acaatagtgt
     1261 atcactttaa taaaattttt ggttaccatg aaaaaaaaaa aaaaaaaa
```

FIG. 8G-1

DOR71g

```
LOCUS       XXXXX        1252 bp    DNA             INV       07-FEB-1999
DEFINITION  Drosophila melanogaster odorant receptor DOR71g, GENSCAN
predicted complete cds.
ACCESSION   ;
KEYWORDS    .
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1252)
  AUTHORS   Leslie B. Vosshall, Hubert Amrein, Pavel S. Morozov, Andrey
            Rzhetsky and Richard Axel.
  TITLE     A Spatial Map of Olfactory Receptor Expression in the Drosophila
            Antenna
  JOURNAL   Cell (1999) In press
REFERENCE   2  (bases 1 to 1252)
  AUTHORS   Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
            Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
            Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
            Pfeiffer,B., Poon,L., Punch,E., Sequeira,A., Sethi,H., Snir,E.,
            Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R.,
            Zieran,L.L. and Rubin,G.M.
  TITLE     Sequencing of Drosophila melanogaster
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1252)
  AUTHORS   Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and Axel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-FEB-1999) Department of Biochemistry and Molecular
            Biophysics, HHMI-Columbia University, 701 West 168th Street, New
            York, NY 10032, USA
FEATURES             Location/Qualifiers
     Comment:       /tissue_type='adult maxillary palp'
                    /note='putative seven transmembrane G protein coupled
                    receptor'
                    /note='sequence annotation for BDGP P1 clone DS07071;
                    predicted using GENSCAN; join (26150-24899)'
     source          1..1252
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /chromosome="II"
                     /map="33B1-2"
     exon            1..731
                     /gene="DOR71g"
                     /note="exon"
     mRNA            join(1..731,811..1234)
                     /gene="DOR71g"
     CDS             join(1..731,811..1234)
                     /gene="DOR71g"
                     /note="odorant receptor"
                     /codon_start=1
                     /product="DOR71g"
```

FIG. 8G-2

```
/translation="MVIIDSLSFYRPFWICMRLLVPTFFKDSSRPVQLYVVLLHILVT
LWFPLHLLLHLLLLPSTAEFFKNLTMSLTCVACSLKHVAHLYHLPQIVEIESLIEQLD
TFIASEQEHRYYRDHVHCHARRFTRCLYISFGMIYALFLFGVFVQVISGNWELLYPAY
FPFDLESNRFLGAVALGYQVFSMLVEGFQGLGNDTYTPLTLCLLAGHVHLWSIRMGQL
GYFDDETVVNHQRLLDYIEQHKLLVRFHNLVSRTISEVQLVQLGGCGATLCIIVSYML
FFVGDTISLVYYLVFFGVVCVQLFPSCYFASEVAEELERLPYAIFSSRWYDQSRDHRF
DLLIFTQLTLGNRGWIIKAGGLIELNLNAFFATLKMAYSLFAVVVRAKGI"
     gene            1..1234
                     /note="odorant receptor"
                     /gene="DOR71g"
     intron          732..810
                     /gene="DOR71g"

                     /note="intron"
     exon            811..1231
                     /gene="DOR71g"
                     /note="exon"
     polyA_signal    1246..1252
                     /note="polyA_signal"
BASE COUNT      269 a    299 c    305 g    379 t
ORIGIN
        1 atggtcatta tcgacagtct tagtttttat cgtccattct ggatctgcat gcgattgctg
       61 gtaccgactt tcttcaagga ttcctcacgt cctgtccagc tgtacgtggt gttgctgcac
      121 atcctggtca ccttgtggtt tccactgcat ctgctgctgc atcttctgct acttccatct
      181 accgctgagt tctttaagaa cctgaccatg tctctgactt gtgtggcctg cagtctgaag
      241 catgtggccc acttgtatca cttgccgcag attgtggaaa tcgaatcact gatcgagcaa
      301 ttagacacat ttattgccag cgaacaggag catcgttact atcgggatca cgtacattgc
      361 catgctaggc gctttacaag atgtctctat attagctttg gcatgatcta tgcgcttttc
      421 ctgttcggcg tcttcgttca ggttattagc ggaaattggg aacttctcta tccagcctat
      481 ttccccattcg acttggagag caatcgcttt ctcggcgcag tagccttggg ctatcaggta
      541 ttcagcatgt tagttgaagg cttccagggg ctgggcaacg atacctatac cccactgacc
      601 ctatgccttc tggccggaca tgtccatttg tggtccatac gaatgggtca actgggatac
      661 ttcgatgacg agacggtggt gaatcatcag cgtttgctgg attacattga gcagcataaa
      721 ctcttggtgc ggtaagcttt gattaactaa cttttgacaa gaagtttatt cactttaact
      781 ggttccaaaa acgatgcact caatgtgcag attccacaac ctggtgagcc ggaccatcag
      841 cgaagtgcaa ctggtgcagc tgggcggatg tggagccact ctgtgcatca ttgtctccta
      901 catgctcttc tttgtgggcg acacaatctc gctggtctac tacttggtgt tctttggagt
      961 ggtctgcgtg cagctctttc ccagctgcta ttttgccagc gaagtagccg aggagttgga
     1021 acggctgcca tatgcgatct tctccagcag atggtacgat caatcgcggg atcatcgatt
     1081 cgatttgctc atctttacac aattaacact gggaaaccgg gggtggatca tcaaggcagg
     1141 aggtcttatc gagctgaatt tgaatgcctt tttcgccacc ctgaagatgg cctattcccct
     1201 ttttgcagtt gtggtgcggg caaagggtat atagagagtc tgtttaatta aa
```

FIG. 8H-1

DOR72g

```
LOCUS       XXXXX        1321 bp    DNA             INV       08-FEB-1999
DEFINITION  Drosophila melanogaster odorant receptor DOR72g, GENSCAN
predicted complete cds.
ACCESSION   ;
KEYWORDS    .
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1321)
  AUTHORS   Leslie B. Vosshall, Hubert Amrein, Pavel S. Morozov, Andrey
            Rzhetsky and Richard Axel.
  TITLE     A Spatial Map of Olfactory Receptor Expression in the Drosophila
            Antenna
  JOURNAL   Cell (1999) In press
REFERENCE   2  (bases 1 to 1321)
  AUTHORS   Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
            Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
            Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
            Pfeiffer,B., Poon,L., Punch,E., Sequeira,A., Sethi,H., Snir,E.,
            Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R.,

            Zieran,L.L. and Rubin,G.M.
  TITLE     Sequencing of Drosophila melanogaster
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1321)
  AUTHORS   Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and Axel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-FEB-1999) Department of Biochemistry and Molecular
            Biophysics, HHMI-Columbia University, 701 West 168th Street, New
            York, NY 10032, USA
FEATURES             Location/Qualifiers
     Comment:       /tissue_type='adult antenna'
                    /note='putative seven transmembrane G protein coupled
                    receptor'
                    /note='sequence annotation for BDGP P1 clone DS07071;
                    predicted using GENSCAN; join (27938-26618)'
     source            1..1321
                       /organism="Drosophila melanogaster"
                       /db_xref="taxon:7227"
                       /chromosome="II"
                       /map="33B1-2"
     mRNA              join(1..728,910..1321)
                       /gene="DOR72g"
     gene              1..1321
                       /note="odorant receptor"
                       /gene="DOR72g"
     exon              1..728
                       /gene="DOR72g"
                       /note="exon"
     CDS               join(1..728,910..1321)
                       /gene="DOR72g"
                       /note="odorant receptor"
                       /codon_start=1
                       /product="DOR72g"
```

FIG. 8H-2

```
/translation="MDLKPRVIRSEDIYRTYWLYWHLLGLESNFFLNRLLDLVITIFV
TIWYPIHLILGLFMERSLGDVCKGLPITAACFFASFKFICFRFKLSEIKEIEILFKEL
DQRALSREECEFFNQNTRREANFIWKSFIVAYGLSNISAIASVLFGGGHKLLYPAWFP
YDVQATELIFWLSVTYQIAGVSLAILQNLANDSYPPMTFCVVAGHVRLLAMRLSRIGQ
GPEETIYLTGKQLIESIEDHRKLMKIVELLRSTMNISQLGQFISSGVNISITLVNILF
FADNNFAITYYGVYFLSMVLELFPCCYYGTLISVEMNQLTYAIYSSNWMSMNRSYSRI
LLIFMQLTLAEVQIKAGGMIGIGMNAFFATVRLAYSFFTLAMSLR"
     intron          729..909
                     /gene="DOR72g"
                     /note="intron"
     exon            910..1321
                     /gene="DOR72g"
                     /note="exon"
BASE COUNT      361 a    255 c    283 g    422 t
ORIGIN
        1 atggacttaa aaccgcgagt cattcgaagt gaagatatct acagaaccta ttggttatat
       61 tggcatcttt tgggcctgga aagcaatttc tttctgaatc gcttgttgga tttggtgatt
      121 acaattttcg taaccatttg gtatccaatt cacctgattc tgggactgtt tatggaaaga
      181 tctttggggg atgtctgcaa gggtctacca attacggcag catgcttttt cgccagcttt
      241 aaatttattt gttttcgctt caagctatct gaaattaaag aaatcgaaat attatttaaa
      301 gagctggatc agcgagcttt aagtcgagag gaatgcgagt tttcaatca aaatacgaga
      361 cgtgaggcga atttcatttg gaaaagtttc attgtggcct atggactgtc gaatatctcg
      421 gctattgcat cagttctttt cggcggtgga cataagctat tatatcccgc ctggtttcca.
      481 tacgatgtgc aggccacgga actaatattt tggctaagtg taacatacca aattgccgga
      541 gtaagtttgg ccatacttca gaatttggcc aatgattcct atccaccgat gacattttgc
      601 gtggttgccg gtcatgtaag acttttggcg atgcgcttga gtagaattgg ccaaggtcca
      661 gaggaaacaa tatacttaac cggaaagcaa ttaatcgaaa gcatcgagga tcaccgaaaa
      721 ctaatgaagt aatgtacata tatagaatgg tttttagtta ttatcattaa atgaacgtgt
      781 tgtaggaaaa ccattctgtt tgtcgggtgt cacggaaatc gattttcctt aatttacata
      841 tgatattaaa tacttccttg caaacaatta tcatattagt aatttagaat ctttattatt
      901 tatttccaga atagtggaat tactgcgcag caccatgaat atttcgcagc tcggccagtt
      961 tatttcaagt ggtgttaata tttccataac actagtcaac attctcttct ttgcggataa
     1021 taatttcgct ataacctact acggagtgta cttcctatcg atggtgttgg aattattccc
     1081 gtgctgctat tacggcaccc tgatatccgt ggagatgaac cagctgacct atgcgattta
     1141 ctcaagtaac tggatgagta tgaatcggag ctacagccgc atcctactga tcttcatgca
     1201 actcaccctg gcggaagtgc agatcaaggc cggtgggatg attggcatcg gaatgaacgc
     1261 cttctttgcc accgtgcgat tggcctactc cttcttcact ttggccatgt cgctgcgtta
     1321 a
```

FIG. 8I-1

DOR73g

```
LOCUS       XXXXX        1212 bp    DNA              INV       08-FEB-1999
DEFINITION  Drosophila melanogaster odorant receptor DOR73g, GENSCAN
predicted complete cds.
ACCESSION
KEYWORDS
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1212)
  AUTHORS   Leslie B. Vosshall, Hubert Amrein, Pavel S. Morozov, Andrey
            Rzhetsky and Richard Axel.
  TITLE     A Spatial Map of Olfactory Receptor Expression in the Drosophila
            Antenna
  JOURNAL   Cell (1999) In press
REFERENCE   2  (bases 1 to 1212)
  AUTHORS   Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
            Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
            Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
            Pfeiffer,B., Poon,L., Punch,E., Sequeira,A., Sethi,H., Snir,E.,
            Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R.,
            Zieran,L.L. and Rubin,G.M.
  TITLE     Sequencing of Drosophila melanogaster
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1212)
  AUTHORS   Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and Axel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-FEB-1999) Department of Biochemistry and Molecular
            Biophysics, HHMI-Columbia University, 701 West 168th Street, New
            York, NY 10032, USA
FEATURES             Location/Qualifiers
    Comment:         /tissue_type='adult antenna'
                     /note='putative seven transmembrane G protein coupled
                     receptor'
                     /note='sequence annotation for BDGP P1 clone DS07071;
                     predicted using GENSCAN; join (29614-28403)'

  source             1..1212
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /chromosome="II"
                     /map="33B1-2"
  mRNA               join(1..722,798..1212)
                     /gene="DOR73g"
  gene               1..1212
                     /note="odorant receptor"
                     /gene="DOR73g"
  exon               1..722
                     /gene="DOR73g"
                     /note="exon"
  CDS                join(1..722,798..1212)
                     /gene="DOR73g"
                     /note="odorant receptor"
                     /codon_start=1
                     /product="DOR73g"
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FIG. 8I-2

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/translation="MDSRRKVRSENLYKTYWLYWRLLGVEGDYPFRRLVDFTITSFIT
ILFPVHLILGMYKKPQIQVFRSLHFTSECLFCSYKFFCFRWKLKEIKTIEGLLQDLDS
RVESEEERNYFNQNPSRVARMLSKSYLVAAISAIITATVAGLFSTGRNLMYLGWFPYD
FQATAAIYWISFSYQAIGSSLLILENLANDSYPPITFCVVSGHVRLLIMRLSRIGHDV
KLSSSENTRKLIEGIQDHRKLMKIIRLLRSTLHLSQLGQFLSSGINISITLINILFFA
ENNFAMLYYAVFFAAMLIELFPSCYYGILMTMEFDKLPYAIFSSNWLKMDKRYNRSLI
ILMQLTLVPVNIKAGGIVGIDMSAFFATVRMAYSFYTLALSFRV"
     intron          723..797
                     /gene="DOR73g"
                     /note="intron"
     exon            798..1212
                     /gene="DOR73g"
                     /note="exon"
BASE COUNT      352 a    231 c    242 g    387 t
ORIGIN
        1 atggattcaa gaaggaaagt ccgaagtgaa aatctttaca aaacctattg gctttactgg
       61 cgacttctgg gagtcgaggg cgattatcct tttcgacggc tagtggattt tacaatcacg
      121 tctttcatta cgattttatt tcccgtgcat cttatactgg gaatgtataa aaagccccag
      181 attcaagtct tcaggagtct gcatttcaca tcggaatgcc ttttctgcag ctataagttt
      241 ttctgttttc gttggaaact taaagaaata aagaccatcg aaggattgct ccaggatctc
      301 gatagtcgag ttgaaagtga agaagaacgc aactacttta atcaaaatcc aagtcgtgtg
      361 gctcgaatgc tttcgaaaag ttacttggta gctgctatat cggccataat cactgcaact
      421 gtagctggtt tatttagtac tggtcgaaat ttaatgtatc tgggttggtt tccctacgat
      481 tttcaagcaa ccgccgcaat ctattggatt agtttttcct atcaggcgat tggctctagt
      541 ctgttgattc tggaaaatct ggccaacgat tcatatccgc cgattacatt ttgtgtggtc
      601 tctggacatg tgagactatt gataatgcgt ttaagtcgaa ttggtcacga tgtaaaatta
      661 tcaagttcgg aaaataccag aaaactcatc gaaggtatcc aggatcacag gaaactaatg
      721 aagtaagaat aaagatttaa gaaccgcatg tttgatagct cagagaactg ataattaatc
      781 aaatgtaact tttccaggat aatacgccta cttcgcagca ctttacatct tagccaactg
      841 ggccagttcc tttctagtgg aatcaacatt tccataacac tcatcaacat cctgttcttt
      901 gcggaaaaca actttgcaat gctttattat gcggtgttct ttgctgcaat gttaatagaa
      961 ctatttccaa gttgttacta tggaattctg atgacaatgg agtttgataa gctaccatat
     1021 gccatcttct ccagcaactg gcttaaaatg gataaaagat acaatcgatc cttgataatt
     1081 ctgatgcaac taacactggt tccagtgaat ataaaagcag gtggtattgt tggcatcgat
     1141 atgagtgcat tttttgccac agttcggatg gcatattcct tttacacttt agccttgtca
     1201 tttcgagtat ag
```

FIG. 8J-1

DOR46

```
LOCUS       XXXXX         1198 bp    DNA              INV       08-FEB-1999
DEFINITION  Drosophila melanogaster odorant receptor DOR46g, GENSCAN
predicted complete cds.
ACCESSION   ;
KEYWORDS    .
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1198)
  AUTHORS   Leslie B. Vosshall, Hubert Amrein, Pavel S. Morozov, Andrey
            Rzhetsky and Richard Axel.
  TITLE     A Spatial Map of Olfactory Receptor Expression in the Drosophila
            Antenna
  JOURNAL   Cell (1999) In press
REFERENCE   2  (bases 1 to 1198)
  AUTHORS   Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
            Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
            Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
            Pfeiffer,B., Poon,L., Punch,E., Sequeira,A., Sethi,H., Snir,E.,
            Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R.,
            Zieran,L.L. and Rubin,G.M.
  TITLE     Sequencing of Drosophila melanogaster
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1198)
  AUTHORS   Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and Axel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-FEB-1999) Department of Biochemistry and Molecular
            Biophysics, HHMI-Columbia University, 701 West 168th Street, New
            York, NY 10032, USA
FEATURES             Location/Qualifiers
     Comment:      /note='putative seven transmembrane G protein coupled
                   receptor'
                   /note='sequence annotation for BDGP P1 clone DS07462;
                   predicted using GENSCAN'
     source          1..1198
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /chromosome="II"
                     /map="59D5-7"
     mRNA            join(1..725,784..1198)
                     /gene="DOR46g"
     gene            1..1198
                     /note="odorant receptor"
                     /gene="DOR46g"
     exon            1..725
                     /gene="DOR46g"
     CDS             join(1..725,784..1198)
                     /gene="DOR46g"
                     /note="odorant receptor"
                     /codon_start=1
                     /product="DOR46g"
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FIG. 8J-2

```
/translation="MAEVRVDSLEFFKSHWTAWRYLGVAHFRVENWKNLYVFYSIVSN
LLVTLCYPVHLGISLFRNRTITEDILNLTTFATCTACSVKCLLYAYNIKDVLEMERLL
RLLDERVVGPEQRSIYGQVRVQLRNVLYVFIGIYMPCALFAELSFLFKEERGLMYPAW
FPFDWLHSTRNYYIANAYQIVGISFQLLQNYVSDCFPAVVLCLISSHIKMLYNRFEEV
GLDPARDAEKDLEACITDHKHILELFRRIEAFISLPMLIQFTVTALNVCIGLAALVFF
VSEPMARMYFIFYSLAMPLQIFPSCFFGTDNEYWFGRLHYAAFSCNWHTQNRSFKRKM
MLFVEQSLKKSTAVAGGMMRIHLDTFFSTLKGAYSLFTIIIRMRK"
     intron          726..783
                     /gene="DOR46g"
     exon            784..1198
                     /gene="DOR46g"
BASE COUNT     251 a    325 c    310 g    312 t
ORIGIN
        1 atggcagagg tcagagtgga cagtctggag tttttcaaga gccattggac cgcctggcgg
       61 tacttgggag tggctcattt tcgggtcgag aactggaaga acctttacgt gttttacagc
      121 attgtgtcga atcttctcgt gaccctgtgc taccccgttc acctgggaat atccctcttt
      181 cgcaaccgca ccatcaccga ggacatcctc aacctgacca cctttgcgac ctgcacagcc
      241 tgttcggtga agtgcctgct ctacgcctac aacatcaagg atgtgctgga gatggagcgg
      301 ctgttgaggc ttttggatga acgcgtcgtg ggtccggagc aacgcagcat ctacggacaa
      361 gtgagggtcc agctgcgaaa tgtgctatac gtgttcatcg gcatctacat gccgtgtgcc
      421 ctgttcgccg agctatcctt tctgttcaag gaggagcgcg gtctgatgta tcccgcctgg
      481 tttcccttcg actggctgca ctccaccagg aactattaca tagcgaacgc ctatcagata
      541 gtgggcatct cgtttcagct gctgcaaaac tatgttagcg actgctttcc ggcggtggtg
      601 ctgtgcctga tctcatccca catcaaaatg ttgtacaaca gattcgagga ggtgggcctg
      661 gatccagcca gagatgcgga gaaggacctg gaggcctgca tcaccgatca caagcatatt
      721 ctagagtggg caggcggctc attgtaacgt tcgtgttcta ttcactttcc aacttttttc
      781 cagactattc cgacgcatcg aggccttcat ttccctgccc atgctaattc agttcacagt
      841 gaccgccttg aatgtgtgca tcggtttagc agccctggtg tttttcgtca gcgagcccat
      901 ggcacggatg tacttcatct tctactccct ggccatgccg ctgcagatct ttccgtcctg
      961 ctttttcggc accgacaacg agtactggtt cggacgcctc cactacgcgg ccttcagttg
     1021 caattggcac acacagaaca ggagctttaa gcggaaaatg atgctgttcg ttgagcaatc
     1081 gttgaagaag agcaccgctg tggctggcgg aatgatgcgt atccacctgg acacgttctt
     1141 ttccacccta aaggggcct actccctctt taccatcatt attcggatga gaaagtag
```

FIG. 8K-1

DOR19g

```
LOCUS       XXXXX       1293 bp    DNA            INV       09-FEB-1999
DEFINITION  Drosophila melanogaster odorant receptor DOR19g, GENSCAN
predicted complete cds.
ACCESSION   ;
KEYWORDS    .
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1293)
  AUTHORS   Leslie B. Vosshall, Hubert Amrein, Pavel S. Morozov, Andrey
            Rzhetsky and Richard Axel.
  TITLE     A Spatial Map of Olfactory Receptor Expression in the Drosophila
            Antenna
  JOURNAL   Cell (1999) In press
REFERENCE   2  (bases 1 to 1293)
  AUTHORS   Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
            Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
            Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
            Pfeiffer,B., Poon,L., Punch,E., Sequeira,A., Sethi,H., Snir,E.,
            Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R.,
            Zieran,L.L. and Rubin,G.M.
  TITLE     Sequencing of Drosophila melanogaster
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1293)
  AUTHORS   Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and Axel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-1999) Department of Biochemistry and Molecular
            Biophysics, HHMI-Columbia University, 701 West 168th Street, New
            York, NY 10032, USA
FEATURES             Location/Qualifiers
     Comment:       /note='putative seven transmembrane G protein coupled
                    receptor'
                    /note='sequence annotation for BDGP P1 clone DS01913;
                    predicted using GENSCAN; join (72218-70926)'
     source            1..1293
                       /organism="Drosophila melanogaster"
                       /db_xref="taxon:7227"
                       /chromosome="II"
                       /map="46F5-6"
     mRNA              1..1293
                       /gene="DOR19g"
     gene              1..1293
                       /note="odorant receptor"
                       /gene="DOR19g"
     exon              1..1293
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     CDS               1..1293
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                       /note="odorant receptor"
                       /codon_start=1
                       /product="DOR19g"
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FIG. 8K-2

```
/translation="MVTEDFYKYQVWYFQILGVWQLPTWAADHQRRFQSMRFGFILVI
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PEFGVKSEQEMQMLELDRVAVVRMRNSYGIMSLGAASLILIVPCFDNFGELPLAMLEV
CSIEGWICYWSQYLFHSICLLPTCVLNITYDSVAYSLLCFLKVQLQMLVLRLEKLGPV
IEPQDNEKIAMELRECAAYYNRIVRFKDLVELFIKGPGSVQLMCSVLVLVSNLYDMST
MSIANGDAIFMLKTCIYQLVMLWQIFIICYASNEVTVQSSRLCHSIYSSQWTGWNRAN
RRIVLLMMQRFNSPMLLSTFNPTFAFSLEAFGSVGQQKFLYISFITGYALLLSDRQLL
LQLLRTAEARQQLNFETPQHLKIFKPIFKSTQNVMHVH"
BASE COUNT      290 a    322 c    307 g    374 t
ORIGIN
        1 atggttacgg aggactttta taagtaccag gtgtggtact tccaaatcct tggtgtttgg
       61 cagctcccca cttgggccgc agaccaccag cgtcgttttc agtccatgag gtttggcttc
      121 atcctggtca tcctgttcat catgctgctg cttttctcct tcgaaatgtt gaacaacatt
      181 tcccaagtta gggagatcct aaaggtattc ttcatgttcg ccacggaaat atcctgcatg
      241 gccaaattat tgcatttgaa gttgaagagc cgcaaactcg ctggcttggt tgatgcgatg
      301 ttgtccccag agttcggcgt taaaagtgaa caggaaatgc agatgctgga attggataga
      361 gtggcggttg tccgcatgag gaactcctac ggcatcatgt ccctgggcgc ggcttccctg
      421 atccttatag ttccctgttt cgacaacttt ggcgagctac cactggccat gttggaggta
      481 tgcagcatcg agggatggat ctgctattgg tcgcagtacc ttttccactc gatttgcctg
      541 ctgcccactt gtgtgctgaa tataacctac gactcggtgg cctactcgtt gctctgtttc
      601 ttgaaggttc agctacaaat gctggtcctg cgattagaaa agttgggtcc tgtgatcgaa
      661 ccccaggata atgagaaaat cgcaatggaa ctgcgtgagt gtgccgccta ctacaacagg
      721 attgttcgtt tcaaggacct ggtggagctg ttcataaagg ggccaggatc tgtgcagctc
      781 atgtgttctg ttctggtgct ggtgtccaac ctgtacgaca tgtccaccat gtccattgca
      841 aacggcgatg ccatctttat gctcaagacc tgtatctatc agctggtgat gctctggcag
      901 atcttcatca tttgctacgc ctccaacgag gtaactgtcc agagctctag gttgtgtcac
      961 agcatctaca gctcccaatg gacgggatgg aacagggcaa accgccggat tgtccttctc
     1021 atgatgcagc gctttaattc cccgatgctc ctgagcacct ttaaccccac ctttgctttc
     1081 agcttggagg cctttggttc tgtagggcag cagaaattcc tttatatatc atttattact
     1141 ggttatgctc ttctcctttc agatcgtcaa ctgctcctac agctacttcg cactgctgaa
     1201 gcgcgtcaac agttaaattt cgaaacaccg cagcacctaa agattttcaa gccgattttt
     1261 aaaagcactc aaaacgttat gcacgtacat taa
```

FIG. 8L-1

DOR24g

```
LOCUS       XXXXX        2075 bp    DNA             INV       09-FEB-1999
DEFINITION  Drosophila melanogaster odorant receptor DOR24g, GENSCAN
predicted complete cds.
ACCESSION   ;
KEYWORDS    .
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 2075)
  AUTHORS   Leslie B. Vosshall, Hubert Amrein, Pavel S. Morozov, Andrey
            Rzhetsky and Richard Axel.
  TITLE     A Spatial Map of Olfactory Receptor Expression in the Drosophila
            Antenna
  JOURNAL   Cell (1999) In press
REFERENCE   2  (bases 1 to 2075)
  AUTHORS   Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
            Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
            Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
            Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
            Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
            Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
            Pfeiffer,B., Poon,L., Punch,E., Sequeira,A., Sethi,H., Snir,E.,
            Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R.,
            Zieran,L.L. and Rubin,G.M.
  TITLE     Sequencing of Drosophila melanogaster
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 2075)
  AUTHORS   Vosshall,L.B., Amrein,H., Morozov,P.S., Rzhetsky,A. and Axel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-1999) Department of Biochemistry and Molecular
            Biophysics, HHMI-Columbia University, 701 West 168th Street, New
            York, NY 10032, USA
FEATURES             Location/Qualifiers
     Comment:       /tissue_type='adult antenna'
                    /note='putative seven transmembrane G protein coupled
                    receptor'
                    /note='sequence annotation for BDGP P1 clone DS00724;
                    predicted using GENSCAN; join (62623-64697)'
     source            1..2075
                       /organism="Drosophila melanogaster"
                       /db_xref="taxon:7227"
                       /chromosome="II"
                       /map="47D6-E2"
     mRNA              join(1..185,739..1038,1338..1953,2025..2075)
                       /gene="DOR24g"
     gene              1..2075
                       /note="odorant receptor"
                       /gene="DOR24g"
     CDS               join(1..185,739..1038,1338..1953,2025..2075)
                       /gene="DOR24g"
                       /note="odorant receptor"
                       /codon_start=1
                       /product="DOR24g"
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FIG. 8L-2

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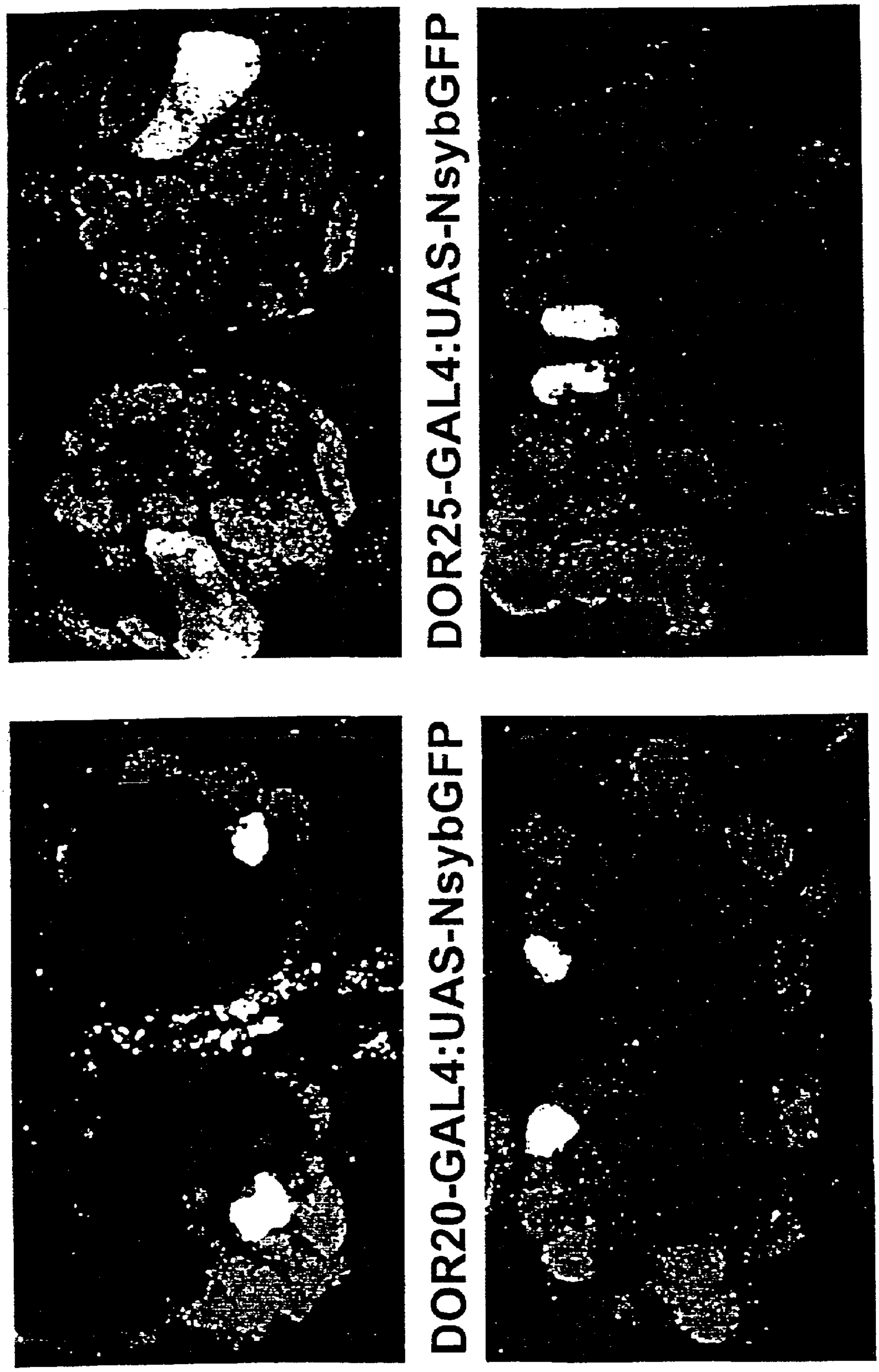
/translation="MRPTLQVLISVLCLVSAYAWDHTDCNDHYIEFMDYPDERATAYS
NESSEWDFFEFWRQVFGLFLQVQKSTIALLGFDLFSENREMWKRPYRAMNVFSIAAIF
PFILAAVLHNWKNVLLLADAMVALLITILGLFKFSMILYLRRDFKRLIDKFRLLMSNG
EFFPWNIHIIRNYVLSFIWSAFASTGVVLPAVSLDTIFCSFTSNLCAFFKIAQYKVVR
FKGGSLKESQATLNKVFALYQTSLDMCNDLNQCYQPIICAQFFISSLQLCMLGYLFSI
TFAQTEGVYYASFIATIIIQAYIYCYCGENLKTESASFEWAIYDSPWHESLGAGGAST
SICRSLLISMMRAHRGFRITGYFFEANMEAFSSIVRTAMSYITMLRSFS"
     exon            1..185
                     /gene="DOR24g"
     intron          186..738
                     /gene="DOR24g"
     exon            739..1038
                     /gene="DOR24g"
     intron          1039..1337
                     /gene="DOR24g"
     exon            1338..1953
                     /gene="DOR24g"
     intron          1954..2024
                     /gene="DOR24g"
     exon            2025..2075
                     /gene="DOR24g"
BASE COUNT      548 a    460 c    447 g    620 t
ORIGIN
        1 atgcgcccaa cactccaggt cctcatcagt gtcctttgtc tggtctctgc ctacgcctgg
       61 gatcataccg actgtaacga tcactatatc gaattcatgg actatcccga tgagagagct
      121 accgcctata gcaatgaatc ctcagaatgg gatttctttg aattttggag gcaagtgttt
      181 ggcctgtagc aattctgaca tcgctgacca cgcctctggt caaagcaatc acttggcgag
      241 acatgtgacc ctcggatgtc agggcgtgaa taaagaacat taaaatttaa ccggagttct
      301 catttactat gcctaaagag gtgtcaaacg gaggtattat ttgggcgtga tatattatac
      361 cctctaaagg agtatcccca ccaggtgaaa ccctataaaa cccttgacgt cgttaatgga
      421 aagtactgaa ccggaaatga aagtgggcac tttctaatgg tagaaatttg tcgggatgaa
      481 atatataagt agatatatat aatattatat cttgattatc cagcatcaat cacaagataa
      541 aaaaaaaata taattcataa ttcataattc atatgtaata ggcatttgta aatgttgtaa
      601 acaaaggaag ggtattaaag agctgtactt tcgcatctgt atttcattta ttcctactca
      661 attgaaaggt ttaaaacccc tgaactgaac acacttgact tagtgtgagg ccgaattaac
      721 ccttgtcgac atggacagtt ttctgcaagt acagaagagc accattgccc ttctgggctt
      781 tgatctcttt agtgaaaatc gagaaatgtg gaaacgcccc tatagagcaa tgaatgtgtt
      841 tagcatagct gccatttttc cctttatcct ggcagctgtg ctccataatt ggaagaatgt
      901 attgctgctg gccgatgcca tggtggccct actaataacc attctgggcc tattcaagtt
      961 tagcatgata ctttacttac gtcgcgattt caagcgactg attgacaaat ttcgtttgct
     1021 catgtcgaat ggtgagttgt aatccatttc ggccagaatg tgtatcattt catttactat
     1081 tttatagagg cggaacaggg cgaggaatac gccgagattc tcaatgcagc aaacaagcag
     1141 gatcaacgaa tgtgcactct gtttaggact tgtttcctcc tcgcctgggc cttgaatagt
     1201 gttctgcccc tcgtgagaat gggtctcagc tattggttag caggtcatgc agagcccgag
     1261 ttgccttttc cctgtctgta tgtacaaatg atatatatga tatatggtga tcaagttatc
     1321 aggctttgtt cctaaagttt tccctggaat atccacatca ttcgcaatta tgttttgagc
     1381 ttcatctgga gcgctttcgc ctcgacaggt gtggttttac ctgctgtcag cttggatacc
     1441 atattctgtt ccttcaccag caacctgtgc gccttcttca aaattgcgca gtacaaggtg
     1501 gttagattta agggcggatc ccttaaagaa tcacaggcca cattgaacaa agtctttgcc
     1561 ctgtaccaga ccagcttgga tatgtgcaac gatctgaatc agtgctacca accgattatc
     1621 tgcgcccagt tcttcatttc atctctgcaa ctctgcatgc tgggatatct gttctccatt
     1681 acttttgccc agacagaggg cgtctactat gcctcattca tagccacaat cattatacaa
     1741 gcctatatct actgctactg cggggagaac ctgaagacgg agagtgccag cttcgagtgg
     1801 gccatctacg acagtccgtg gcacgagagt ttgggtgctg gtggagcctc tacctcgatc
     1861 tgccgatcct tgctgatcag catgatgcgg gctcatcggg gattccgcat tacgggatac
     1921 tttttcgagg caaacatgga ggccttctca tcggtgggtg aatcatttcc attgtacaat
     1981 acatggattt acatgaatac tctttttctaa ctttccgttt ttagattgtt cgcacggcga
     2041 tgtcctacat cacaatgctg agatcattct cctaa
```

FIG. 9



DOR25-GAL4:UAS-NsybGFP

DOR53-GAL4:UAS-NsybGFP

DOR20-GAL4:UAS-NsybGFP

DOR24-GAL4:UAS-NsybGFP

FIG. 10A-1

ClustalW Alignment of the DOR53 Family

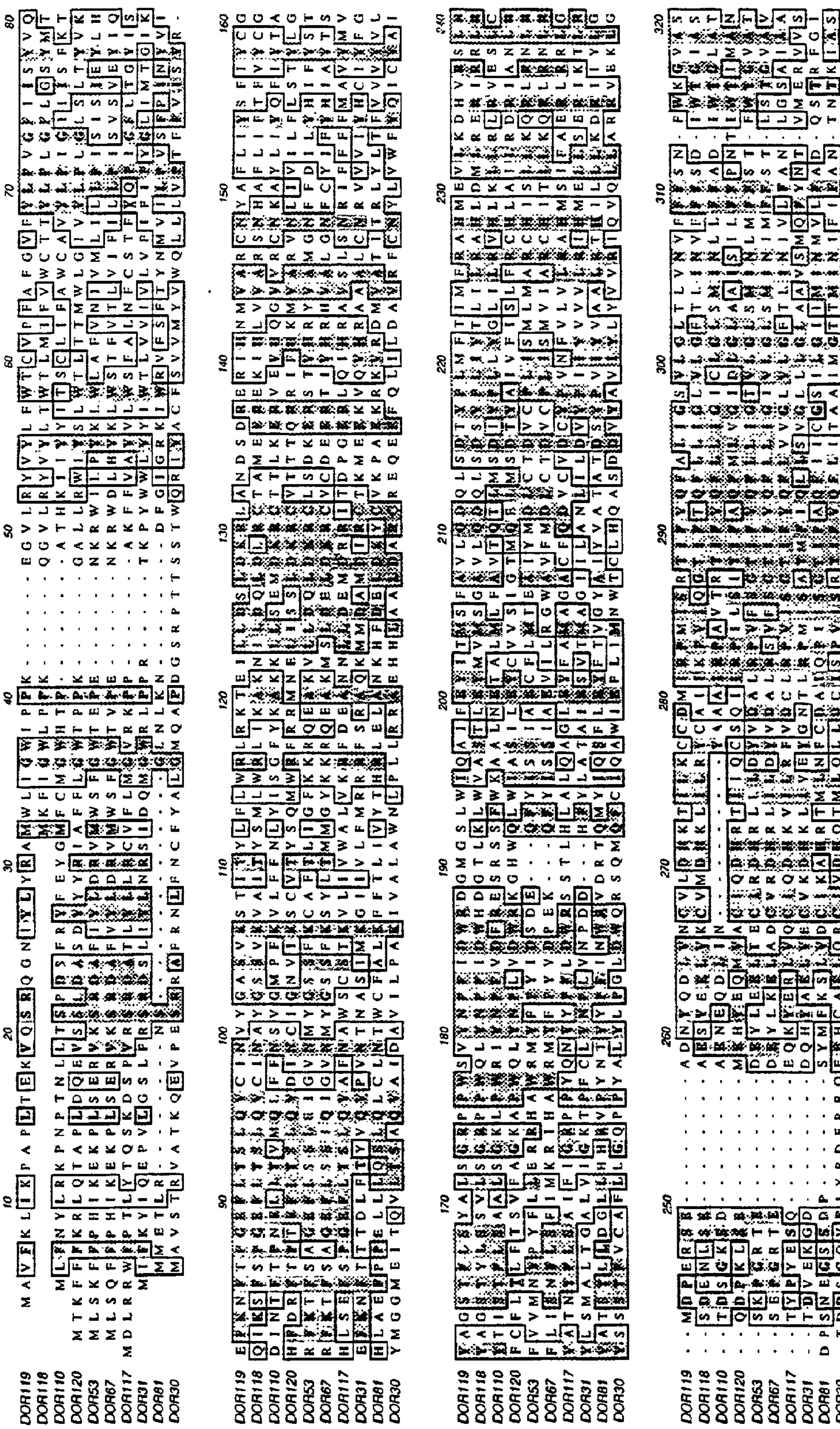
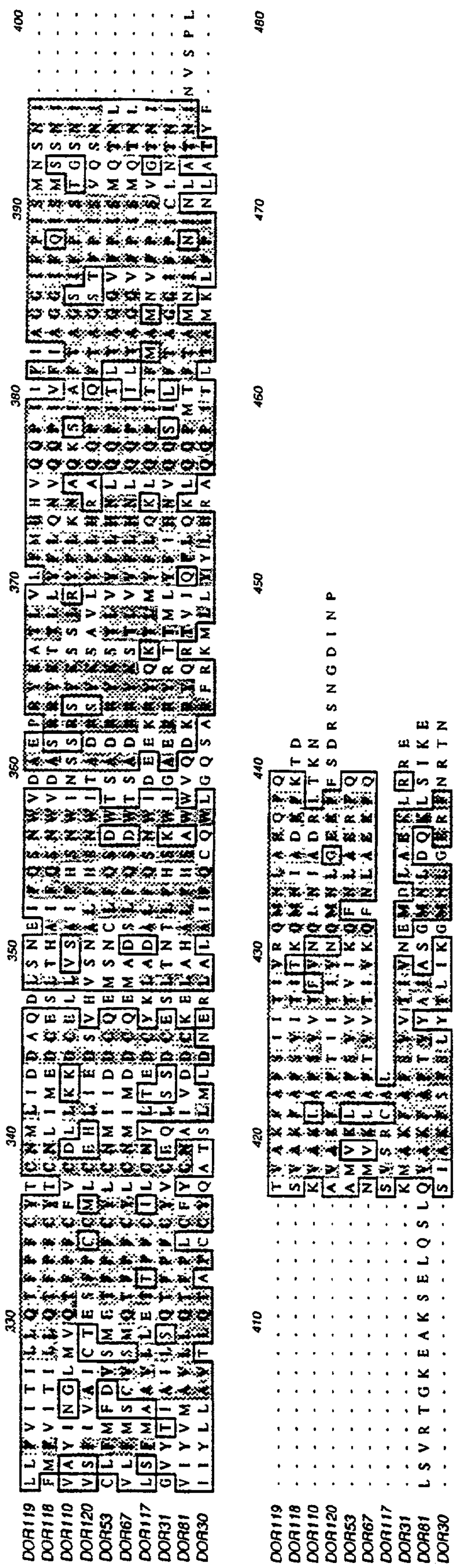


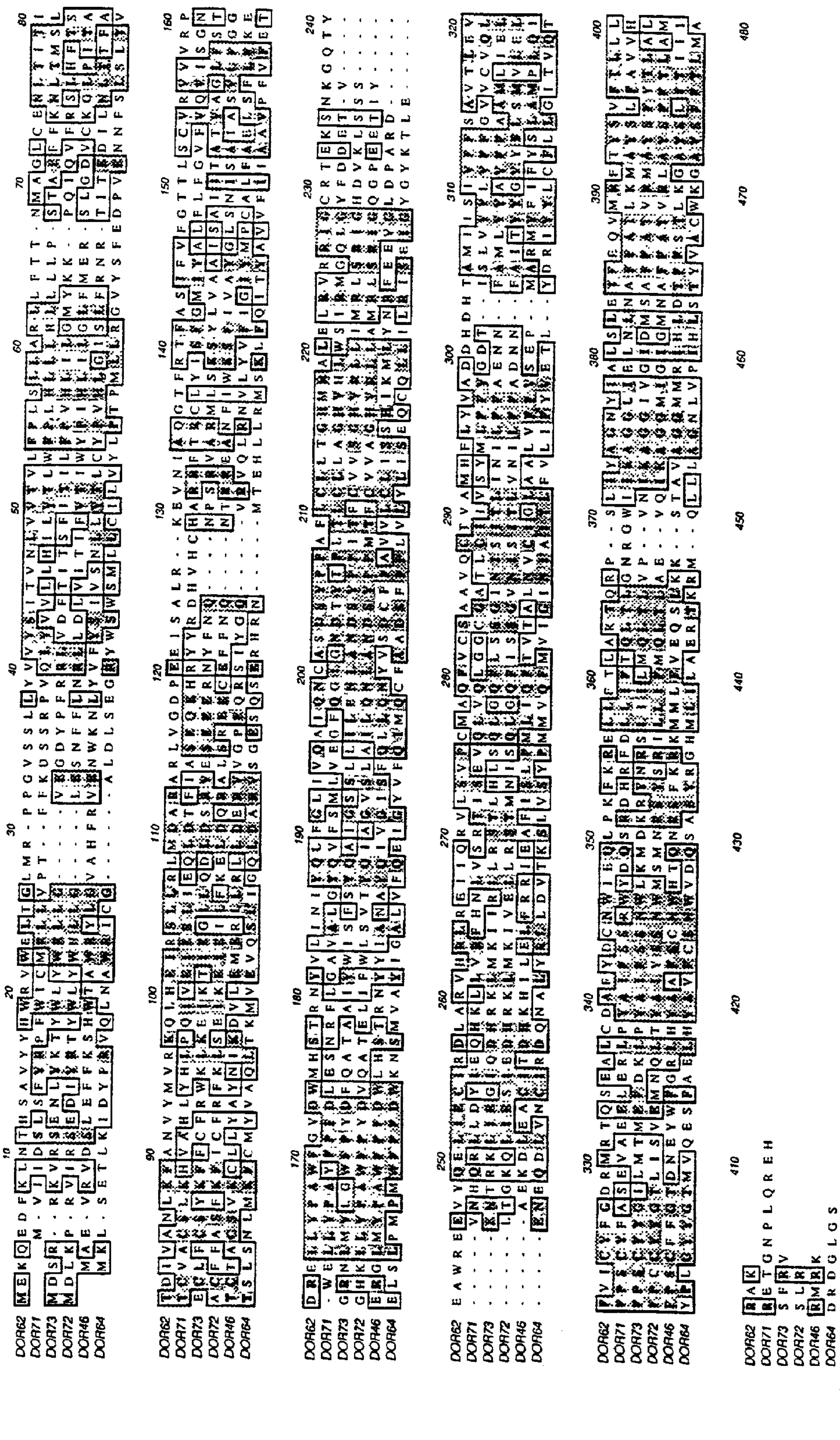
FIG. 10A-2



DOR119
DOR118
DOR110
DOR120
DOR53
DOR67
DOR117
DOR31
DOR81
DOR30
330
340
350
360
370
380
390
400
DOR119
DOR118
DOR110
DOR120
DOR53
DOR67
DOR117
DOR31
DOR81
DOR30
410
420
430
440
450
460
470
480

FIG. 10B

ClustalW Alignment of the DOR64 Family



GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF

[0001] This application claims priority and is a continuation-in-part application of U.S. Ser. No. 09/257,706, filed Feb. 25, 1999, the contents of which is hereby incorporated by reference.

[0002] The invention disclosed herein was made with Government support under NIH:NIMH, 5P50, MH50733-05 and the NINDS, NS29832-07 from the Department of Health and Human Services. Accordingly, the U.S. Government has certain rights in this invention.

[0003] Throughout this application, various publications are referred to by arabic numeral within parentheses. Full citations for these publications are presented immediately before the claims. Disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

BACKGROUND OF THE INVENTION

[0004] All animals possess a "nose," an olfactory sense organ that allows for the recognition and discrimination of chemosensory information in the environment. Humans, for example, are thought to recognize over 10,000 discrete odors with exquisite discriminatory power such that subtle differences in chemical structure can often lead to profound differences in perceived odor quality. What mechanisms have evolved to allow the recognition and discrimination of complex olfactory information and how is olfactory perception ultimately translated into appropriate behavioral responses? The recognition of odors is accomplished by odorant receptors that reside on olfactory cilia, a specialization of the dendrite of the olfactory sensory neuron. The odorant receptor genes encode novel serpentine receptors that traverse the membrane seven times. In several vertebrate species, and in the invertebrate *Caenorhabditis elegans*, as many as 1000 genes encode odorant receptors, suggesting that 1-5% of the coding potential of the genome in these organisms is devoted to the recognition of olfactory sensory stimuli (Buck and Axel, 1991; Levy et al., 1991; Parmentier et al., 1992; Ben-Arie et al., 1994; Troemel et al., 1995; Sengupta et al., 1996; Robertson, 1998). Thus, unlike color vision in which three photoreceptors can absorb light across the entire visible spectrum, these data suggest that a small number of odorant receptors are insufficient to recognize the full spectrum of distinct molecular structures perceived by the olfactory system. Rather, the olfactory sensory system employs an extremely large number of receptors, each capable of recognizing a small number of odorous ligands.

[0005] The discrimination of olfactory information requires that the brain discern which of the numerous receptors have been activated by an odorant. In mammals, individual olfactory sensory neurons express only one of a thousand receptor genes such that the neurons are functionally distinct (Ngai et al., 1993; Ressler et al., 1993; Vassar et al., 1993; Chess et al., 1994; Dulac and Axel, unpublished). The axons from olfactory neurons expressing a specific receptor converge upon two spatially invariant glomeruli among the 1800 glomeruli within the olfactory bulb (Ressler et al., 1994; Vassar et al., 1994; Mombaerts et al., 1996; Wang et al., 1998). The bulb therefore provides a spatial map that identifies which of the numerous receptors has been activated within the sensory epithelium. The quality of an olfactory stimulus would therefore be encoded by specific combinations of glomeruli activated by a given odorant.

[0006] The logic of olfactory discrimination is quite different in the nematode, *C. elegans*. Despite the large size of the odorant receptor gene family, volatile odorants are recognized by only three pairs of chemosensory cells each likely to express a large number of receptor genes (Bargmann and Horvitz, 1991; Colbert and Bargmann, 1995; Troemel et al., 1995). Activation of any one of the multiple receptors in one cell will lead to chemoattraction, whereas activation of receptors in a second cell will result in chemorepulsion (Troemel et al., 1997). The specific neural circuit activated by a given sensory neuron is therefore the determinant of the behavioral response. Thus, this invertebrate olfactory sensory system retains the ability to recognize a vast array of odorants but has only limited discriminatory power.

[0007] Vertebrates create an internal representation of the external olfactory world that must translate stimulus features into neural information. Despite the elucidation of a precise spatial map, it has been difficult in vertebrates to discern how this information is decoded to relate the recognition of odors to specific behavioral responses. Genetic analysis of olfactory-driven behavior in invertebrates may ultimately afford a system to understand the mechanistic link between odor recognition and behavior. Insects provide an attractive model system for studying the peripheral and central events in olfaction because they exhibit sophisticated olfactory-driven behaviors under control of an olfactory sensory system that is significantly simpler anatomically than that of vertebrates (Siddiqi, 1987; Carlson, 1996). olfactory-based associative learning, for example, is robust in insects and results in discernible modifications in the neural representation of odors in the brain (Faber et al., 1998). It may therefore be possible to associate modifications in defined olfactory connections with in vivo paradigms for learning and memory.

[0008] Olfactory recognition in the fruit fly Drosophila is accomplished by sensory hairs distributed over the surface of the third antennal segment and the maxillary palp. olfactory neurons within sensory hairs send projections to one of 43 glomeruli within the antennal lobe of the brain (Stocker, 1994; Laissue et al, 1999). The glomeruli are innervated by dendrites of the projection neurons, the insect equivalent of the mitral cells in the vertebrate olfactory bulb, whose cell bodies surround the glomeruli. These antennal lobe neurons in turn project to the mushroom body and lateral horn of the protocerebrum (reviewed in Stocker, 1994). 2-deoxyglucose mapping in the fruit fly (Rodrigues, 1988) and calcium imaging in the honeybee (Joerges et al., 1997; Faber et al., 1998) demonstrate that different odorants elicit defined patterns of glomerular activity, suggesting that in insects as in vertebrates, a topographic map of odor quality is represented in the antennal lobe. However, in the absence of the genes encoding the receptor molecules, it has not been possible to define a physical basis for this spatial map.

[0009] In this study, we identify a large family of genes that are likely to encode theodorant receptors of *Drosophila melanogaster*. Difference cloning, along with analysis of

Drosophila genomic sequences, has led to the identification of a novel family of putative seven transmembrane domain receptors likely to be encoded by 100 to 200 genes within the Drosophila genome. Each receptor is expressed in a small subset of sensory cells (0.5-1.5%) that is spatially defined within the antenna and maxillary palp. Moreover, different neurons express distinct complements of receptor genes such that individual neurons are functionally distinct. Identification of a large family of putative odorant receptors in insects indicates that, as in other species, the diversity and specificity of odor recognition is accommodated by a large family of receptor genes. The identification of the family of putative odorant receptor genes may afford insight into the logic of olfactory perception in Drosophila.

[0010] Insects provide an attractive system for the study of olfactory sensory perception. We have identified a novel family of seven transmembrane domain proteins, encoded by 100 to 200 genes, that is likely to represent the family of Drosophila odorant receptors. Members of this gene family are expressed in topographically defined subpopulations of olfactory sensory neurons in either the antenna or the maxillary palp. Sensory neurons express different complements of receptor genes, such that individual neurons are functionally distinct. The isolation of candidate odorant receptor genes along with a genetic analysis of olfactory-driven behavior in insects may ultimately afford a system to understand the mechanistic link between odor recognition and behavior.

SUMMARY OF THE INVENTION

[0011] This invention provides an isolated nucleic acid molecule encoding an insect odorant receptor. In an embodiment, the isolated nucleic acid molecule comprise: (a) one of the nucleic acid sequences as set forth in **FIG. 8**, (b) a sequence being degenerated to a sequence of (a) as a result of the genetic code; or (c) a sequence encoding one of the amino acid sequences as set forth in **FIG. 8**.

[0012] This invention provides a nucleic acid molecule of at least 12 nucleotides capable of specifically hybridizing with the sequence of the above-described nucleic acid molecule. This invention provides a vector which comprises the above-described isolated nucleic acid molecule. In another embodiment, the vector is a plasmid.

[0013] This invention also provides a host vector system for the production of a polypeptide having the biological activity of an insect odorant receptor which comprises the above described vector and a suitable host.

[0014] This invention provides a method of producing a polypeptide having the biological activity of an insect odorant receptor which comprising growing the above described host vector system under conditions permitting production of the polypeptide and recovering the polypeptide so produced.

[0015] This invention also provides a purified, insect odorant receptor. This invention further provides a polypeptide encoded by the above-described isolated nucleic acid molecule.

[0016] This invention provides an antibody capable of specifically binding to an insect odorant receptor. This invention also provides an antibody capable of competitively inhibiting the binding of the antibody capable of specifically binding to an insect odorant receptor.

[0017] This invention provides a method for identifying cDNA inserts encoding an insect odorant receptors comprising: (a) generating a cDNA library which contains clones carrying cDNA inserts from antennal or maxillary palp sensory neurons; (b) hybridizing nucleic acid molecules of the clones from the cDNA libraries generated in step (a) with probes prepared from the antenna or maxillary palp neurons and probes from heads lacking antenna or maxillary palp neurons or from virgin female body tissue; (c) selecting clones which hybridized with probes from the antenna or maxillary palp neurons but not from head lacking antenna or maxillary palp neurons or virgin female body tissue; and (d) isolating clones which carry the hybridized inserts, thereby identifying the inserts encoding odorant receptors.

[0018] This invention also provides cDNA inserts identified by the above method.

[0019] This invention further provides a method for identifying DNA inserts encoding an insect odorant receptors comprising: (a) generating DNA libraries which contain clones carrying inserts from a sample which contains at least one antennal or maxillary palp neuron; (b) contacting clones from the cDNA libraries generated in step (a) with nucleic acid molecule capable of specifically hybridizing with the sequence which encodes an insect odorant receptor in appropriate conditions permitting the hybridization of the nucleic acid molecules of the clones and the nucleic acid molecule; (c) selecting clones which hybridized with the nucleic acid molecule; and (d) isolating the clones which carry the hybridized inserts, thereby identifying the inserts encoding the odorant receptors.

[0020] This invention also provides a method to identify DNA inserts encoding an insect odorant receptors comprising:

[0021] (a) generating DNA libraries which contain clones with inserts from a sample which contains at least one antenna or maxillary palp sensory neuron; (b) contacting the clones from the DNA libraries generated in step (a) with appropriate polymerase chain reaction primers capable of specifically binding to nucleic acid molecules encoding odorant receptors in appropriate conditions permitting the amplification of the hybridized inserts by polymerase chain reaction; (c) selecting the amplified inserts; and (d) isolating the amplified inserts, thereby identifying the inserts encoding the odorant receptors.

[0022] This invention also provides a method to isolate DNA molecules encoding insect odorant receptors comprising:(a) contacting a biological sample known to contain nucleic acids with appropriate polymerase chain reaction primers capable of specifically binding to nucleic acid molecules encoding insect odorant receptors in appropriate conditions permitting the amplification of the hybridized molecules by polymerase chain reaction; (b) isolating the amplified molecules, thereby identifying the DNA molecules encoding the insect odorant receptors.

[0023] This invention also provides a method of transforming cells which comprises transfecting a host cell with a suitable vector described above. This invention also provides transformed cells produced by the above method.

[0024] This invention provides a method of identifying a compound capable of specifically bind to an insect odorant receptor which comprises contacting a transfected cells or membrane fractions of the above described transfected cells with an appropriate amount of the compound under conditions permitting binding of the compound to such receptor, detecting the presence of any such compound specifically bound to the receptor, and thereby determining whether the compound specifically binds to the receptor.

[0025] This invention provides a method of identifying a compound capable of specifically binding to an insect odorant receptor which comprises contacting an appropriate amount of the purified insect odorant receptor with an appropriate amount of the compound under conditions permitting binding of the compound to such purified receptor, detecting the presence of any such compound specifically bound to the receptor, and thereby determining whether the compound specifically binds to the receptor.

[0026] This invention also provides a method of identifying a compound capable of activating the activity of an insect odorant receptor which comprises contacting the transfected cells or membrane fractions of the above-described transfected cells with the compound under conditions permitting the activation of a functional odorant receptor response, the activation of the receptor indicating that the compound is capable of activating the activity of a odorant receptor.

[0027] This invention also provides a method of identifying a compound capable of activating the activity of an odorant receptor which comprises contacting a purified insect odorant receptor with the compound under conditions permitting the activation of a functional odorant receptor response, the activation of the receptor indicating that the compound is capable of activating the activity of a odorant receptor. In an embodiment, the purified receptor is embedded in a lipid bilayer.

[0028] This invention also provides a method of identifying a compound capable of inhibiting the activity of a odorant receptor which comprises contacting the transfected cells or membrane fractions of the above-described transfected cells with an appropriate amount of the compound under conditions permitting the inhibition of a functional odorant receptor response, the inhibition of the receptor response indicating that the compound is capable of inhibiting the activity of a odorant receptor.

[0029] This invention provides a method of identifying a compound capable of inhibiting the activity of a odorant receptor which comprises contacting an appropriate amount of the purified insect odorant receptor with an appropriate amount of the compound under conditions permitting the inhibition of a functional odorant receptor response, the inhibition of the receptor response indicating that the compound is capable of activating the activity of a odorant receptor. In an embodiment, the purified receptor is embedded in a lipid bilayer.

[0030] This invention also provides the compound identified by the above-described methods.

[0031] This invention provides a method of controlling pest populations which comprises identifying odorant ligands by the above-described method which are alarm odorant ligands and spraying the desired area with the identified odorant ligands.

[0032] Finally, this invention provides a method of controlling a pest population which comprises identifying odorant ligands by the above-described method which interfere with the interaction between the odorant ligands and the odorant receptors which are associated with fertility.

BRIEF DESCRIPTION OF FIGURES

[0033] **FIG. 1** Identification of Rare Antennal- and Maxillary Palp-Specific Genes

[0034] Candidate antennal/maxillary palp-specific phage were subjected to in vivo excision, digestion of resulting pBLUESCRIPT plasmid DNAs with BamHI/Asp718, and electrophoresis on 1.5% agarose gels. Southern blots were hybridized with ^{32}P-labeled cDNA probes generated from antennal/maxillary palp mRNA (Panel A), head minus antennal/maxillary palp mRNA (Panel B), or virgin female body mRNA (Panel C). The ethidium bromide stained gel is shown in Panel D. Of the thirteen clones displayed in this figure, four appear to be antennal/maxillary palp specific (lanes 5, 7, 9, and 11). However, only two are selectively expressed in subsets of cells in chemosensory organs of the adult fly. DOR104, a putative maxillary palp odorant receptor, is in Lane 9. The clone in Lane 11 (RN106) is homologous to lipoprotein and triglyceride lipases and is expressed in a restricted domain in the antenna (data not shown).

[0035] **FIG. 2** Expression of DOR104 in a Subset of Maxillary Palp Neurons

[0036] (A) A frontal section of an adult maxillary palp was hybridized with a digoxigenin-labeled antisense RNA probe and visualized with anti-digoxigenin conjugated to alkaline phosphatase. Seven cells expressing DOR104 are visible in this 15 μm section, which represents about one third of the diameter of the maxillary palp. Serial sections of multiple maxillary palps were scored for DOR104 expression and on average 20 cells per maxillary palp are positive for this receptor.

[0037] (B) Transgenic flies carrying a DOR104-lacZ reporter transgene were stained with X-GAL in a whole mount preparation. Maxillary palps were dissected from the head and viewed in a flattened cover slipped preparation under Nomarski optics, which allows the visualization of all 20 cells expressing DOR104-lacZ.

[0038] (C) Dendrites and axons of neurons expressing DOR104-lacZ are visible in this horizontal section of a maxillary palp. LacZ expression was visualized with a polyclonal anti-β-galactosidase primary antibody and a CY3-conjugated secondary antibody. Sections were viewed under epifluorescence and photographed on black and white film.

[0039] **FIG. 3** Predicted Amino Acid Sequences of Drosophila odorant Receptor Genes

[0040] Deduced amino acid sequences of 12 DOR genes are aligned using ClustalW (MacVector, Oxford Molecular). Predicted positions of transmembrane regions (I-VII) are indicated by bars above the alignment. Amino acids identities are marked with dark shading and similarities are indicated with light shading. Protein sequences of DOR87, 53, 67, 104, and 64 were derived from cDNA clones. All others were derived from GENSCAN predictions of intron-exon arrangements in genomic DNA, as indicated by the letter "g" after the gene name. We obtained a partial cDNA clone for DOR62 and found it to be 100% identical to the GENSCAN protein in the region of amino acids 245-381. A 40 amino acid extension for DOR 19 was predicted by GENSCAN analysis. This has been replaced with an asterisk in the alignment, and isolation of cDNA clones for this receptor will resolve whether this extension is physically present in the protein.

[0041] **FIG. 4** Receptor Gene Expression in Spatially Restricted Regions of the Antenna Digoxigenin-labeled antisense RNA probes against 8 DOR genes each hybridize to a small number of cells distributed in distinct regions in the antenna. The total number of cells per antenna expressing a given receptor was obtained by counting positive cells in serial sections of multiple antennae. There are approximately 20 positive cells per antenna for DOR67 (A), 53 (B), and 24 (data not shown); 15 positive cells for DOR62 (C) and 87 (D); and 10 positive cells for DOR64 (E). The actual number of cells staining in these sections is a subset of this total number. With the exception of DOR53 and DOR67, which strongly cross-hybridize, the receptor genes likely identify different olfactory neurons, such that the number of cells staining with a mixed probe (F) is equal to the sum of those staining with the individual probes (A-E). The mixture of DOR53, 67, 62, 87 and 64 labels a total of about 60 cells per antenna. A total of 34 cells stain with the mixed probe in this 15 μm section. Expression of the linked genes DOR71, DOR72, and DOR73 is shown in panels (G), (H), and (I), respectively. DOR71 is expressed in approximately 10 cells in the maxillary palp. Five positive cells are seen in the horizontal section in panel (G). We also examined the expression of the other members of this linkage group and found DOR72 in approximately 15 cells (of which 3 label in this section) (H) and DOR73 in 1 to 2 cells per antenna (I).

[0042] **FIG. 5** Odorant Receptors are Restricted to Distinct Populations of Olfactory Neurons

[0043] (A-C) Flies of the C155 eIav-GAL4; UAS-lacZ genotype express cytoplasmic lacZ in all neuronal cells. Panels (A-C) show confocal images of a horizontal maxillary palp section from such a fly incubated with an antisense RNA probe against DOR104 (red) and anti-β-galactosidase antibody (green). DOR104 recognizes five cells in this maxillary palp section (A), all of which also express elav-lacZ (B), as demonstrated by the yellow cells in the merged image in panel©).

[0044] (D, E) DOR64 and DOR87 are expressed in non-overlapping neurons at the tip of the antenna. Antisense RNA probes for DOR64 (digoxigenin-RNA; red) and DOR87 (FITC-RNA; green) were annealed to the same antennal sections and viewed by confocal microscopy. Panel (D) is a digital superimposition of confocal images taken at 0.5 μm intervals through a 10 μm section of the antenna. Cells at different focal planes express both receptors, but no double labeled cells are found.

[0045] (F, G) Two color RNA in situ hybridization with odorant receptors and odorant binding proteins demonstrates that these proteins are expressed in different populations of cells. DORS3 (FITC-RNA; green) labels a few cells internal to the cuticle at the proximal-medial edge, while PBPRP2 (digoxigenin-RNA; red) labels a large number of cells apposed to the cuticle throughout the antenna (F). The more restricted odorant binding protein OS-F (digoxigenin-RNA; red) also stains cells distinct from those expressing DOR67 (FITC-RNA; green) (G).

[0046] **FIG. 6** Receptor Expression is Conserved Between Individuals

[0047] Frontal sections of antennae from six different individuals were hybridized with digoxigenin-labeled antisense RNA probes against DOR53 (A-C) or DOR87 (D-F). DOR53 labels approximately 20 cells on the proximal-medial edge of the antenna, of which approximately 5 are shown labeling in these sections. DOR87 is expressed in about the same number of cells at the distal tip. Both the position and number of staining cells is conserved between different individuals and is not sexually dimorphic.

[0048] **FIG. 7** Drosophila Odorant Receptors are Highly Divergent

[0049] Oregon R genomic DNA isolated from whole flies was digested with BamHI (B), EcoRI (E), or HindIII (H), electrophoresed on 0.8% agarose gels, and blotted to nitrocellulose membranes. Blots were annealed with ^{32}P-labeled probes derived from DOR53 cDNA (A), DOR67 cDNA (B), or DNA fragments generated by RT-PCR from antennal mRNA for DOR 24 (C), DOR62 (D), and DOR72 (E). Strong crosshybridization of DOR53 and DOR67 is seen at both high and low stringency (A, B), while DOR24, 62, and 72 reveal only a single hybridizing band in each lane at both low stringency (C-E) and high stringency (data not shown).

[0050] **FIG. 8** DOR 62, 104, 87, 53, 67, 64, 71g, 72g, 73g, 46, 19g, and 24g

[0051] Both nucleic acid sequence of each DOR and its encoded amino acid sequence are described.

[0052] **FIG. 9** Analysis of axonal projections of olfactory receptor neurons expressing a given Drosophila odorant receptor. Result: all neurons expressing a given receptor send their axons to a single glomerulus, or discrete synaptic structure, in the olfactory processing center of the fly brain. This result is identical to that obtained with mouse odorant receptors: each glomerulus is dedicated to receiving axonal input from neurons expressing a given odorant receptor. Therefore, this result strengthens the argument that these genes indeed function as odorant receptors in Drosophila.

[0053] **FIG. 10** ClustalW alignments of two subfamilies of the Drosophila odorant receptors, the DOR53 (A-1 and A-2) and DOR64 (B) families. This figure highlights sequence similarities between DOR genes, that are diagnostic hallmarks of the proteins. Residues that are identical in different DOR genes are highlighted in black, while residues that are similar are highlighted in gray.

DETAILED DESCRIPTION OF THE INVENTION

[0054] In order to facilitate an understanding of the Experimental Procedures section which follow, certain frequently occurring methods and/or terms are described in Sambrook, et al. (1989).

[0055] Throughout this application, the following standard abbreviations are used throughout the specification to indicate specific nucleotides:

[0056] C=cytosine A=adenosine

[0057] T=thymidine G=guanosine

[0058] This invention provides an isolated nucleic acid molecule encoding an insect odorant receptor. The nucleic acid includes but is not limited to DNA, cDNA, genomic DNA, synthetic DNA or RNA. In an embodiment, the nucleic acid molecule encodes a Drosophila odorant receptor.

[0059] In a further embodiment, the isolated nucleic acid molecule comprise: (a) one of the nucleic acid sequences as set forth in **FIG. 8**, (b) a sequence being degenerated to a sequence of (a) as a result of the genetic code; or (c) a sequence encoding one of the amino acid sequences as set forth in **FIG. 8**.

[0060] The nucleic acid molecules encoding a insect receptor includes molecules coding for polypeptide analogs, fragments or derivatives of antigenic polypeptides which differ from naturally-occurring forms in terms of the identity or location of one or more amino acid residues (deletion analogs containing less than all of the residues specified for the protein, substitution analogs wherein one or more residues specified are replaced by other residues and addition analogs where in one or more amino acid residues is added to a terminal or medial portion of the polypeptides) and which share some or all properties of naturally-occurring forms. These molecules include but not limited to: the incorporation of codons "preferred" for expression by selected non-mammalian hosts; the provision of sites for cleavage by restriction endonuclease enzymes; and the provision of additional initial, terminal or intermediate sequences that facilitate construction of readily expressed vectors. Accordingly, these changes may result in a modified insect odorant receptor. It is the intent of this invention to include nucleic acid molecules which encodes modified insect odorant receptor. Also, to facilitate the expression of receptor in different host cells, it may be necessary to modify the molecule such that the expressed receptors may reach the surface of the host cells. The modified insect odorant receptor should have biological activities similar to the unmodified insect odorant receptor. The molecules may also be modified to increase the biological activity of the expressed receptor.

[0061] This invention provides a nucleic acid molecule of at least 12 nucleotides capable of specifically hybridizing with the sequence of the above-described nucleic acid molecule. In an embodiment, the nucleic acid molecule hybridizes with a unique sequence within the sequence of the above-described nucleic acid molecule. This nucleic acid molecule may be DNA, cDNA, genomic DNA, synthetic DNA or RNA.

[0062] This invention provides a vector which comprises the above-described isolated nucleic acid molecule. In another embodiment, the vector is a plasmid.

[0063] In an embodiment, the above described isolated nucleic acid molecule is operatively linked to a regulatory element.

[0064] Regulatory elements required for expression include promoter sequences to bind RNA polymerase and transcription initiation sequences for ribosome binding. For example, a bacterial expression vector includes a promoter such as the lac promoter and for transcription initiation the Shine-Dalgarno sequence and the start codon AUG. Similarly, a eukaryotic expression vector includes a heterologous or homologous promoter for RNA polymerase II, a downstream polyadenylation signal, the start codon AUG, and a termination codon for detachment of the ribosome. Such vectors may be obtained commercially or assembled from the sequences described by methods well-known in the art, for example the methods described above for constructing vectors in general.

[0065] This invention also provides a host vector system for the production of a polypeptide having the biological activity of an insect odorant receptor which comprises the above described vector and a suitable host.

[0066] This invention also provides a host vector system, wherein the suitable host is a bacterial cell, yeast cell, insect cell, or animal cell. The host cell of the above expression system may be selected from the group consisting of the cells where the protein of interest is normally expressed, or foreign cells such as bacterial cells (such as *E. coli*), yeast cells, fungal cells, insect cells, nematode cells, plant or animal cells, where the protein of interest is not normally expressed. Suitable animal cells include, but are not limited to Vero cells, HeLa cells, Cos cells, CV1 cells and various primary mammalian cells.

[0067] This invention provides a method of producing a polypeptide having the biological activity of an insect odorant receptor which comprising growing the above described host vector system under conditions permitting production of the polypeptide and recovering the polypeptide so produced.

[0068] This invention also provides a purified, insect odorant receptor. This invention further provides a polypeptide encoded by the above-described isolated nucleic acid molecule.

[0069] This invention provides an antibody capable of specifically binding to an insect odorant receptor. This invention also provides an antibody capable of competitively inhibiting the binding of the antibody capable of specifically binding to an insect odorant receptor. In an embodiment, the antibody is monoclonal. In another embodiment, the antibody is polyclonal.

[0070] Monoclonal antibody directed to an insect odorant receptor may comprise, for example, a monoclonal antibody directed to an epitope of an insect odorant receptor present on the surface of a cell. Amino acid sequences may be analyzed by methods well known to those skilled in the art to determine whether they produce hydrophobic or hydrophilic regions in the proteins which they build. In the case of cell membrane proteins, hydrophobic regions are well known to form the part of the protein that is inserted into the lipid bilayer which forms the cell membrane, while hydrophilic regions are located on the cell surface, in an aqueous environment.

[0071] Antibodies directed to an insect odorant receptor may be serum-derived or monoclonal and are prepared using methods well known in the art. For example, monoclonal antibodies are prepared using hybridoma technology by fusing antibody producing B cells from immunized animals with myeloma cells and selecting the resulting hybridoma cell line producing the desired antibody. Cells such as NIH3T3 cells or 293 cells which express the receptor may be used as immunogens to raise such an antibody. Alternatively, synthetic peptides may be prepared using commercially available machines.

[0072] As a still further alternative, DNA, such as a cDNA or a fragment thereof, encoding the receptor or a portion of the receptor may be cloned and expressed. The expressed polypeptide recovered and used as an immunogen.

[0073] The resulting antibodies are useful to detect the presence of insect odorant receptors or to inhibit the function of the receptor in living animals, in humans, or in biological tissues or fluids isolated from animals or humans.

[0074] This antibodies may also be useful for identifying or isolating other insect odorant receptors. For example, antibodies against the Drosophila odorant receptor may be used to screen an cockroach expression library for a cockroach odorant receptor. Such antibodies may be monoclonal or monospecific polyclonal antibody against a selected insect odorant receptor. Different insect expression libraries are readily available and may be made using technologies well-known in the art.

[0075] One means of isolating a nucleic acid molecule which encodes an insect odorant receptor is to probe a libraries with a natural or artificially designed probes, using methods well known in the art. The probes may be DNA or RNA. The library may be cDNA or genomic DNA.

[0076] This invention provides a method for identifying cDNA inserts encoding an insect odorant receptors comprising: (a) generating a cDNA library which contains clones carrying cDNA inserts from antennal or maxillary palp sensory neurons; (b) hybridizing nucleic acid molecules of the clones from the cDNA libraries generated in step (a) with probes prepared from the antenna or maxillary palp neurons and probes from heads lacking antenna or maxillary palp neurons or from virgin female body tissue; (c) selecting clones which hybridized with probes from the antenna or maxillary palp neurons but not from head lacking antenna or maxillary palp neurons or virgin female body tissue; and (d) isolating clones which carry the hybridized inserts, thereby identifying the inserts encoding odorant receptors.

[0077] In an embodiment of the above method, after step (c), it further comprises: (a) amplifying the inserts from the selected clones by polymerase chain reaction; (b) hybridizing the amplified inserts with probes from the antennal or maxillary palp neurons; and (c) isolating the clones which carry the hybridized inserts, thereby identifying the inserts encoding the odorant receptors.

[0078] In an embodiment, the probes are cDNA probes.

[0079] The appropriate polymerase chain reaction primers may be chosen from the conserved regions of the known insect odorant receptor sequences. Alternatively, the primers may be chosen from the regions which are the active sites for the binding of ligands.

[0080] This invention also provides cDNA inserts identified by the above method.

[0081] This invention further provides a method for identifying DNA inserts encoding an insect odorant receptors comprising: (a) generating DNA libraries which contain clones carrying inserts from a sample which contains at least one antennal or maxillary palp neuron; (b) contacting clones from the cDNA libraries generated in step (a) with nucleic acid molecule capable of specifically hybridizing with the sequence which encodes an insect odorant receptor in appropriate conditions permitting the hybridization of the nucleic acid molecules of the clones and the nucleic acid molecule; (c) selecting clones which hybridized with the nucleic acid molecule; and (d) isolating the clones which carry the hybridized inserts, thereby identifying the inserts encoding the odorant receptors.

[0082] This invention also provides a method to identify DNA inserts encoding an insect odorant receptors comprising: (a) generating DNA libraries which contain clones with inserts from a sample which contains at least one antenna or maxillary palp sensory neuron; (b) contacting the clones from the DNA libraries generated in step (a) with appropriate polymerase chain reaction primers capable of specifically binding to nucleic acid molecules encoding odorant receptors in appropriate conditions permitting the amplification of the hybridized inserts by polymerase chain reaction; (c) selecting the amplified inserts; and (d) isolating the amplified inserts, thereby identifying the inserts encoding the odorant receptors.

[0083] This invention also provides a method to isolate DNA molecules encoding insect odorant receptors comprising:(a) contacting a biological sample known to contain nucleic acids with appropriate polymerase chain reaction primers capable of specifically binding to nucleic acid molecules encoding insect odorant receptors in appropriate conditions permitting the amplification of the hybridized molecules by polymerase chain reaction; (b) isolating the amplified molecules, thereby identifying the DNA molecules encoding the insect odorant receptors.

[0084] This invention also provides a method of transforming cells which comprises transfecting a host cell with a suitable vector described above.

[0085] This invention also provides transformed cells produced by the above method. In an embodiment, the host cells are not usually expressing odorant receptors. In another embodiment, the host cells are expressing odorant receptors.

[0086] This invention provides a method of identifying a compound capable of specifically binding to an insect odorant receptor which comprises contacting a transfected cells or membrane fractions of the above described transfected cells with an appropriate amount of the compound under conditions permitting binding of the compound to such receptor, detecting the presence of any such compound specifically bound to the receptor, and thereby determining whether the compound specifically binds to the receptor.

[0087] This invention provides a method of identifying a compound capable of specifically bind to an insect odorant receptor which comprises contacting an appropriate amount of the purified insect odorant receptor with an-appropriate amount of the compound under conditions permitting binding of the compound to such purified receptor, detecting the presence of any such compound specifically bound to the receptor, and thereby determining whether the compound specifically binds to the receptor. In an embodiment, the purified receptor is embedded in a lipid bilayer. The purified receptor may be embedded in the liposomes with proper orientation to carry out normal functions. Liposome technology is well-known in the art.

[0088] This invention also provides a method of identifying a compound capable of activating the activity of an insect odorant receptor which comprises contacting the transfected cells or membrane fractions of the above-described transfected cells with the compound under conditions permitting the activation of a functional odorant receptor response, the activation of the receptor indicating that the compound is capable of activating the activity of a odorant receptor.

[0089] This invention also provides a method of identifying a compound capable of activating the activity of an odorant receptor which comprises contacting a purified insect odorant receptor with the compound under conditions permitting the activation of a functional odorant receptor response, the activation of the receptor indicating that the compound is capable of activating the activity of a odorant receptor. In an embodiment, the purified receptor is embedded in a lipid bilayer.

[0090] This invention also provides a method of identifying a compound capable of inhibiting the activity of a odorant receptor which comprises contacting the transfected cells or membrane fractions of the above-described transfected cells with an appropriate amount of the compound under conditions permitting the inhibition of a functional odorant receptor response, the inhibition of the receptor response indicating that the compound is capable of inhibiting the activity of a odorant receptor.

[0091] This invention provides a method of identifying a compound capable of inhibiting the activity of a odorant receptor which comprises contacting an appropriate amount of the purified insect odorant receptor with an appropriated amount of the compound under conditions permitting the inhibition of a functional odorant receptor response, the inhibition of the receptor response indicating that the compound is capable of activating the activity of a odorant receptor. In an embodiment, the purified receptor is embedded in a lipid bilayer.

[0092] In a separate embodiment of the above method, the compound is not previously known. This invention also provides the compound identified by the above-described methods.

[0093] This invention provides a method of controlling pest populations which comprises identifying odorant ligands by the above-described method which are alarm odorant ligands and spraying the desired area with the identified odorant ligands.

[0094] Finally, this invention provides a method of controlling a pest population which comprises identifying odorant ligands by the above-described method which interfere with the interaction between the odorant ligands and the odorant receptors which are associated with fertility.

[0095] This invention will be better understood from the Experimental Procedures which follow. However, one skilled in the art will readily appreciate that the specific methods and results discussed are merely illustrative of the invention as described more fully in the claims which follow thereafter.

[0096] Experimental Procedures

[0097] Experimental Animals

[0098] Oregon R flies (*Drosophila melanogaster*) were raised on standard cornmeal-agar-molasses medium at 25° C. Transgenic constructs were injected into yw embryos. CISS elav-GAL4 flies were obtained from Corey Goodman (Lin and Goodman, 1994) and Gary Struhl provided the UAS- (cytoplasmic) lacZ stock.

[0099] Preparation and Differential Screening of a Drosophila Antennal/Maxillary Palp cDNA Library

[0100] Drosophila antennae and maxillary palps were obtained by manually decapitating and freezing 5000 adult flies and shaking antennae and maxillary palps through a fine metal sieve. mRNA was prepared using a polyA+ RNA Purification Kit (Stratagene). An antennal/maxillary palp cDNA library was made from 0.5 μg mRNA using the LambdaZAPIIXR kit from Stratagene.

[0101] Briefly, phage were plated at low density (500-1000 pfu/150 mm plate) and UV-crosslinked after lifting in triplicate to Hybond-N+ (Amersham). Complex probes were generated by random primed labeling (PrimeItII, Stratagene) of reverse transcribed mRNA (RT-PCR kit, Stratagene) from virgin adult female body mRNA and duplicate lifts hybridized at high stringency for 36 hours (65° C. in 0.5M Sodium Phosphate buffer [pH7.3] containing 1% bovine serum albumin, 4% SDS, and 0.5 mg/ml herring sperm DNA). We prescreened the third lift with a mix of all previously cloned OBPs/PBPs (McKenna et al., 1994; Pikielny et al., 1994; Kim et al., 1998) remove a source of abundant but undesired olfactory-specific clones. Approximately 5000 individual OBP/PBP and virgin female body negative phage clones were isolated, their inserts amplified by PCR with T3 and T7 primers, and approximately 3 μg of DNA were electrophoresed on 1.5% agarose gels. Gels were blotted in duplicate to Hybond-N+ (Amersham), filters were UV-crosslinked, and the resulting Southern blots were subjected to reverse Northern analysis using complex probes generated from virgin female body mRNA. Approximately 500 clones not hybridizing with virgin female body probes were identified and consolidated onto secondary Southern blots in triplicate. These blots were probed with complex probes derived from antennal/maxillary palp, head-minus-antenna/maxillary palp, and virgin female body mRNA. A total of 210 clones negative with head-minus-antenna/maxillary palp and virgin female body probes and strongly positive, weakly positive, or negative with antennal/maxillary palp probes were further analyzed by sequencing and in situ hybridization.

[0102] Analysis of Drosophila Genome Project Sequences for Transmembrane Proteins

[0103] All Drosophila genomic sequences were batch downloaded in April 1998 from the Berkeley Drosophila Genome Project (Berkeley Drosophila Genome Project, unpublished). Genomic P1 sequences were first analyzed with the GENSCAN program (Burge and Karlin, 1997; http://CcR-081.mit.edu/GENSCAN.html), which predicts intron-exon structures and generates hypothetical coding sequences (CDS) and open reading frames. GENSCAN predicted proteins shorter than 50 amino acids were discarded. The remaining open reading frames were used to search for putative transmembrane regions greater than 15 amino acids with two programs that were obtained from the authors and used in stand-alone mode locally (see Persson and Argos, 1994; Cserzo et al., 1997). The Dense Surface Alignment (DAS) program is available at http://www.biokemi.su.se/~ server/DAS/ or from M. Cserzo (miklos@pugh.bip.bham.ac.uk). TMAP is available at ftp://ftp.ebi.ac.uk/pub/software/unix/, or by contacting the author, Bengt Persson (bpn@mbb.ki.se). Scripts were written to apply the DAS and TMAP programs repeatedly to genome scale sequence sets. Genes showing significant sequence similarity to the NCBI non-redundant protein database using BLAST analysis (Altschul et al., 1990; Altschul et al., 1997) were eliminated. All scripts required for these computations were written in standard ANSI C and run on a SUN Enterprise 3000.

[0104] Of 229 novel Drosophila proteins with three or more predicted transmembrane spanning regions, 35 showed no clear sequence similarity to any known protein and were selected for further analysis by in situ hybridization. Probes for in situ hybridization were generated by RT-PCR using antennal/maxillary palp mRNA as a template.

[0105] Map positions of DOR Genes

[0106] The chromosome position of DOR104 was determined by in situ hybridization of a biotin-labeled probe to salivary gland polytene chromosome squashes as described (Amrein et al., 1988).

[0107] Chromosomal positions of all other DOR genes were eased on chromosome assignments of the P1 clones to which they map, as determined by the Berkeley Drosophila Genome Project (personal communication; http://www.fruitfly.org; see also Hartl et al., 1994; Kimmerly et al., 1996). DOR62 maps to a cosmid sequenced by the European Drosophila Genome Project (unpublished; http://edgp.ebi.ac.uk/; Siden-Kiamos et al., 1990).

RECEPTOR	MAP POSITION	P1 CLONE ACCESSION NUMBER
DOR62	(X) 2F	62D9 (EDGP cosmid)
DOR67	(2L) 22A3	DS00676
DOR53	(2L) 22A2-3	DS05342
DOR64	(2L) 23A1-2	DS06400
DOR72	(2L) 33B1-2	DS07071
DOR72	(2L) 33B1-2	DS07071
DOR73	(2L) 33B1-2	DS07071
DOR87	(2R) 43B1-2	DS08779
DOR19	(2R) 46F5-6	DS01913
DOR24	(2R) 47D6-E2	DS00724

-continued

RECEPTOR	MAP POSITION	P1 CLONE ACCESSION NUMBER
DOR46	(2R) 59D5-7	DS07462
DOR104	(3L) 85B	not applicable

[0108] The Isolation of DOR cDNA Clones and Southern Blotting

[0109] We screened 3×10^{6} clones of the antennal/maxillary palp library described above with PCR probes for the genes DOR87, DOR53, DOR67, DOR64, and DOR62. cDNAs were present at a frequency ranging from 1:200,000 (DOR67) to 1:1,000,000 (DOR62) in the library and their sequences were remarkably similar to the hypothetical CDS predicted by the GENSCAN program. The frequency of these genes is similar to that of DOR104, which is present at 1:125,000 in the antennal/maxillary palp library. All sequencing was with ABI cycle sequencing kits and reactions were run on an ABI 310 or 377 sequencing system.

[0110] Five μg of Oregon R genomic DNA isolated from whole flies were digested with BamHI, EcoRI, or HindIII, electrophoresed on 0.8% agarose gels, and blotted to Nitropure nitrocellulose membranes (Micron Separations Inc.). Blots were baked and annealed with ^{32}P-labeled probes derived from cDNA probes of DORS3 and DOR67, or PCR fragments from DOR24, DOR62, and DOR72. Hybridization was at 42° C. for 36 hours in 5× SSCP, 10× Denhardts, 500 μg/ml herring sperm DNA, and either 50% (high stringency) or 25% (low stringency) formamide (Sambrook et al., 1989). Blots were washed for 1 hour in 0.2× SSC, 0.5% SDS at 65° C. (high stringency) or 1× SSC, 0.5% SDS at 42° C. (low stringency).

[0111] In situ Hybridization

[0112] RNA in situ hybridization was carried out essentially as described (Schaeren-Wiemers and Gerfin-Moser, 1993). This protocol was modified to include detergents in most steps to increase sensitivity and reduce background. The hybridization buffer contained 50% formamide, 5× SSC, 5× Denhardts, 250 μg/ml yeast tRNA, 500 μg/ml herring sperm DNA, 50 μg/ml Heparin, 2.5 mM EDTA, 0.1% Tween-20, 0.25% CHAPS. All antibody steps were in the presence of 0.1% Triton X-100, and the reaction was developed in buffer containing 0.1% Tween-20. Slides were mounted in Glycergel (DAKO) and viewed with Nomarski optics.

[0113] Fluorescent in situ hybridization was carried out as above with either digoxigenin or FITC labeled RNA probes. The digoxigenin probe was visualized with sheep anti-digoxigenin (Boehringer) followed by donkey anti-sheep CY3 (Jackson). FITC probes were visualized with mouse anti-FITC (Boehringer) and goat anti-mouse Alexa 488 (Molecular Probes) following preincubation with normal goat serum. Sections were mounted in vectashield reagent (Vector Labs) and viewed on a Biorad 1024 Confocal Microscope.

[0114] For double labeling with a neural marker, animals of the genotype C155 elav-Gal4; UAS-lacZ were sectioned and first hybridized with a digoxigenin labeled antisense DOR104 RNA probe and developed as described above. Neuron-specific expression of lacZ driven by the elav-Gal4 enhancer trap was visualized with a polyclonal rabbit anti-β-galactosidase antibody (Organon-Technika/Cappel), visualized by a goat anti-rabbit Alexa488 conjugated secondary antibody (Molecular Probes) following preincubation with normal goat serum.

[0115] The proportion of neurons in the third antennal segment was calculated by comparing the number of nuclei staining with the 44C11 ELAV monoclonal (kindly provided by Lily Jan) and those staining with TOTO-3 (Molecular Probes), a nucleic acid counterstain, in several confocal sections of multiple antennae. On average, 36% of the nuclei in the antenna were ELAV positive.

[0116] DOR104-lacZ Transaene Construction and Histochemical Staining

[0117] A genomic clone containing the DOR104 coding region and several kb of upstream sequence was isolated from a genomic library prepared from flies isogenic for the third chromosome (a gift of Kevin Moses and Gerry Rubin). Approximately 3 kb of DNA immediately upstream of the putative translation start site of DOR104 were isolated by PCR and subcloned into the pCasperAUGβGal vector (Thummel et al., 1988). β-galactosidase activity staining was carried out with whole mount head preparations essentially as described in Wang et al. (1998). Frozen sections of DOR104-lacZ maxillary palps were incubated with a polyclonal rabbit anti-β-galactosidase antibody and as described above.

[0118] Experimental Results

[0119] Cloning Candidate Odorant Receptors

[0120] In initial experiments, we isolated a cDNA encoding a putative odorant receptor by a difference cloning strategy designed to detect cDNA copies of mRNA present at extremely low frequencies in an mRNA population. In the antenna and maxillary palp, about 30% of the cells are olfactory neurons. If each neuron expressed only one of a possible 100 different odorant receptor genes at a level of 0.1% of the mRNA in a sensory neuron, then a given receptor mRNA would be encountered at a frequency of one in 300,000 in antennal mRNA. If 100 different receptor genes were expressed, then the entire family of receptor genes would be represented at a frequency of one in 3,000 mRNAs. We therefore introduced experimental modifications into standard difference cloning to allow for the identification of extremely rare mRNAs whose expression is restricted to either the antenna or the maxillary palp.

[0121] Briefly, 5000 insets from an antennal/maxillary palp cDNA library were prescreened (see Experimental Procedures) and then subjected to Southern blot hybridization with cDNA probes from antennal/maxillary palp, head minus antenna/maxillary palp, or virgin female body mRNA (see **FIG. 1**). This Southern blot hybridization (or reverse Northern) to candidate cDNAs allows for the detection of sequences present at a frequency of 1 in 100,000 in the probe, a sensitivity about one hundred-fold greater than that of plaque screening (see Experimental Procedures). This procedure led to the identification of multiple antennal/maxillary palp-specific cDNAs that were analyzed by DNA sequencing and in situ hybridization. One cDNA, DOR104 (for Drosophila Odorant Receptor) (**FIG. 1**, Lane 9), encodes a putative seven-transmembrane domain protein with no obvious sequence similarity to known serpentine receptors (**FIG. 3**). In situ hybridization revealed that this cDNA anneals to about 15% of the 120 sensory neurons within the maxillary palp but does not anneal with neurons in either the brain or antenna. Seven cells expressing DOR104 are shown in the frontal maxillary palp section in **FIG. 2A**.

[0122] These observations suggested that DOR104 might be one member of a larger family of odorant receptor genes within the Drosophila genome. However, we were unable to identify additional genes homologous to DOR104 by low stringency hybridization to genomic DNA and cDNA libraries or upon analysis of linked genes in a genomic walk. We therefore analyzed the Drosophila genome database for families of multiple transmembrane domain proteins that share sequence similarity with DOR104. Sequences representing about 10% of the Drosophila genome were downloaded (Berkeley Drosophila Genome Project) and subjected to GENSCAN analysis (Burge and Karlin, 1997) to predict the intron-exon structure of all sequences within the database. Open reading frames greater than 50 amino acids were searched for proteins with three or more predicted transmembrane-spanning regions using the dense alignment surface (DAS) and TMAP algorithms (Persson and Argos, 1994; Cserzo et al., 1997; also see Experimental Procedures). Of 229 candidate genes identified in this manner, 11 encoded proteins that define a novel divergent family of presumed seven transmembrane domain proteins with sequence similarity to the DOR104 sequence. This family of candidate odorant receptors does not share any conserved sequence motifs with previously identified families of seven transmembrane domain receptors. cDNA clones containing the coding regions for 5 of the 11 genes identified by GENSCAN analysis have been isolated from an antennal/maxillary palp cDNA library and their sequences are provided in **FIG. 3**. The remaining 6 protein sequences derive from GENSCAN predictions for intron-exon arrangement. Their organization conforms well to the actual structure determined from the cDNA sequences of other members of the gene family (**FIG. 3**).

[0123] The receptors consist of a short extracellular N-terminal domain (usually less than 50 amino acids) and seven presumed membrane-spanning domains. Analysis of presumed transmembrane domains (Kyte and Doolittle, 1982; Persson and Argos, 1994; Cserzo et al., 1997) reveals multiple hydrophobic segments, but it is not possible from this analysis to unequivocally determine either the number or placement of the membrane spanning domains. At present, our assignment of transmembrane domains is therefore tentative.

[0124] The individual family members are divergent and most exhibit from 17-26% amino acid identity. Two linked clusters of receptor genes constitute small subfamilies of genes with significantly greater sequence conservation. Two linked genes, DOR53 and DOR67, exhibit 76% amino acid identity, whereas the three linked genes, DOR71, 72 and 73, reveal 30-55% identity (**FIG. 3**; see below). Despite the divergence, each of the genes shares short, common motifs in fixed positions within the putative seven transmembrane domain structure that define these sequences as highly divergent members of a novel family of putative receptor molecules.

[0125] Expression of the DOR Gene Family in Olfactory Neurons

[0126] If this gene family encodes putative odorant receptors in the fly, we might expect that other members of the family in addition to DOR104 would also be expressed in olfactory sensory neurons. We therefore performed in situ hybridization to examine the pattern of receptor expression of each of the 11 additional members of the gene family in adult and developing organisms. In Drosophila, olfactory sensory neurons are restricted to the maxillary palp and third antennal segment. The third antennal segment is covered with approximately 500 fine sensory bristles or sensilla (Stocker, 1994), each containing from one to four neurons (Venkatesh and Singh, 1984). The maxillary palp is covered with approximately 60 sensilla, each of which is innervated by two or three neurons (Singh and Nayak, 1985). Thus, the third antennal segment and maxillary palp contain about 1500 and 120 sensory neurons, respectively.

[0127] RNA in situ hybridization experiments were performed with digoxigenin-labeled RNA antisense probes to each of the 11 new members of the gene family under conditions of high stringency. One linked pair of homologous genes, DOR53 and DOR67, crosshybridizes, whereas the remaining 10 genes exhibit no crosshybridization under these conditions (see below). Eight of the 11 genes hybridize to a small subpopulation (0.5-1.5%) of the 1500 olfactory sensory neurons in the third antennal segment (**FIG. 4**). One gene, DOR71, is expressed in about 10% of the sensory neurons in the maxillary palp but not in the antenna (**FIG. 4G**). We have not detected expression of DOR46 or DOR19 in the antenna or the maxillary palp. Expression of this gene family is only observed in cells within the antenna and maxillary palp. No hybridization was observed in neurons of the brain, nor was hybridization observed in any sections elsewhere in the adult fly or in any tissue at any stage during embryonic development. However, we do find hybridization to a small number of cells in the developing antennae in the late pupal stage (data not shown). We have not yet determined whether this family of receptors is expressed in the larval olfactory apparatus.

[0128] Only about one third of the cells in the third antennal segment and the maxillary palp are neurons (data not shown), which are interspersed with non-neuronal sensillar support cells and glia. We have performed two experiments to demonstrate that the family of seven transmembrane domain receptor genes is expressed in sensory neurons rather than support cells or glia within the antenna and maxillary palp. First, we developed two-color fluorescent antibody detection schemes to co-localize receptor expression in cells that express the neuron-specific RNA binding protein, ELAV (Robinow and White, 1988). An enhancer trap line carrying an insertion of GAL4 at the elav locus expresses high levels of lacZ in neurons when crossed to a transgenic UAS-lacZ responder line (Lin and Goodman, 1994). Fluorescent antibody detection of lacZ identifies the sensory neurons in a horizontal section of the maxillary palp (**FIG. 5B**). Hybridization with the receptor probe DOR104 reveals expression in 5 of the 12 lacZ positive cells in a horizontal section of the maxillary palp (**FIG. 5A**). All cells that express DOR104 are also positive for lacZ (**FIG. 5C**), indicating that this receptor is expressed only in neurons.

[0129] In a second experiment we have demonstrated that the receptor genes are not expressed in non-neuronal cells. The support cells of the antenna express different members of a family of odorant binding proteins (McKenna et al., 1994; Pikielny et al., 1994; Kim et al., 1998). These genes encode abundant low molecular weight proteins thought to transport odorants through the sensillar lymph (reviewed in Pelosi, 1994). Two-color in situ experiments with a probe for the odorant binding protein, PBPRP2 (Pikielny et al., 1994), reveal hybridization to a large number of cells broadly distributed throughout the antenna (**FIG. 5F**). In the same section, however, the probe DOR53 anneals to a non-overlapping subpopulation of neurons restricted to the medial-proximal domain of the antenna. In a similar experiment, in situ hybridization with the odorant binding protein, OS-F (McKenna et al., 1994), identifies a spatially restricted subpopulation of support cells in the antenna, whereas the DOR67 probe identifies a distinct subpopulation of neurons in a medial-proximal domain (**FIG. 5G**). Thus, the putative odorant receptor genes are expressed in a subpopulation of sensory neurons distinct from the support cells that express the odorant binding proteins. Taken together, these data demonstrate that 10 of the 12 family members we have identified are expressed in small subpopulations of olfactory sensory neurons in the antenna and maxillary palp.

[0130] Spatially Defined Patterns of Receptor Expression

[0131] The in situ hybridization experiments reveal that each receptor is expressed in a spatially restricted subpopulation of neurons in the antenna or maxillary palp (**FIG. 4**). The total number of cells expressing each receptor per antenna was obtained by counting the positive cells in serial sections of antennae from multiple flies. These numbers are presented in the legend of **FIG. 4**. DOR67 and 53, for example, anneal to about 20 neurons on the medial proximal edge of the antenna (**FIGS. 4A and B**), whereas DOR62 and 87 anneal to subpopulations of 20 cells at the distal edge of the antenna (FIGS. 4C-D). Approximately 10 cells in the distal domain express DOR64 (**FIG. 4E**). Each of the three linked genes DOR71, 72, and 73 is expressed in different neurons. DOR72 is expressed in approximately 15 antennal cells (**FIG. 4H**), while DOR73 is expressed in 1 to 2 cells at the distal edge of the antenna (**FIG. 4I**). In contrast, DOR71 is expressed in approximately 10 maxillary palp neurons but is not detected in the antenna (**FIG. 4G**). The three sensillar types are represented in a coarse topographic map across the third antennal segment. The proximal-medial region, for example, contains largely basiconic sensilla. Receptors expressed in this region (DOR53 and 67) are therefore likely to be restricted to the large basiconic sensilla. More distal regions contain a mixture of all three sensilla types and it is therefore not possible from these data to assign specific receptors to specific sensillar types.

[0132] The spatial pattern of neurons expressing a given receptor is conserved between individuals. In situ hybridization with two receptor probes to three individual flies reveals that both the frequency and spatial distributions of the hybridizing neurons is conserved in different individuals (**FIG. 6**). At present, we cannot determine the precision of this topographic map and can only argue that given receptors are expressed in localized domains.

[0133] In preliminary experiments, we have demonstrated that the spatial pattern of expression of one receptor, DOR104, can be recapitulated in transgenic flies with a promoter fragment flanking the DOR104 gene. The fusion of the presumed DOR104 promoter (consisting of 3 kb of 5' DNA immediately adjacent to the coding region) to the lacZ reporter gene has allowed us to visualize a subpopulation of neurons expressing DOR104 within the maxillary palp. Whole mount preparations of the heads of transgenic flies reveal a small subpopulation of sensory neurons within the maxillary palp whose cell bodies exhibit blue color after staining with X-gal (**FIG. 2B**). The number of positive cells, approximately 20 per maxillary palp, corresponds well with that seen for DOR104 RNA expression. Immunofluorescent staining of sections with antibodies directed against β-galactosidase more clearly reveals the dendrites and axons of these bipolar neurons in the maxillary palp (**FIG. 2C**). Levels of lacZ expression in these transgenic lines are low and further amplification will be necessary to allow us to trace the axons to glomeruli in the antennal lobe. Nonetheless, the data suggest that the information governing the spatial pattern of DOR104 expression in a restricted subpopulation of maxillary palp neurons resides within 3 kb of DNA 5' to the DOR104 gene.

[**0134**] Individual Neurons Express Different Complements of Receptors

[**0135**] An understanding of the logic of olfactory discrimination in Drosophila will require a determination of the diversity and specificity of receptor expression in individual neurons. In the vertebrate olfactory epithelium, a given neuron is likely to express only one receptor from the family of 1,000 genes (Ngai et al., 1993; Ressler et al., 1993; Vassar et al., 1993; Chess et al., 1994; Dulac and Axel, unpublished). In the nematode *C. elegans*, however, individual chemosensory neurons are thought to express multiple receptor genes (Troemel et al., 1995). Our observations with the putative Drosophila odorant receptors indicate that a given receptor probe anneals with 0.5-1.5% of antennal neurons, suggesting that each cell expresses only a subset of receptor genes. If we demonstrate that each of the different receptor probes hybridizes with distinct, nonoverlapping subpopulations of neurons, this would provide evidence that neurons differ with respect to the receptors they express.

[**0136**] In situ hybridization was therefore performed with either a mix of five receptor probes (**FIG. 4F**) or individually with each of the five probes (FIGS. 4A-E). We observe that the number of olfactory neurons identified with the mixed probe (about 60 per antenna) approximates the sum of the positive neurons detected with the five individual probes. These results demonstrate that individual receptors are expressed in distinct nonoverlapping populations of olfactory neurons.

[**0137**] We have performed an additional experiment using two-color RNA in situ hybridization to ask whether two receptor genes, DOR64 and DOR87, expressed in interspersed cells in the distal antenna are expressed in different neurons. Antisense RNA probes for the two genes were labeled with either digoxigenin- or FITC-UTP and were used in pairwise combinations in in situ hybridization to sections through the Drosophila antenna. Although these two genes are expressed in overlapping lateral-distal domains, two-color in situ hybridization reveals that neurons expressing DOR64 do not express DOR87, rather each gene is expressed in distinct cell populations (**FIGS. 5D and E**). Taken together, these data suggest that olfactory sensory neurons within the antenna are functionally distinct and express different complements of odorant receptors. At the extreme, the experiments are consistent with a model in which individual neurons express only a single receptor gene.

[**0138**] Our differential cloning procedure identified one additional gene, A45, which shares weak identity (24%) with the DOR gene family over a short region (93 amino acids). This gene, however, does not appear to be a classical member of the DOR family: it is far more divergent and significantly larger than the other family members (486 amino acids). This gene is expressed in all olfactory sensory neurons (data not shown). If A45 does encode a divergent odorant receptor, then it would be present in all sensory neurons along with different complements of the more classical members of the DOR gene family.

[**0139**] The Size and Organization of the Odorant Receptor Gene Family

[**0140**] How large is the family of odorant receptor genes in Drosophila? Unlike vertebrate odorant receptors, which share 40-98% sequence identity at the amino acid level, the fly receptors are extremely divergent. The extent of sequence similarity between receptor subfamilies ranges from 20-30%. The maxillary palp receptor DOR104 is the most distantly related member of the family with about 17% identity to the other receptor genes. Inspection of the receptor sequences suggests that Southern blot hybridizations, even those performed at low stringency, are unlikely to reveal multiple additional members of a gene family. In accord with this, Southern blot hybridization with receptor probes DOR24, 62, and 72, performed at either high or low stringency, reveals only a single hybridizing band following cleavage of genomic DNA with three different restriction endonucleases (FIGS. 7C-E). The two linked clusters of receptors contain genes with a greater degree of sequence conservation and define small subfamilies of receptor genes. A cluster of three receptors, DOR71, 72, and 73, is located at map position 33B1-2. The antennal receptors DOR72 and 73 are 55% identical and both exhibit about 30% identity to the third gene at the locus, DOR71, which is expressed in the maxillary palp. DOR67 and DOR53, members of a second subfamily, reside within 1 kb of each other at map position 22A2-3 and exhibit 76% sequence identity. Not surprisingly, these two linked genes crosshybridize at low stringency. Southern blots probed with either DOR67 or DOR53 reveal two hybridizing bands corresponding to the two genes within the subfamily but fail to detect additional subfamily members in the chromosome (**FIGS. 7A and B**).

[**0141**] The members of the receptor gene family described here are present on all but the small fourth chromosome. No bias is observed toward telomeric or centromeric regions. The map positions, as determined from P1 and cosmid clones (Berkeley Drosophila Genome Project; European Drosophila Genome Project) are provided in Experimental Procedures. A comparatively large number of receptor genes map to chromosome 2 because the Berkeley Drosophila Genome Project has concentrated its efforts on this chromosome. Unlike the distribution of odorant receptors in nematodes and mammals (Ben-Arie et al., 1994; Troemel et al., 1995; Robertson, 1998), only small linked arrays have been identified and the majority of the family members are isolated at multiple, scattered loci in the Drosophila genome.

[**0142**] The high degree of divergence among members of the Drosophila odorant receptor gene family is more reminiscent of the family of chemoreceptors in *C. elegans* than the more highly conserved odorant receptors of vertebrates. Estimates of the size of the Drosophila receptor gene family, therefore, cannot be obtained by either Southern blot hybridization o**[text missing or illegible when filed]** PCR analysis of genomic DNA. Rather, our estimates of the gene family derive from the statistics of small numbers. We detect 12 members of the odorant receptor gene family from a Drosophila genome database that includes roughly 10% of the genome. Recognizing a possible bias in our estimate, it seem reasonable at present to estimate that the odorant recepto**[text missing or illegible when filed]** family is likely to include 100 to 200 genes. This is i**[text missing or illegible when filed]** accord with independent estimates from in situ hybridizatio**[text missing or illegible when filed]** experiments that demonstrate that a given receptor prob**[text missing or illegible when filed]** hybridizes with 0.5-1.5% of the neurons. If we assume tha**[text missing or illegible when filed]** a given neuron expresses only a single receptor gene, thes**[text missing or illegible when filed]** observations suggest that the gene family would include 10**[text missing or illegible when filed]** to 200 members.

[0143] Experimental Discussion

[0144] The Size and Divergence of the Gene Family

[0145] We have identified a novel family of seven transmembrane domain proteins that is likely to encode the Drosophila odorant receptors. The number of different receptor genes expressed in the neurons of the antenna and maxillary palp will reflect the diversity and specificity of odor recognition in the fruit fly. How large is the Drosophila odorant receptor gene family? We have identified 11 members of this divergent gene family in the Drosophila DNA database. The potential for bias notwithstanding, it seems reasonable to assume then that since only 10% of genomic sequence has been deposited, this gene family is likely to contain from 100 to 200 genes. However, significant errors in our estimates could result from bias in the nature of the sequences represented in the 10% of the Drosophila genome analyzed to date. In situ hybridization experiments demonstrating that each of the receptor genes labels from 0.5-1.5% of the olfactory sensory neurons are in accord with the estimate of 100 to 200 receptor genes.

[0146] Several divergent odorant receptor gene families, each encoding seven transmembrane proteins, have been identified in vertebrate and invertebrate species. In mammals, volatile odorants are detected by a family of as many as 1,000 receptors each expressed in the main olfactory epithelium (Buck and Axel, 1991; Levy et al., 1991; Parmentier et al., 1992; Ben-Arie et al., 1994). This gene family shares features with the serpentine neurotransmitter receptors and is conserved in all vertebrates examined. Terrestrial vertebrates have a second anatomically and functionally distinct olfactory system, the vomeronasal organ, dedicated to the detection of pheromones. Vomeronasal sensory neurons express two distinct families of receptors each thought to contain from 100 to 200 genes: one novel family of serpentine receptors (Dulac and Axel, 1995), and a second related to the metabotropic neurotransmitter receptors (Herrada and Dulac, 1997; Matsunami and Buck, 1997; Ryba and Tirindelli, 1997).

[0147] In the invertebrate *C. elegans*, chemosensory receptors are organized into four gene families that share 20-40% sequence similarity within a family and essentially no sequence similarity between families (Troemel et al., 1995; Sengupta et al., 1996; Robertson, 1998). The four gene families in *C. elegans* together contain about 1,000 genes engaged in the detection of odors. The nematode receptors exhibit no sequence conservation with the three distinct families of vertebrate odorant receptor genes. Our studies reveal that Drosophila has evolved an additional divergent gene family of serpentine receptors comprised of from 100 to 200 genes. The observation that a similar function, chemosensory detection, is accomplished by at least eight highly divergent gene families, sharing little or no sequence similarity, is quite unusual.

[0148] Why is the evolutionary requirement for odorant receptors so often met by recruitment of novel gene families rather than exploiting pre-existing odorant receptor families in ancestral genomes? The character of natural odorants along with their physical properties (e.g. aqueous or volatile) represent important selectors governing the evolution of receptor gene families. The use of common "anthropomorphic" odorant sets in the experimental analysis of olfactory specificity has led to the prevailing view that significant overlap exists in the repertoire of perceived odors between different species. Studies of odorant specificity in different species often employ odors at artificially high concentrations and may present an inaccurate image of the natural repertoire of odorants. We simply do not know the nature of the odors that initially led to the ancestral choice of receptor genes during the evolution of the nematode, insect, or vertebrate species. Clearly, vastly different properties in salient odors could dictate the recruitment of new gene families to effect an old function, olfaction. The character of the odor is not the only evolutionary selector. Odorant receptors must interact with other components in the signal transduction pathway [G proteins (for review see Buck, 1996; Bargmann and Kaplan, 1998) and perhaps even RAMPs (McLatchie et al, 1998) and rho (Mitchell et al., 1998)] that may govern the choice of one family of serpentine receptors over another. Moreover, mammalian receptors not only recognize odorants in the environment but are likely to recognize guidance cues governing formation of a sensory map in the brain (Wang et al., 1998). Thus, the multiple properties required of the odorant receptors might change vastly over evolutionary time and this might underlie the independent origins of the multiple chemosensory receptor gene families.

[0149] Establishing a Topographic Map in the Antenna and the Brain

[0150] We observe that individual receptor genes in the fly are expressed in topographically conserved domains within the antenna. This highly ordered spatial distribution of receptor expression differs from that observed in the mammalian olfactory epithelium. In mammals, a given receptor can be expressed in one of four broad but circumscribed zones in the main olfactory epithelium (Ressler et al., 1993; Vassar et al., 1993). A given zone can express up to 250 different receptors and neurons expressing a given receptor within a zone appear to be randomly dispersed (Ressler et al., 1993; Vassar et al., 1993). The highly ordered pattern of expression observed in the Drosophila antenna might have important implications for patterning the projections to the antennal lobe. In visual, somatosensory, and auditory systems the peripheral receptor sheet is highly ordered and neighbor relations in the periphery are maintained in the projections to the brain. These observations suggest that the relative position of the sensory neuron in the periphery will determine the pattern of projections to the brain.

[0151] Our data on the spatial conservation of receptor expression in the antenna suggest that superimposed upon coarse spatial patterning of olfactory sensilla (Venkatesh and Singh, 1984; Ray and Rodrigues, 1995; Reddy et al., 1997) must be more precise positional information governing the choice of receptor expression This spatial information might dictate the fixed topographic pattern of receptor expression in the peripheral receptor sheet and at the same time govern the ordered sensory projections to the brain. This relationship between positional identity and the pattern of neuronal projections has been suggested for both peripheral sensory neurons (Merritt and Whitington, 1995; Grillenzoni et al., 1998) and neurons in the embryonic central nervous system of Drosophila (Doe and Skeath, 1996).

[0152] Implications for Sensory Processing

[0153] In mammals, olfactory neurons express only one of the thousand odorant receptor genes. Neurons expressing a given receptor project with precision to 2 of the 1800 glomeruli in the mouse olfactory bulb. Odorants will therefore elicit spatially defined patterns of glomerular activity such that the quality of an olfactory stimulus is encoded by the activation of a specific combination of glomeruli (Stewart et al., 1979; Lancet et al., 1982; Kauer et al., 1987; Imamura et al., 1992; Mori et al., 1992; Katoh et al., 1993; Friedrich and Korsching, 1997). Moreover, the ability of an odorant to activate a combination of glomeruli allows for the discrimination of a diverse array of odors far exceeding the number of receptors and their associated glomeruli. In the nematode, an equally large family of receptor genes is expressed in 16 pairs of chemosensory cells, only three of which respond to volatile odorants (Bargmann and Horvitz, 1991; Bargmann et al., 1993). This immediately implies that a given chemosensory neuron will express multiple receptors and that the diversity of odors recognized by the nematode might approach that of mammals, but the discriminatory power is necessarily dramatically reduced.

[0154] What does the character of the gene family we have identified in Drosophila tell us about the logic of olfactory processing in this organism? We estimate that the Drosophila odorant receptors comprise a family of from 100 to 200 genes. Moreover, the pattern of expression of these genes in the third antennal segment suggests that individual sensory neurons express a different complement of receptors and, at the extreme, our data are consistent with the suggestion that individual neurons express one or a small number of receptors. As in the case of mammals, the problem of odor discrimination therefore reduces to a problem of the brain discerning which receptors have been activated by a given odorant. If the number of different types of neurons exceeds the number of glomeruli (43) (Stocker, 1994; Laissue et al., 1999), it immediately follows that a given glomerulus must receive input from more than one kind of sensory neuron. This implies that a single glomerulus will integrate multiple olfactory stimuli. One possible consequence of this model would be a loss of discriminatory power while maintaining the ability to recognize a vast array of odors. Alternatively, significant processing of sensory input may occur in the fly antennal lobe to afford discrimination commensurate with the large number of receptors.

[0155] This model of olfactory coding is in sharp contrast with the main olfactory system of vertebrates in which sensory neurons express only a single receptor and converge on only a single pair of spatially fixed glomeruli in the olfactory bulb. Moreover, each projection neuron in the mammalian bulb extends its dendrite to only a single glomerulus. Thus the integration and decoding of spatial patterns of glomerular activity, in vertebrates, must occur largely in the olfactory cortex. In the fruit fly, the observation that the number of receptors may exceed the number of glomeruli suggests that individual glomeruli will receive input from more than one type of sensory neuron. A second level of integration in the antennal lobe is afforded by subsets of projection neurons that elaborate extensive dendritic arbors that synapse with multiple glomeruli. Thus, the Drosophila olfactory system reveals levels of processing and integration of sensory input in the antennal lobe that is likely to be restricted to higher cortical centers in the main olfactory system of vertebrates.

[0156] Protein and Nucleic Acid (nt) Sequences of 55 Drosophila Odorant Receptor Genes

[0157] The following includes those genes first identified in 1998-1999. Protein sequences used single letter amino acid codes.

[0158] DOR10

[0159] MEKLRSYEDFIFMANMMFKTLGYDLFHT-
PKPWWRYLLVRGYFVLCTISNFYEASMVTT
RIIEWESLAGSPSKIMRQGLH-
FFYMLSSQLKFITFMINRKRLLQLSHRLKELYPHKEQ
NQRKYEVNKYYLSCSTRNVLYVYYFVMN-
VVMALEPLVQSQFIVNVSLGTDLWMMCVSSQ ISM-
HLGYLANMLASIRPSPETEQQDCD-
FLASIIKRHQLMIRLQKDVNYVFGLLLASNL
FTTSCLLCCMAYYTVVEGFNWEGISYM-
MLPASVAAQFYVVSSHGQMLIDLLMTITYRF
FAVIRQTVEK

[0160] DOR10nt

[0161] ATGGAAAAACTACGTTCCTATGAG-
GATTTCATCTTCATGGCCAACATGATGTTCAAGA
CCCTTGGCTACGATCTATTCCATACAC-
CCAAACCCTGGTGGCGCTATCTGCTTGTGCG
AGGATACTTCGTTTTGTGCACGATCAG-
CAACTTTTACGAGGCTTCCATGGTGACGACA
AGGATAATTGAGTGGGAATCCTTGGCCG-
GAAGTCCCTCCAAAATAATGCGACAGGGTC
TGCACTTCTTTTACATGTTGAGTAGC-
CAATTGAAATTTATCACATTCATGATAAATCG
CAAACGCCTACTGCAGCTGAGC-
CATCGTTTGAAAGAGTTGTATCCTCAT-
AAAGAGCAA AATCAAAGGAAGTACGAGGT-
GAATAAATACTACCTATCCTGTTCCACGCGCAATG
TTT TGTACGTGTACTACTTTGTAATGGTCGT-
CATGGCACTGGAACCCCTCGTTCAGTCCCA
GTTCATAGTGAATGTGAGCCTGGGCACA-
GATCTGTGGATGATGTGCGTCTCAAGCCAA ATATC-
GATGCACTTGGGCTATCTGGCCAATAT-
GTTGGCCTCCATTCGACCAAGTCCAG
AAACGGAACAACAAGACTGTGACTTCT-
TGGCCAGCATTATAAAGAGACATCAACTAAT GAT-
CAGGCTTCAAAAGGACGTGAACTAT-
GTTTTTGGACTCTTATTGGCATCTAATCTG

TTTACCACATCCTGTTTACTTTGCTG-CATGGCGTACTATACCGTCGTCGAAGGTTTCA ATTGGGAGGGCATTTCCTATATGAT-GCTCTTTGCTAGTGTAGCTGCCCAGTTCTACGT TGTCAGCTCACACGGACAAATGTTAATA-GATTTGTTGATGACCATCACATACAGATTT TTCGCGGTTATACGACAAACTGTAGAAAAG

[0162] DOR104

[0163] MASLQFHGNVDADIRYDISLDPARESN-LFRLLMGLQLANGTKPSPRLPKWWPKRLEMI GKV-LPKAYCSMVI FTSLHLGVLFTKTTLDVLPTGELQAIT-DALTMT IYFFTGYGTIY WCLRSRRLLAYMEHMNREYRHHSLAGVT-FVSSHAAFRMSRNFTVVWIMSCLLGVISWG VSPLM-LGIRMLPLQCWYPFDALGPG-TYTAVYATQLFGQIMVGMTFGFGGSLFVTLSLL LLGQFDVLYCSLKNLDAHTKLLGGES-VNGLSSLQEELLLGDSKRELNQYVLLQEHPTD LLRL-SAGRKCPDQGNAFHNALVECIRLHRFIL-HCSQELENLFSPYCLVKSLQITFQLC LLVFVGVSGTREVLRIVNQLQYLGL-TIFELLMFTYCGELLSRHSIRSGDAFWRGAWWK HAHFIRQDILIFLVNSRRAVHVTAGK-FYVMDVNRLRSVITQAFSFLTLLQKLAAKKTE SEL

[0164] DOR104nt

[0165] GAATTCGGCACGAGCAGTCGATGGC-CAGTCTTCAGTTCCACGGCAACGTCGATGCGGA CATCAGGTATGATATTAGCCTGGATCCG-GCTAGGGAATCGAATCTCTTCCGTCTGCTA ATGG-GACTCCAGTTGGCGAATGGCACGAAGC-CATCGCCGCGGTTACCCAAATGGTGGC CAAAGCGGCTGGAAATGATTGGTAAAGT-GCTGCCCAAAGCCTATTGTTCCATGGTGAT TTTCACCTCCCTGCATTTGGGTGTCCT-GTTCACGAAAACCACACTGGATGTCCTGCCG ACGGGGGAGCTGCAGGCCATAACGGAT-GCCCTCACCATGACCATAATATACTTTTTCA CGGGCTACGGCACCATCTACTGGTGCCT-GCGCTCCCGGCGCCTCTTGGCCTACATGGA GCA-CATGAACCGGGAGTATCGCCATCAT-TCGCTGGCCGGGGTGACCTTTGTGAGTAGC CATGCGGCCTTTAGGATGTCCAGAAACT-TCACGGTGGTGTGGATAATGTCCTGCCTGC TGGGCGTGATTTCCTGGGGCGTTTCGC-CACTGATGCTGGGCATCCGGATGCTGCCGCT CCAATGTTGGTATCCCTTCGACGC-CCTGGGTCCCGGCACATATACGGCGGTCTATGCT ACACAACTTTTCGGTCAGATCATG-GTGGGCATGACCTTTGGATTCGGGGGATCACTGT TTGTCACCCTGAGCCTGCTACTCCTGG-GACAATTCGATGTGCTCTACTGCAGCCTGAA GAACCTGGATGCCCATACCAAGT-TGCTGGGCGGGGAGTCTGTAAATGGCCTGAGTTCG CTGCAAGAGGAGTTGCTGCTGGGG-GACTCGAAGAGGGAATTAAATCAGTACGTTTTGC TCCAGGAGCATCCGACGGATCTGCT-GAGATTGTCGGCAGGACGAAAATGTCCTGACCA AGGAAATGCGTTTCACAACGCCTTGGTG-GAATGCATTCGCTTGCATCGCTTCATTCTG CACT-GCTCACAGGAGTTGGAGAATCTAT-TCAGTCCATATTGTCTGGTCAAGTCACTGC AGATCACCTTTCAGCTTTGCCTGCTG-GTCTTTGTGGGCGTTTCGGGTACTCGAGAGGT CCT-GCGGATTGTCAACCAGCTACAGTACT-TGGGACTGACCATCTTCGAGCTCCTAATG TTCACCTATTGTGGCGAACTCCT-CAGTCGGCATAGTATTCGATCTGGCGACGCCTTTT GGAGGGGTGCGTGGTGGAAGCACGC-CCATTTCATCCGCCAGGACATCCTCATCTTTCT GGT-CAATAGTAGACGTGCAGTTCACGTGACT-GCCGGCAAGTTTTATGTGATGGATGTG AATCGTCTAAGATCGGTTATAACGCAG-GCGTTCAGCTTCTTGACTTTGCTGCAAAAGT TGGCTGCCAAGAAGACGGAATCG-GAGCTCTAAACTGGTACCACGCATCGATATTTATT TAGCGCATTGTCGAGTAAAAG-CAAAAAAAASAASAAAAA

[0166] DOR105

[0167] MFEDIQLIYMNIKILRFWALLYDKNLR-RYVCIGLASFHIFTQIVYMMSTNEGLTGIIR NSYMLV-LWINTVLRAYLLLADHDRYLALIQKL-TEAYYDLLNLNDSYISEILDQVNKVG KLMARGNLFFGMLTSMGFGLY-PLSSSERVLPFGSKIPGLNEYESPYYEMWYIFQMLIT PMGCCMYIPYTSLIVGLIMFGIVRCK-ALQHRLRQVALKHPYGDRDPRELREEIIACIR YQQSI-IEYMDHINELTTMMFLFELMAFSALL-CALLFMLIIVSGTSQLIIVCMYINMIL AQILALYWYANELREQNLAVATAAY-ETEWFTFDVPLRKNILFMMMRAQRPAAILLGNI RPITLELFQNLLNTTYTFFTVLKRVYG

[0168] DOR105nt

[0169] ATGTTTGAAGACATTCAGCTAATCTA-CATGAATATCAAGATATTGCGATTCTGGGCCC TGCTCTATGACAAAAACTTGAGGCGT-TATGTGTGCATTGGACTGGCCTCATTCCACAT CTTCACCCAAATCGTCTACATGATGAG-TACCAATGAAGGACTAACCGGGATAATTCGT AACT-CATATATGCTCGTCCTTTGGAT-TAATACGGTGCTGCGAGCTTATCTCTTGCTGG CGGATCACGACAGATATTTG-GCTTTGATCCAAAAACTAACTGAGGC-CTATTACGATTT ACTGAATCTGAACGATTCG-TATATATCGGAAATATTGGACCAGGTGAACAAGGT GGGA AAGTTGATGGCTAGGGGCAATCTGT-TCTTTGGCATGCTCACATCCATGGGATTCGGTC TGTACCCATTGTCCTCCAGCGAAA-GAGTCCTGCCATTTGGCAGCAAAATTCCTGGTCT AAATGAGTACGAGAGTCCGTACTAT-GAGATGTGGTACATCTTTCAGATGCTCATCACC CCGATGGGCTGTTGCATGTACATTCCG-TACACCAGTCTGATTGTGGGCTTGATAATGT TCG-GCATTGTGAGGTGCAAGGCTTTGCAG-CATCGCCTCCGCCAGGTGGCGCTTAAGCA TCCGTACGOAGATCGCGATCCCCGT-GAACTGAGGGAGGAGATCATAGCCTGCATACGT TACCAGCAGAGCATTATCGAGTACATG-GATCACATAAACGAGCTGACCACCATGATGT TCCTATTCGAACTGATGGCCTTTTCG-GCGCTGCTCTGTGCGCTGCTCTTTATGCTGAT TATCGTCAGCGGCACCAGTCAGCT-GATAATTGTTTGCATGTACATTAACATGATTCTG GCCCAAATACTGGCCCTCTATTGGTATG-CAAATGAGTTAAGGGAACAGAATCTGGCGG TGGC-

CACCGCAGCCTACGAAACGGAGTGGT-
TCACCTTCGACGTTCCACTGCGCAAAAA
CATCCTGTTCATGATGATGAGGGCA-
CAGCGGCCAGCTGCAATACTACTGGGCAATATA
CGCCCCATCACTTTGGAACTGTTC-
CAAAACCTACTGAACACAACCTATACATTTTTA
CGGTTCTCAAGCGAGTCTACGGA

[**0170**] DOR107

[**0171**] MYPRFLSRNYPLAKHLFFVTRYSF-
GLLGLRFGKEQSWLHLLWLVFNFVNLAHCCQAEF
VFGWSHLRTSPVDAMDAFCPLACSFT-
TLFKLGWMWWRRQEVADLMDRIRLLIGEQEKR
EDSRRKVAQRSYYLMVTRCGMLVFTLG-
SITTGAFVLRSLWEMWVRRHQEFKFDMPFRM LFHD-
FAHRMPWFPVFYLYSTWSGQVTVYAF-
AGTDGFFFGFTLYMAFLLQALRYDIQDA
LKPIRDPSLRESKICCQRLADI-
VDRHNEIEKIVKEFSGIMAAPTFVHFVSASLVIATS
VIDILLYSGYNIIRYVVYTFTVSSAI-
FLYCYGGTEMSTESLSLGEAAYSSAWYTWDRE
TRRRVFLIIL-
RAQRPITVRVPFFAPSLPVFTSVIKFTGSIVALAKTIL

[**0172**] DOR107nt

[**0173**] ATGTATCCGCGATTCCTCAGCCGTAAC-
TATCCGCTGGCCAAGCATTTGTTCTTCGTCA CCA-
GATACTCCTTTGGCCTGCTGGGCCT-
GAGATTTGGCAAAGAGCAATCGTGGCTTCA
CCTCTTGTGGCTGGTGTTCAATTTCGT-
TAACCTGGCGCACTGCTGCCAGGCGGAGTTC
GTCTTCGGCTGGAGTCACTTGCGCAC-
CAGTCCCGTGGATGCCATGGACGCCTTTTGTC
CTCTGGCCTGCAGTTTCACCACGCTCT-
TCAAGCTGGGATGGATGTGGTGGCGTCGCCA
GGAAGTAGCTGATCTAATGGACCGCATC-
CGCTTGCTCATCGGGGAGCAGGAGAAGAGG GAG-
GACTCCCGGAGAAAGGTGGCTCAAAG-
GAGCTACTATCTCATGGTCACCAGGTGCG
GTATGCTGGTCTTCACCCTGGGCAGCAT-
TACCACTGGAGCCTTCGTTCTGCGTTCCCT TTGG-
GAAATGTGGGTGCGTCGTCATCAGGAGT-
TCAAATTCGATATGCCCTTTCGCATG
CTGTTCCACGACTTTGCGCATCGCATGC-
CCTGGTTTCCAGTTTTCTATCTCTACTCCA CATG-
GAGTGGCCAGGTCACTGTGTACGC-
CTTTGCTGGTACAGATGGTTTCTTC TTGG
CTTTACCCTCTACATGGCCTTCTTGCTG-
CAGGCCTTAAGATACGATATCCAGGATGCC
CTCAAGCCAATAAGAGATCCCTCGCT-
TAGGGAATCCAAAATCTGCTGTCAGCGATTGG
CGGACATCGTGGATCGCCACAAT-
GAGATAGAGAAGATAGTCAAGGAATTTTCTGGAAT
TATGGCTGCTCCAACTTTTGTTCACT-
TCGTATCAGCCAGCTTAGTGATAGCCACCAGC
GTCATTGATATACTATTGTATTCCGGC-
TATAACATCATCCGTTACGTGGTGTACACCT TCACG-
GTTTCCTCGGCCATCTTCCTCTATTGC-
TACGGAGGCACAGAAATGTCAACTGA
GAGCCTTTCCTTGGGAGAAGCAGCCTA-
CAGCAGTGCCTGGTATACTTGGGATCGAGAG
ACCCGCAGGCGGGTCTTTCTCATTATC-
CTGCGTGCTCAACGACCCATTACGGTGAGGG TGC-
CCTTTTTTGCACCATCGTTACCAGTCT-
TCACATCGGTCATCAAGTTTACAGGTTC
GATTGTGGCACTGGCTAAGACGATACTG

[**0174**] DOR108

[**0175**] MDKHKDRIESMRLILQVMQLFGLWPWS-
LKSEEEWTFTGFVKRNYRFLLHLPITFTFIG
LMWLEAFISSNLEQAGQVLYMSITE-
MALVVKILSIWHYRTEAWRLMYELQHAPDYQLH
NQEEVDFWRREQRFFKWFFYIYILIS-
LGVVYSGCTGVLFLEGYELPFAYYVPFEWQNE RRY-
WFAYGYDMAGMTLTCISNITLDTLGCY-
FLFHISLLYRLLGLRLRETKNMKNDTIF
GQQLRAIFIMHQRIRSLTLTCQRIVSPY-
ILSQIILSALIICFSGYRLQHVGIRDNPGQ FISMLQFVS-
VMILQIYLPCYYGNEITVYANQLT-
NEVYHTNWLECRPPIRKLLNAYMEH
LKKPVTIRAGNSFAVGLPIFVKTINNAY-
SFLALLLNVSN

[**0176**] DOR108nt

[**0177**] ATGGATAAACACAAGGATCGCAT-
TGAATCCATGCGCCTAATTCTTCAGGTCATGCAAC
TATTTGGCCTCTGGCCGTGGTCCT-
TGAAATCGGAAGAGGAGTGGACTTTCACCGGTTT
TGTAAAGCGCAACTATCGCTTCCTGCTC-
CATCTGCCCATTACCTTCACCTTTATTGGA CTCAT-
GTGGCTGGAGGCCTTCATCTCGAG-
CAATCTGGAGCAGGCTGGCCAGGTTCTGT
ACATGTCCATCACCGAGATGGCTTTG-
GTGGTGAAAATCCTGAGCATTTGGCACTATCG CAC-
CGAAGCTTGGCGGCTGATGTACGAACTC-
CAACATGCTCCGGACTACCAACTCCAC
AACCAGGAGGAGGTAGACTTTTGGCGC-
CGGGAGCAACGATTCTTCAAGTGGTTCTTCT
ACATCTACATTCTGATTAGCT-
TGGGCGTGGTATATAGTGGCTGCACTG-
GAGTACTTTT TCTGGAGGGCTACGAACTGC-
CCTTTGCCTACTACGTGCCCTTCGAATGGCAGAAC
GAG AGAAGGTACTGGTTCGCCTATGGTTAC-
GATATGGCGGGCATGACGCTGACCTGCATCT CAAA-
CATTACCCTGGACACCCTGGGTTGC-
TATTTCCTGTTCCATATCTCTCTTTTGTA
CCGACTGCTTGGTCTGCGATTGAGG-
GAAACGAAGAATATGAAGAATGATACCATTTTT
GGCCAGCAGTTGCGTGCCATCTTCAT-
TATGCATCAGAGGATTAGAAGCCTAACCCTGA CCT-
GCCAGAGAATCGTATCTCCCTATATC-
CTATCTCAGATCATTTTGAGTGCCCTGAT
CATCTGCTTTAGTGGATACCGCTTGCAG-
CATGTGGGAATTCGCGATAATCCCGGCCAG
TTTATATCCATGTTGCAGTTTGTCAGT-
GTGATGATCCTGCAGATTTACTTGCCCTGCT ACT-
ATGGAAACGAGATAACCGTGTATGC-
CAATCAGCTGACCAACGAGGTTTACCATAC
CAATTGGCTGGAATGTCGGCCACCGAT-
TCGAAAGTTACTCAATGCCTACATGGAGCAC
CTGAAGAAACCGGTGACCATCCGGGCTG-
GCAACTCCTTCGCCGTGGGACTACCAATTT TTGT-
TAAGACCATCAACAACGCCTA-
CAGTTTCTTGGCTTTATTACTAAATGTATCGAA T

[**0178**] DOR109

[**0179**] MESTNRLSAIQTLLVIQRWIGLLKWE-
NEGEDGVLTWLKRIYPFVLHLPLTFTYIALMW

YEAITSSDFEEAGQVLYMSITELALVT-KLLNIWYRRHEAASLIHELQHDPAFNLRNSE EIKF-WQQNQRNFKRIFYWYIWGSLFVAVMGY-ISVFFQEDYELPFGYYVPFEWRTRERY FYAWGYNVVAMTLCCLSNILLDTLGCY-FMFHIASLFRLLGMRLEALKNAAEEKARPEL RRIFQLHTKVRRLTRECEVLVSPYV-LSQVVFSAFIICFSAYRLVHMGFKQRPGLFVTT VQFVAVMIVQIFLPCYYGNELTFHAN-ALTNSVFGTNWLEYSVGTRKLLNCYMEFLKRP VKVRAGVFFEIGLPIFVKTINNAYSFFALLLKISK

[0180] DOR109nt

[0181] ATGGAGTCTACAAATCGCCTAAGTGC-CATCCAAACACTTTTAGTAATCCAACGTTGGA TAG-GACTTCTTAAATGGGAAAACGAGGGC-GAGGATGGAGTATTAACCTGGCTAAAACG AATATATCCTTTTGTACTGCACCTTC-CACTGACCTTCACGTATATTGCCTTAATGTGG TAT-GAAGCTATTACATCGTCAGATTTTGAG-GAAGCTGGTCAAGTTCTGTACATGTCCA TCACCGAACTGGCATTGGTCACTAAACT-GCTGAATATTTGGTATCGTCGTCATGAAGC TGCTAGTCTAATCCACGAATTGCAACAC-GATCCCGCATTTAATCTGCGCAATTCGGAG GAAAT-CAAATTCTGGCAGCAAAATCAGAG-GAACTTTAAGAGAATATTTTACTGGTACA TCTGGGGCAGCCTTTTCGTGGCTG-TAATGGGTTATATAAGCGTGTTTTTCCAGGAGGA TTACGAGCTGCCCTTTGGCTACTACGT-GCCATTCGAGTGGCGCACCAGGGAACGATAC TTC-TACGCTTGGGGCTATAATGTGGTGGC-CATGACCCTGTGCTGTCTATCCAACATCC TACTGGACACACTAGGCTGTTATTTCAT-GTTCCACATCGCCTCGCTTTTCAGGCTTTT GGGAATGCGACTGGAGGCCTTGAAAAAT-GCAGCCGAAGAGAAAGCCAGACCGGAGTTG CGC-CGCATTTTCCAACTGCACACTAAAGTC-CGCCGATTGACGAGGGAATGCGAAGTGT TAGTTTCACCCTATGTTCTATC-CCAAGTGGTCTTCAGTGCCTTCATCATCTGCTTCAG TGCCTATCGACTGGTGCACATGGGCT-TCAAGCAGCGACCTGGACTCTTCGTGACCACC GTGCAATTCGTGGCCGTCATGATCGTC-CAGATTTTCTTGCCCTGTTACTACGGCAATG AGT-TGACCTTTCATGCCAATGCACTCAC-TAATAGTGTCTTCGGTACCAATTGGCTGGA GTACTCCGTGGGCACTCGCAAGCTGCT-TAACTGCTACATGGAGTTCCTCAAGCGACCG GTTAAAGTGCGAGCTGGGGTGT-TCTTTGAAATAGGACTACCCATCTTTGTGAAGACCA TCAACAATGCCTACAGTTTCTTCGCCCT-GCTGCTAAAGATATCCAAG

[0182] DOR110

[0183] MLFNYLRKPNPTNLLTSPDSFRYFEYGM-FCMGWHTPATHKIIYYITSCLIFAWCAVYL PIGIIISFK-TDINTFTPNELLTVMQLFFNSVGMPFKV-LFFNLYISGFYKAKKLLSEMD KRCTTLKERVEVHQGVVRCNKAY-LIYQFIYTAYTISTFLSAALSGKLPWRIYNPFVDF RESRSSFWKAALNETALMLFAVTQTLMS-DIYPLLYGLILRVHLKLLRLRVESLCTDSG KSDAENEQDLINYAAAIRPAVTRTIFVQ-FLLIGICLGLSMINLLFFADIWTGLATVAY INGLM-VQTFPFCFVCDLLKKDCELLVSAIFHSN-WINSSRSYKSSLRYFLKNAQKsIAF TAGSIFPISTGSNIKVAKLAFSVVTFVN-QLNIADRLTKN

[0184] DOR110nt

[0185] ATGTTGTTCAACTATCTGCGAAAGC-CGAATCCCACAAACCTTTTGACTTCTCCGGACT CATTTAGATACTTTGAGTATGGAAT-GTTTTGCATGGGATGGCACACACCAGCAACGCA TAAGATAATCTACTATATAACATCCT-GTTTGATTTTTGCTTGGTGTGCCGTATACTTG CCAATCGGAATCATCATT-AGTTTCAAAACGGATATTAACACATTCA-CACCGAATGAAC TGTTGACAGTTATGCAAT-TATTTTTCAATTCAGTGGGAATGCCATTCAAGGTT CTGTT CTTCAATTTGTATATTTCTGGATTTTA-CAAGGCCAAAAAGCTCCTTAGCGAAATGGAC AAACGTTGCACCACTTTGAAGGAGC-GAGTGGAAGTGCACCAAGGTGTGGTCCGTTGCA ACAAGGCCTACCTCATTTACCAGT-TCATTTATACCGCGTACACTATTTCAACATTTCT ATCGGCGGCTCTTAGTGGAAAATTGC-CATGGCGCATCTATAATCCTTTTGTGGATTTT CGAGAAAGTAGATCCAGTTTTTG-GAAAGCTGCCCTCAACGAGACAGCACTTATGCTAT TTGCTGTGACTCAAACCCTAATGAGT-GATATATATOCACTGCTTTATGGTTTGATCCT GAGAGTTCACCTCAAACTTTTGCGAC-TAAGAGTGGAGAGCCTGTGCACAGATTCTGGA AAAAGCGATGCTGAAAACGAGCAA-GATTTGATTAACTATGCTGCAGCAATACGACCAG CGGTTACCCGCACAATTTTCGTTCAAT-TCCTCTTGATCGGAATTTGCCTTGGCCTTTC AAT-GATCAATCTACTCTTCTTTGCCGA-CATCTGGACAGGATTGGCCACAGTGGCTTAC ATCAATGGTCTAATOTGCAGACATTTC-CATTTTGCTTCGTTTGTGATCTACTCAAAA AGGAT-TGTGAACTTCTTGTGTCGGC-CATATTTCATTCCAACTGGATTAATTCAAGCCG CAGTTACAAGT-CATCTTTGAGATATTTCTGAAGAACGC-CCAGAAATCAATTGCTTTT ACAGCCGGC TCTATTTTTCCCATTTCTACTGGCTC-GAATATTAAGGTGGCTAAGCTGG CATTTTCGGTG-GTTACTTTTGTCAATCAACTTAACAT-AGCTGACAGATTGACAAAGAA C

[0186] DOR 111

[0187] MLFRKRKPKSDDEVITFDELTRFPMT-FYKTIGEDLYSDRDPNVIRRYLLRFYLVLGFL NFNAYVVGEIAYFIVHIMSTTTLLEATA-VAPCIGFSFMADFKQFGLTVNRKRLVRLLD DLKEIF-PLDLEAQRKYNVSFYRKHMNRVMTLFT-ILCMTYTSSFSFYPAIKSTIKYYLM GSEIFERNYGFHILFPYDAETDLTVYWF-SYWGLAHCAYVAGVSYVCVDLLLIATITQL TMHFN-FIANDLEAYEGGDHTDEENIKYLHNLV-VYHARALDINKKCTFQSSRIGHSAFN QNWLPCSTKYKRILQFIIARSQKPASIR-PPTFPPISFNTFMKVISMSYQFFALLRTTY YG

[0188] DOR111nt

[0189] ATGCTGTTCCGCAAACGTAAGC-CAAAAAGTGACGATGAAGTCATCACCT-

TCGACGAAC TTACCCGGTTTCCGATGACTTTCTA-CAAGACCATCGGCGAGGATCTGTACTCCGATAG GGATCCGAATGTGATAAGGCGTTACCT-GCTACGTTTTTATCTGGTACTCGGTTTTCTC AACT-TCAATGCCTATGTGGTGGGC-GAAATCGCGTACTTTATAGTCCATATAATGTCGA CGACTACTCTTTTGGAGGCCACTG-CAGTGGCACCGTGCATTGGCTTCAGCTTCATGGC CGACTTTAAGCAGTTCGGTCTCACAGT-GAATAGAAAGCGATTGGTCAGATTGCTGGAT GATCTCAAGGAGATATTTCCTTTAGATT-TAGAAGCGCAGCGGAAGTATAACGTATCGT TTTAC-CGGAAACACATGAACAGGGTCATGAC-CCTATTCACCATCCTCTGCATGACCTA CACCTCGTCATTTAGCTTTTATCCAGC-CATCAAGTCGACCATAAAGTATTACCTTATG GGATCGGAAATCTTTGAGCGCAACTACG-GATTTCACATTTTGTTTCCCTACGACGCAG AAACG-GATCTGACGGTCTACTGGTTTTC-CTACTGGGGATTGGCTCATTGTGCCTATGT GGCCGGAGTTTCCTACGTCTGCGTG-GATCTCCTGCTGATCGCGACCATAACCCAGCTG ACCATGCACTTCAACTTTATAGCGAAT-GATTTGGAGGCCTACGAAGGAGGTGATCATA CGGATGAAGAAAATATCAAATACCTGCA-CAACTTGGTCGTCTATCATGCCAGGGCGCT GGATATTAACAAGAAATGTACATTTCA-GAGCTCTCGGATTGGCCATTCGGCATTTAAT CAGAACTGGTTGCCATGCAGCAC-CAAATACAAACGCATCCTGCAATTTATTATCGCGC GCAGCCAGAAGCCCGCCTCTATAAGAC-CGCCTACCTTTCCACCCATATCTTTTAATAC CTTTAT-GAAGGTAATCAGCATGTCGTAT-CAGTTTTTTGCACTGCTCCGCACCACATAT TATGGT

[0190] DOR114

[0191] MLTKKDTQSAKEQEKLKAIPLHSFLKY-ANVFYLSIGMMAYDHKYSQKWKEVLLHWTFI AQM-VNLNTVLISELIYVFLAIGKGSNFLEAT-MNLSFIGFVIVGDFKIWNISRQRKRLT QVVSRLEELHPQGLAQQEPYNIGHHLS-GYSRYSKFYFGMHMVLIWTYNLYWAVYYLVC DFWLGMRQFERMLPYYCWVPWDWST-GYSYYFMYISQNIGGQACLSGQLAADMLMCALV TLVvMHFIRLSAHIESHVAGIGS-FQHDLEFLQATVAYHQSLIHLCQDINEIFGVSLLS NFVSSSFIICFVGFQMTIGSKIDNLVM-LVLFLFCAMVQVFMIATHAQRLVDASEQIGQ AVYN-HDWFRADLRYRKMLILIIKRAQQPSRLK-ATMFLNISLVTVSDLLQLSYKFFALL RTMYVN

[0192] DOR114nt

[0193] ATGTTGACTAAGAAGGATACTCAAAGT-GCCAAGGAGCAGGAAAAGTTGAAGGCCATTC CAT-TGCACAGCTTTCTGAAATATGCCAACGT-GTTCTATTTATCGATTGGAATGATGGC CTACGATCACAAGTACAGTCAAAAGTG-GAAGGAGGTCCTGCTGCACTGGACATTCATT GCCCAGATGGTCAATCTGAATACAGT-GCTCATCTCGGAACTGATTTACGTATTCCTGG CGATCGGCAAAGGTAGCAATTTTCTG-GAGGCCACCATGAATCTGTCTTTCATTGGATT TGT-CATCGTTGGTGACTTCAAAATCTGGAA-CATTTCGCGGCAGAGAAAGAGACTCACC CAAGTGGTCAGCCGATTGGAAGAACTG-CATCCGCAAGGCTTGGCTCAACAAGAACCCT ATAATATAGGGCATCATCTGAGCGGC-TATAGCCGATATAGCAAATTTTACTTCGGCAT GCA-CATGGTGCTGATATGGACGTACAACCTG-TATTGGGCCGTTTACTATCTGGTCTGT GATTTCTGGCTGGGAATGCGT-CAATTTGAGAGGATGCTGCCCTACTACT-GCTGGGTTC CCTGGGATTGGAGTACCGGATATAGC-TACTATTTCATGTATATCTCACAGAATATCGG CGGTCAGGCTTGTCTGTCCGGT-CAGCTAGCAGCTGACATGTTAATGT-GCGCCCTGGTC ACTTTGGTGGTGATGCACTTCATC-CGGCTTTCCGCTCACATCGAGAGTCATGTTGCGG GCATTGGCTCATTCCAGCACGATTTG-GAGTTCCTCCAAGCGACGGTGGCGTATCACCA GAGCTTGATCCACCTCTGCCAGGATAT-CAATGAGATATTCGGTGTTTCACTGTTGTCC AACTTTGTATCCTCGTCGTTTATCATCT-GCTTCGTGGGTTTCCAGATGACCATCGGCA GCAA-GATCGACAACCTGGTAATGCTTGT-GCTTTTCCTGTTTTGTGCCATGGTTCAGGT CTTCATGATTGCCACCCATGCTCAGAG-GCTCGTTGATGCGAGTGAACAGATTGGTCAA GCG-GTCTATAATCACGACTGGTTCCGTGCT-GATCTGCGGTATCGTAAAATGCTGATCC TGATTATTAAGAGGGCCCAACAGC-CGAGTCGACTCAAGGCCACAATGTTCCTGAACAT CTCACTGGTCACCGTGTCGGATCTCTTG-CAACTCTCGTACAAATTCTTTGCCCTTCTG CGCA-CAATGTACGTGAAT

[0194] DOR115

[0195] MEKLMKYASFFYTAVGIRPYTNGEESK-MNKLIFHIVFWSNVINLSFVGLFESIYVYSA FMDNK-FLEAVTALSYIGFVTVGMSKMFFIRWKK-TAITELINELKEIYPNGLIREERYN LPMYLGTCSRISLIYSLLYSVLIWTFN-LFCVMEYWVYDKWLNIRVVGKQLPYLMYIPW KWQDNWSYYYPLLFSQNFAGYTSAAG-QISTDVLLCAVATQLVMHFDFLSNSMERHELSG DWKKDSRFLVDIVRYHERILRLSDAVN-DIFGIPLLLNFMVSSFVICFVGFQMTVGVPP DIV-VKLFLFLVSSMSQVYLICHYGQLVA-DASYGFSVATYNQKWYKADVRYKRALVIII ARSQKVTFLKATIFLDITRSTMTDVRNCVLSV

[0196] DOR115nt

[0197] ATGGAGAAGCTAATGAAGTACGCTAGCT-TCTTCTACACAGCAGTGGGCATACGGCCAT ATAC-CAATGGTGAAGAATCCAAAATGAA-CAAACTTATATTTCACATAGTTTTTTGGTC CAATGTGATTAACCTCAGCTTCGTTG-GATTATTTGAGAGCATTTACGTTTACAGTGCC TTCATGGATAATAAGTTCCTGGAAG-CAGTCACTGCGTTGTCCTACATTGGCTTCGTAA CCGTAGGCATGAGCAAGATGTTCT-TCATCCGGTGGAAGAAAACGGCTATAACTGAACT GATTAATGAATTGAAGGAGATCTATC-CGAATGGTTTGATCCGAGAGGAAAGATACAAT CTGCCGATGTATCTGGGCACCTGCTCCA-GAATCAGCCTTATATATTCCTTGCTCTACT CTGT-TCTCATCTGGACATTCAACTTGTTTTGT-GTAATGGAGTATTGGGTCTATGACAA

GTGGCTCAACATTCGAGTGGTGGGCAAA-
CAGTTGCCGTACCTCATGTACATTCCTTGG AAATG-
GCAGGATAACTGGTCGTACTATCCACT-
GTTATTCTCCCAGAATTTTGCAGGAT
ACACATCTGCAGCTGGTCAAATTTCAAC-
CGATGTCTTGCTCTGCGCGGTGGCCACTCA GTTGG-
TAATGCACTTCGACTTTCTCTCAAATAG-
TATGGAACGCCACGAATTGAGTGGA
GATTGGAAGAAGGACTCCCGATTTCTG-
GTGGACATTGTTAGGTATCACGAACGTATAC
TCCGCCTTTCAGATGCAGTGAAC-
GATATATTTGGAATTCCACTACTACTCAACTTCAT
GGTATCCTCGTTCGTCATCTGCT-
TCGTGGGATTCCAGATGACTGTTGGAGTTCCGCCG
GATATAGTTGTGAAGCTCTTCCTCTTC-
CTTGTCTCTTCGATGAGTCAGGTCTATTTGA TTTGT-
CACTATGGTCAACTGGTGGCCGAT-
GCTAGCTACGGATTTTCGGTTGCCACCTA
CAATCAGAAGTGGTATAAAGCCGATGT-
GCGCTATAAACGAGCCTTGGTTATTATTATA GCTA-
GATCGCAGAAGGTAACTTTTCTAAAGGC-
CACTATATTCTTGGATATTACCAGGT
CCACTATGACAGATGTACGCAACTGTG-
TATTGTCAGTG

[0198] DOR116

[0199] MELLPLAMLMYDGTRVTAM-
QYLIPGLPLENNYCYVVTYMIQTVTM-
LVQGVGFYSGDLF VFLGLTQILTFADMLQVKVKELN-
DALEQKAEYRALVRVGASIDGAENRQRLLLDVIRW
HQLFTDYCRAINALYYELIATQVLS-
MALAMMLSFCINLSSFHMPSAIFFVVSAYSMSI
YCILGTILEFAYDQVYESICNVTWYELS-
GEQRKLFGFLLRESQYPHNIQILGVMSLSV RTAL-
QIVKLIYSVSMMMMNRA

[0200] DOR116nt

[0201] ATGGAACTCCTGCCATTGGCCAT-
GCTAATGTACGATGGAACCCGGGTTACTGCGATGC
AGTATTTAATTCCGGGTCTACCGCT-
TGAGAACAATTATTGCTACGTAGTCACGTACAT
GATTCAGACGGTGACAATGCTCGTG-
CAAGGAGTCGGATTCTACTCCGGTGATTTGTTC
GTATTTCTCGGCTTAACGCAGATC-
CTAACTTTCGCCGATATGCTGCAGGTGAAGGTGA
AAGAGCTAAACGATGCCCTGGAA-
CAAAAAGCGGAATACAGAGCTCTAGTCCGAGTTGG
AGCTTCTATTGATGGAGCGGAAAATCGT-
CAACGCCTTCTCTTGGATGTTATAAGATGG CAT-
CAATTATTCACGGACTACTGTCGCGC-
CATAAATGCCCTCTACTACGAATTGATCG
CCACTCAGGTTCTTTCGATGGCTTTGGC-
CATGATGCTCAGCTTCTGCATTAATTTGAG
CAGCTTTCACATGCCTTCGGC-
TATCTTTTTCGTGGTTTCTGCCTACAGCATGTCCATC
TATTGCATTCTGGGCACCATTCT-
TGAGTTTGCATATGACCAGGTGTACGAGAGCATCT
GTAATGTGACCTGGTATGAGTTGAGTG-
GCGAACAGCGAAAGCTTTTTGGTTTTTTGTT
GCGGGAATCCCAGTATCCGCACAATAT-
TCAGATACTTGGAGTTATGTCGCTTTCCGTG
AGAACGGCTCTGCAGATTGTTAAAC-
TAATTTATAGCGTATCCATGATGATGATGAATC
GGGCG

[0202] DOR117

[0203] MDLRRWFPTLYTQSKDSPVRSRDAT-
LYLLRCVFLMGVRKPPAKFFVAYVLWSFALNFC
STFYQPIGFLTGYISHLSEFSPGE-
FLTSLQVAFNAWSCSTKVLIVWALVKRFDEANNL
LDEMDRRITDPGERLQIHRAVSLSN-
RIFFFFMAVYMVYATNTFLSAIFIGRPPYQNYY PFLD-
WRSSTLHLALQAGLEYFAMAGACFQD-
VCVDCYPVNFVLVLRAHMSIFAERLRRL
GTYPYESQEQKYERLVQCIQDHKVILR-
FVDCLRPVISGTIFVQFLVVGLVLGFTLINI VLFANLG-
SAIAALSFMAAVLLETTPFCILCNYLT-
EDCYKLADALFQSNWIDEEKRYQK
TLMYFLQKLQQPITFMAMNVFPISVGTNISVSRCAL

[0204] DOR117nt

[0205] ATGGATCTGCGAAGGTGGTTTCCGACCT-
TGTACACCCAGTCGAAGGATTCGCCAGTTC GCTC-
CCGAGACGCGACCCTGTACCTC-
CTACGCTGCGTCTTCTTAATGGGCGTCCGCAA
GCCACCTGCCAAGTTTTTCGTGGC-
CTACGTGCTCTGGTCCTTCGCACTGAATTTCTGC
TCAACATTTTATCAGCCAATTG-
GCTTTCTCACAGGCTATATAAGCCATTTATCAGAGT
TCTCCCCGGGAGAGTTTCTAACTTCGCT-
GCAGGTGGCCTTTAATGCTTGGTCCTGCTC
TACAAAAGTCCTGATAGTGTGGGCAC-
TAGTTAAGCGCTTTGACGAGGCTAATAACCTT CTC-
GACGAGATGGATAGGCGTATCACAGAC-
CCCGGAGAGCGTCTTCAGATTCATCGCG
CTGTCTCCCTCAGTAACCGTATATTCT-
TCTTTTTCATGGCAGTCTACATGGTTTATGC CAC-
TAATACGTTTCTGTCGGCGATCTTCAT-
TGGAAGGCCACCGTACCAAAATTACTAC
CCTTTTCTGGACTGGCGATCTAG-
CACTCTGCATCTAGCTCTGCAGGCCGGTCTGGAAT
ACTTCGCCATGGCTGGCGCCTGCTTC-
CAGGACGTTTGCGTTGATTGCTACCCAGTCAA
TTTCGTTTTGGTCCTGCGTGCCCACAT-
GTCGATCTTCGCGGAGCGCCTTCGACGTTTG
GGAACTTATCCTTATGAAAGCCAGGAG-
CAGAAATATGAACGATTGGTTCAGTGCATAC
AAGATCACAAAGTAATTTTGCGATTTGT-
TGACTGCCTGCGTCCTGTTATTTCTGGTAC CATCT-
TCGTGCAATTCTTGGTTGTGGGGTTGGT-
GCTGGGCTTTACCCTAATTAACATT
CTCCTGTTCGCCAACTTGGGATCGGC-
CATCGCAGCGCTCTCGTTTATGGCCGCAGTGC
TTCTAGAGACGACTCCCTTCTGCATAT-
TGTGCAATTATCTCACAGAAGACTGCTACAA GCTG-
GCCGATGCCCTGTTTCAGTCAAACTG-
GATTGATGAGGAGAAACGATACCAAAAG
ACACTCATGTACTTCCTACAGAAACTG-
CAGCAGCCTATAACCTTCATGGCTATGAACG
TGTTTCCAATATCTGTGGGAACTAACAT-
CAGTGTAAGCAGATGTGCCCTT

[0206] DOR118

[0207] MKFIGWLPPKQGVLRYVYLTWTLMT-
FVWCTTYLPLGFLGSYMTQIKSFSPGEFLTSLQ VCI-
NAYGSSVKVAITYSMLWRLIKAK-
NILDQLDLRCTAMEEREKIHLVVARSNHAFLI
FTFVYCGYAGSTYLSSVLSGRPPWQLYN-
PFIDWHDGTLKLWVASTLEYMVMSGAVLQD QLS-

DSYPLIYTLILRAHLDMLRERIRRLRS-DENLSEAESYEELVKCVMDHKLILRYCA IIKPVIQGTIFTQFLLIGLVLGFTLIN-VFFFSDIWTGIASFMFVITILLQTFPFCYTC NLIMED-CESLTHAIFQSNWVDASRRYKTTLLY-FLQNVQQPIVFIAGGIFQISMSSNIS VAKFAFSVITITKQMNIADKFKTD

[0208] DOR118nt

[0209] ATGAAGTTTATTGGATGGCTGC-CCCCCAAGCAGGGTGTGCTCCGGTATGT-GTACCTCA CCTGGACGCTAATGACGTTCGTGTGGT-GTACAACGTACCTGCCGCTTGGCTTCCTTGG TAGCTACATGACGCAGATCAAGTCCT-TCTCCCCTGGAGAGTTTCTCACTTCACTCCAG GTGTGCATTAATGCCTACGGCTCATCGG-TAAAAGTTGCAATCACATACTCCATGCTCT GGCGC-CTTATCAAGGCCAAGAACATTTTGGAC-CAGCTGGACCTGCGCTGCACCGCCAT GGAGGAGCGCGAAAAGATCCACCTAGTG-GTGGCCCGCAGCAACCATGCCTTTCTCATC TTCAC-CTTTGTCTACTGCGGATATGCCGGCTC-CACCTACCTGAGCTCGGTTCTCAGCG GGCGTCCGCCCTGGCAGCTGTACAATC-CCTTTATTGATTGGCATGACGGCACACTCAA GCTCTGGGTGGCCTCCACGTTGGAGTA-CATGGTGATGTCAGGCGCCGTTCTGCAGGAT CAACTCTCGGACTCTTACCCATTGATC-TATACCCTCATCCTTCGTGCTCACTTGGACA TGCTAAGGGAGCGCATCCGACGCCTC-CGTTCCGATGAGAACCTGAGCGAGGCCGAGAG CTATGAAGAGCTGGTCAAATGTGTGATG-GACCACAAGCTCATTCTAAGATACTGCGCG ATTAT-TAAACCAGTAATCCAGGGGACCATCT-TCACACAGTTTCTGCTGATCGGCCTGG TTCTGGGCTTCACGCTGATCAACGT-GTTTTTCTTCTCAGACATCTGGACGGGCATCGC ATCATTTATGTTTGTTATAAC-CATTTTGCTGCAGACCTTCCCCTTCTGC-TACACATGC AACCTCATCATGGAGGACTGC-GAGTCCTTGACCCATGCTATTTTCCAGTCCAACTG GG TGGATGCCAGTCGTCGCTACAAAACAA-CACTACTGTATTTTCTCCAAAACGTGCAGCA GCCTATCGTTTTCATTGCAGGCGG-TATCTTTCAGATATCCATGAGCAGCAACATAAGT GTGGCAAAGTTTGCTTTCTCCGT-GATAACCATTACCAAGCAAATGAATATAGCTGACA AATTTAAGACGGAC

[0210] DOR119

[0211] MAVFKLIKPAPLTEKVQSRQGNIY-LYRAMWLIGWIPPKEGVLRYVYLFWTCVPFAFGV FYLPVGFIISYVQEFKNFTPGE-FLTSLQVCINVYGASVKSTITYLFLWRLRKTEILLD SLDKRLANDSDRERIHNMVARCN-YAFLIYSFIYCGYAGSTFLSYALSGRPPWSVYNPF IDWRDGMGSLWIQAIFEYITMSFAV-LQDQLSDTYPLMFTIMFRAHMEVLKDHVRSLRM DPERSEADNYQDLVNCVLDHKTILKCCD-MIRPMISRTIPVQFALIGSVLGLTLVNVFF FSNF-WKGVASLLFVITILLQTFPFCYTCNM-LIDDAQDLSNEIFQSNWVDAEPRYKATL VLFMHHVQQPIIFIAGGIFPISMNSNIT-VAKFAFSIITIVRQMNLAEQFQATGGCGGT GTTCAAGCTAATCAAACCGGCTCCGT-TGACCGAGAAGGTGCAGTCCCGCCAGGGGAAT ATATATCTGTACCGTGCCATGTGGCT-CATCGGATGGATTCCGCCGAAGGAGGGAGTCC TGCGCTACGTGTATCTCTTCTGGACCT-GCGTGCCCTTCGCCTTCGGGGTGTTTTACCT GCCCGTGGGCTTCATCATCAGCTACGTG-CAGGAGTTCAAGAACTTCACGCCGGGCGAG TTC-CTTACCTCGCTGCAGGTGTGCATCAAT-GTGTATGGCGCCTCGGTGAAGTCCACCA TCACCTACCTCTTCCTCTGGCGACTGCG-CAAGACGGAGATCCTTCTGGACTCCCTGGA CAA-GAGGCTGGCGAACGACAGCGATCGC-GAGAGGATCCACAATATGGTGGCGCGCTGC AACTACGCCTTTCTCATCTACAGCT-TCATCTACTGCGGATACGCGGGTTCCACTTTCC TGTCCTACGCCCTCAGTGGTCGTCCTC-CGTGGTCCGTCTACAATCCCTTCATCGATTG GCGC-GATGGCATGGGCAGCCTGTGGATCCAG-GCCATATTCGAGTACATCACCATGTCC TTCGCCGTGCTGCAGGACCAGCTATC-CGACACGTATCCCCTGATGTTCACCATTATGT TCCGGGCCCACATGGAGGTCCTCAAG-GATCACGTGCGGAGCCTGCGCATGGATCCCGA GCGCAGTGAGGCAGACAACTATCAG-GATCTGGTGAACTGCGTGCTGGACCACAAGACT ATACTGAAATGCTGTGACATGATTCGC-CCCATGATATCCCGCACCATCTTCGTGCAAT TCGCGCTGATTGGTTCCGTTTTGGGCCT-GACCCTGGTGAACGTGTTCTTCTTCTCGAA CTTCTGGAAGGGCGTGGCCTCGCTCCT-GTTCGTCATCACCATCCTGCTGCAGACCTTC CCGT-TCTGCTACACCTGCAACATGCTGATC-GACGATGCCCAGGATCTGTCCAACGAGA TTTTCCAGTCCAACTGGGTGGACGCG-GAGCCGCGCTACAAGGCGACGCTGGTGCTCTT CATGCACCATGTTCAGCAGCCCAT-AATCTTCATTGCCGGAGGCATCTTTCCCATCTCT ATGAACAGCAACATAACCGTGGCCAAGT-TCGCCTTCAGCATCATTACAATAGTGCGAC AAAT-GAATCTGGCCGAGCAGTTCCAG

[0212] DOR120

[0213] MTKFFFKRLQTAPLDQEVSSLDAS-DYYYRIAFFLGWTPPKGALLRWIYSLWTLTTMWL GIVYLPLGLSLTYVKHFDRFTPTE-FLTSLQVDINCIGNVIKSCVTYSQMWRFRRMNEL ISSLDKRCVTTTQRRIFHKMVARVNLIV-ILFLSTYLGFCFLTLFTSVFAGKAPWQLYN PLVD-WRKGHWQLWIASILEYCVVSIGTM-QELMSDTYAIVFISLFRCHLAILRDRIANL RQDPKLSEMEHYEQMVACIQDHRTIIQC-SQIIRPILSITIFAQFMLVGIDLGLAAISI LFFPNTIWTI-MANVSFIVAICTESFPCCMLCEHLIEDS-VHVSNALFHSNWITADRSYK SAVLYFLHRAQQPIQFTAGSTFPISVQS-NIAVAKFAFTIITIVNQMNLGEKFFSDRSN GDINP

[0214] DOR120nt

[0215] ATGACCAAGTTCTTCTTCAAGCGCCTG-CAAACTGCTCCACTTGATCAGGAGGTGAGTT CCCTTGATGCCAGCGACTACTACTACCG-CATCGCATTTTTCCTGGGCTGGACCCCGCC CAAGGGGGCTCTGCTCCGATGGATC-

TACTCCCTGTGGACTCTGACCACGATGTGGCTG GGTATCGTGTACCTGCCGCTCGGACT-GAGCCTCACCTATGTGAAGCACTTCGATAGAT TCACGCCGACGGAGTTCCTGACCTCCCT-GCAGGTGGATATCAACTGCATCGGGAACGT GAT-CAAGTCATGCGTAACTTATTCCCAGAT-GTGGCGTTTTCGCCGGATGAATGAGCTT ATCTCGTCCCTGGACAAGAGATGTGT-GACTACGACACAGCGTCGAATTTTCCATAAGA TGGTGGCACGGGTTAATCTCATCGTGAT-TCTGTTCTTGTCCACGTACTTGGGCTTCTG CTTTCTAACTCTGTTOACTTCG-GTTTTCGCTGGCAAAGCTCCTTG-GCAGCTGTACAAC CCACTGGTGGACTGGCG-GAAAGGCCATTGGCAGCTATGGATTGCCTCCATC CTGGAGT ACTGTGTGGTCTCCATTGGCACCATG-CAGGAGTTGATGTCCGACACCTACGCCATAGT GTTCATCTCCTTGTTCCGCTGCCACCTG-GCTATTCTCAGAGATCGCATAGCTAATCTG CGGCAGGATCCGAAACTCAGTGAGATG-GAACACTATGAGCAGATGGTGGCCTGCATTC AGGATCATCGAACCATCATACAGTGCTC-CCAGATTATTCGACCCATCCTGTCGATCAC TATCTTTGCCCAGTTCATGCTGGTTG-GCATTGACTTGGGTCTGGCGGCCATCAGCATC CTCTTCTTTCCGAACACCATTTGGAC-GATCATGGCAAACGTGTCGTTCATCGTGGCCA TCT-GTACAGAGTCCTTTCCATGCTGCAT-GCTCTGCGAGCATCTGATCGAGGACTCCGT CCATGTGAGCAACGCCCTGTTCCACT-CAAACTGGATAACCGCGGACAGGAGCTACAAG TCGGCGGTTCTGTATTTCCTGCAC-CGGGCTCAGCAACCCATTCAATTCACGGCCGGCT CCATATTTCCCATTTCGGTGCAGAGCAA-CATAGCCGTGGCCAAGTTCGCGTTCACAAT CATCA-CAATCGTGAACCAAATGAATCTGGGC-GAGAAGTTCTTCAGTGACAGGAGCAAT GGCGATATAAATCCT

[0216] DOR121

[0217] MLTDKFLRLQSALFRLLGLELLHEQD-VGHRYPWRSICCILSVASFMPLTIAFGLQNVQ NVEQLTDSLCSVLVDLLALCKIGLFLW-LYKDFKFLIGQFYCVLQTETHTAVAEMIVTR ESR-RDQFISAMYAYCFITAGLSACLMSPLSM-LISYHEQVNCSRNFHFPVCKKKYCLIS RILRYSFCRYPWDNMKLSNYIISYFWNV-CAALGVALPTVCVDTLFCSLSHNLCALFQI ARHKM-MHFEGRNTKETHENLKHVFQLYALCLN-LGHFLNEYFRPLICQFVAASLHLCVL CYQLSANILQPALLFYAAFTAAV-VGQVSIYCFCGSSIHSECQLFGQAIYESSWPHLLQ ENLQLVSSLKIAMMRSSLGCPIDGY-FFEANRETLITVSKAFIKVSKKTPQVND

[0218] DOR121

[0219] ATGCTGACGGACAAGTTCCTCCGACTG-CAGTCCGCTTTATTTCGCCTTCTCGGACTCG AAT-TGTTGCACGAGCAGGATGTTGGCCATC-GATATCCTTGGCGCAGCATCTGCTGCAT TCTCTCGGTGGCCAGTTTCATGCCCCT-GACCATTGCGTTTGGCCTGCAAAACGTCCAA AAT-GTGGAGCAATTAACCGACTCACTCT-GCTCGGTTCTCGTGGATTTGCTGGCCCTGT GCAAAATCGGGCTTTTCCTTTGGCTTTA-CAAGGACTTCAAGTTCCTAATAGGGCAGTT CTAT-TGTGTTTTGCAAACGGAAACCCACAC-CGCTGTCGCTGAAATGATAGTGACCAGG GAAAGTCGTCGGGATCAGTTCATCAGT-GCTATGTATGCCTACTGTTTCATTACGGCTG GCCTTTCGGCCTGCCTGATGTCCCCTC-TATCCATGCTGATTAGCTACCACGAACAGGT GAAT-TGCAGCCGAAATTTCCATTTCCCAGTGT-GTAAGAAAAAGTACTGCTTAATATCC AGAATATTAAGATACAGTTTCTGCA-GATATCCCTGGGACAATATGAAGCTGTCCAACT ACATCATTTCCTATTTCTGGAATGTGT-GTGCTGCATTGGGCGTGGCACTGCCCACCGT TTGT-GTGGACACACTGTTCTGTTCTCTGAGC-CATAATCTCTGTGCCCTATTCCAGATT GCCAGGCACAAAATGATG-CACTTTGAGGGCAGAAATACCAAA-GAGACTCATGACAACT TAAAGCACGTGTTTCAAC-TATATGCGTTGTGTTTGAACCTGGGCCATTTCTTAA ACGA ATATTTCAGACCGCTCATCTGC-CAGTTTGTGGCAGCCTCACTGCACTTGT-GTGTCCTG TGCTACCAACTGTCTGCCAATATCCTG-CAGCCAGCGTTACTCTTCTATGCCGCATTTA CGGCAGCAGTTGTTGGCCAGGTGTC-TATATACTGCTTCTGCGGATCGAGCATCCATTC GGAGTGTCAGCTATTTGGCCAGGCCATC-TACGAGTCCAGCTGGCCCCATCTGCTGCAG GAAAACCTGCAGCTTGTAAGCTCCT-TAAAAATTGCCATGATGCGATCGAGTTTGGGAT GTCCCATCGATGGTTACTTCTTCGAGGC-CAATCGGGAGACGCTCATCACGGTGAGTAA AGCGTTTATAAAAGTGTCCAAAAAGA-CACCTCAAGTGAATGAT

[0220] DOR14

[0221] MDYDRIRPVRFLTGVLKWWRLWPRKES-VSTPDWTNWQAYALHVPFTFLFVLLLWLEAI KSRDIQHTADVLLICLTTTALGGKVINI-WKYAHVAQGILSEWSTWDLFELRSKQEVDM WRFE-HRRFNRVFMFYCLCSAGVIPFIVIQPLF-DIPNRLPFWMWTPFDWQQPVLFWYAF IYQATTIPIACACNVTMDAVNWYLM-LHLSLCLRMLGQRLSKLQHDDKDLREKFLELIH LHQRLKQQALSIEIFISKSTFTQILVSS-LIICFTIYSMQMDLPGFAAMMQYLVAMIMQ VMLP-TIYGNAVIDSANMLTDSMYNSDWPDMN-CRMRRLVLMFMVYLNRPVTLKAGGFFH IGLPLFTKVVFSTLENPCISYLYFRP

[0222] DOR14nt

[0223] ATGGACTACGATCGAATTCGACCGGTGC-GATTTTTGACGGGAGTGCTGAAATGGTGGC GTCTCTGGCCGAGGAAGGAATCGGTGTC-CACACCGGACTGGACTAACTGGCAGGCATA TGC-CTTGCACGTTCCATTTACATTCT-TGTTTGTGTTGCTTTTGTGGTTGGAGGCAATC AAGAGCAGGGATATACAGCATACCGC-CGATGTCCTTTTGATTTGCCTAACCACCACTG CCT-TGGGAGGTAAAGTTATCAATATCTG-GAAGTATGCCCATGTGGCCCAAGGCATTTT GTCCGAGTGGAGCACGTGGGATCTTTTC-GAGCTGAGGAGCAAACAGGAAGTGGATATG TGGCGATTCGAGCATCGACGTTTCAATCGT-

GTTTTATGTTTTACTGTTTGTGCAGTG CTGGTGTAATCCCATTTATTGTGAT-TCAACCGTTGTTTGATATCCCAAATCGATTGCC CTTCTGGATGTGGACACCATTCGATTG-GCAGCAGCCTGTTCTCTTCTGGTATGCATTC ATC-TATCAGGCCACAACCATTCCTATTGCCT-GTGCTTGCAACGTAACCATGGACGCTG TTAATTGGTACTTGATGCTGCATCTGTC-CTTGTGTTTGCGTATGTTGGGCCAGCGATT GAG-TAAGCTTCAGCATGATGACAAGGATCT-GAGGGAGAAGTTCCTGGAACTGATCCAT CTGCACCAGCGACTCAAGCAACAGGCCT-TGAGCATTGAAATCTTTATTTCGAAGAGCA CGT-TCACCCAAATTCTGGTCAGTTCCCTTAT-CATTTGCTTCACCATTTACAGCATGCA GATGGACTTGCCAGGATTTGCCGCCAT-GATGCAGTACCTAGTGGCCATGATCATGCAG GTCATGCTGCCCACCATATATGG-TAACGCCGTCATCGATTCTGCAAATATGTTGACCG ATTCCATGTACAATTCGGATTGGCCG-GATATGAATTGCCGAATGCGTCGCCTAGTTTT AAT-GTTTATGGTGTACTTAAATCGACCGGT-GACCTTAAAAGCCGGTGGCTTTTTTCAT ATTGGTTTACCTCTGTTTACCAAGGTTG-TATTTTCTACTCTGGAAAATCCTTGTATAA GTTATCTTTATTTCAGACCA

[0224] DOR16

[0225] MTDSGQPAIADHFYRIPRISGLIVGLW-PQRIRGGGGRPWHAHLLFVFAFAMVVVGAVG EVSYGCVHLDNLVVALEAFCPGTT-KAVCVLKLWVFFRSNRRWAELVQRLRAILWESRR QEAQRMLVGLATTANRLSLLLLSSGTAT-NAAFTLQPLIMGLYRWIVQLPGQTELPFNI ILPS-FAVQPGVFPLTYVLLTASGACTVFAFS-FVDGFFICSCLYICGAFRLVQQDIRRI FADLHGDSVDVFTEEMNAEVRHR-LAQVVERHNAIIDFCTDLTRQFTVIVLMHFLSAAF VLCSTILDIMLVSPFSEAFLWGGYPWV-CRATGFSHRLHSAAVLKVFPCFHCLLFFPGF SSRSV-LIRFSRFVCLLCGCGCGSLRWQFISA

[0226] DOR16nt

[0227] ATGACTGACAGCGGGCAGCCTGCCAT-TGCCGACCACTTTTATCGGATTCCCCGCATCT CCG-GCCTCATTGTCGGCCTCTGGCCGCAAAG-GATAAGGGGCGGGGGCGGTCGTCCTTG GCACGCCCATCTGCTCTTCGTGTTCGC-CTTCGCCATGGTGGTGGTGGGTGCGGTGGGC GAG-GTGTCGTACGGCTGTGTCCACCTGGA-CAACCTGGTGGTGGCGCTGGAGGCCTTCT GCCCCGGAACCACCAAGGCGGTCT-GCGTTTTGAAGCTGTGGGTCTTCTTCCGCTCCAA TCGCCGGTGGGCGGAGTTGCTCCAGCGC-CTGCGGGCTATTTTGTGGGAATCGCGGCGG CAG-GAGGCCCAGAGGATGCTGGTCGGACTG-GCCACCACGGCCAACAGGCTCAGCCTGT TGTTGCTCAGCTCTGGCACGGCGA-CAAATGCCGCCTTCACCTTGCAACCGCTGATTAT GGGTCTCTACCGCTGGATTGTGCAGCT-GCCAGGTCAAACCGAGCTGCCCTTTAATATC ATACTGCCCTCGTTTGCCGTGCAGCCAG-GAGTCTTTCCGCTCACCTACGTGCTGCTGA CCGCT-TCCGGTGCCTGCACCGTTTTCGCCT-TCAGCTTCGTGGACGGATTCTTCATTTG CTCGTGCCTCTACATCTGCGGCGCTTTC-CGGCTGGTGCAGCAGGACATTCGCAGGATA TTTGCCGATTTGCATGGCGACTCAGTG-GATGTGTTCACCGAGGAGATGAACGCGGAGG TGCGGCACAGACTGGCCCAAGTTGTC-GAGCGGCACAATGCGATTATCGATTTCTGCAC GGACCTAACACGCCAGTTCACCGT-TATCGTTTTAATGCATTTCCTGTCCGCCGCCTTC GTCCTCTGCTCGACCATCCTGGACAT-CATGTTGGTGAGCCCCTTTTCAGAGGCCTTCC TTTGGGGCGGGTATCCT-TGGGTTTGTCGCGCCACTGGCTTTTCG-CATCGCCTGCATTC GGCGGCTGTTT-TAAAAGTTTTTCCCTGTTTTCACTGTTTGCTGTTT TTCCCTGGCTTT TCCAGCCGCTCCGTTCTGATTCG-GTTTTCCCGATTTGTTTGTTTGCTTTGTGGCTGCG GCTGCGGCTCTCTCCGGTGGCAATT-TATAAGCCCATGA

[0228] DOR19

[0229] MVTEDFYKYQVWYFQILGVWQLPT-WAADHQRRFQSMRFGFILVILFIMLLLFSFEMLN NISQVREILKVFFMFATEISCMAK-LLHLKLKSRKLAGLVDAMLSPEFGVKSEQEMQML ELDRVAVVRMRNSYGIMSLGAAS-LILIVPCFDNFGELPLAMLEVCSIEGWICYWSQYL FHSICLLPTCVLNITYDSVAY-SLLCFLKVQLQMLVLRLEKLGPVIEPQDNEKIAMELR ECAAYYNRIVRFKDLVELFIKGPGS-VQLMCSVLVLVSNLYDMSTMSIANGDAIFMLKT CIYQLVMLWQIFIICYASNEVTVQSSR-LCHSIYSSQWTGWNRANRRIVLLMMQRFNSP MLL-STFNPTFAFSLEAFGSVGQQKFLYIS-FITGYALLLSDRQLLLQLLRTAEARQQLN FETPQHLKIFKPIFKSTQNVMHVH

[0230] DOR19nt

[0231] ATGGTTACGGAGGACTTTTATAAGTAC-CAGGTGTGGTACTTCCAAATCCTTGGTGTTT GGCAGCTCCCCACTTGGGCCGCAGAC-CACCAGCGTCGTTTTCAGTCCATGAGGTTTGG CTTCATCCTGGTCATCCTGTTCATCAT-GCTGCTGCTTTTCTCCTTCGAAATGTTGAAC AACATTTCCCAAGTTAGGGAGATC-CTAAAGGTATTCTTCATGTTCGCCACGGAAATAT CCTGCATGGCCAAATTATTG-CATTTGAAGTTGAAGAGCCG-CAAACTCGCTGGCTTGGT TGATGCGATGTTGTC-CCCAGAGTTCGGCGTTAAAAGTGAACAGGAAAT GCAGATGCTG GAATTGGATAGAGTGGCGGTTGTC-CGCATGAGGAACTCCTACGGCATCATGTCCCTGG GCGCGGCTTCCCTGATCCTTATAGTTC-CCTGTTTCGACAACTTTGGCGAGCTACCACT GGC-CATGTTGGAGGTATGCAGCATCGAGG-GATGGATCTGCTATTGGTCGCAGTACCTT TTCCACTCGATTTGCCTGCTGCCCACT-TGTGTGCTGAATATAACCTACGACTCGGTGG CCTACTCGTTGCTCTGTTTCTTGAAGGT-TCAGCTACAAATGCTGGTCCTGCGATTAGA AAAGT-TGGGTCCTGTGATCGAACCCCAG-GATAATGAGAAAATCGCAATGGAACTGCGT GAGTGTGCCGCCTACTACAACAGGAT-TGTTCGTTTCAAGGACCTGGTGGAGCTGTTCA

TAAAGGGGCCAGGATCTGTGCAGCTCAT-GTGTTCTGTTCTGGTGCTGGTGTCCAACCT GTAC-GACATGTCCACCATGTCCATTGCAAACG-GCGATGCCATCTTTATGCTCAAGACC TGTATCTATCAGCTGGTGATGCTCTG-GCAGATCTTCATCATTTGCTACGCCTCCAACG AGG-TAACTGTCCAGAGCTCTAGGTTGTGTCA-CAGCATCTACAGCTCCCAATGGACGGG ATGGAACAGGGCAAACCGCCGGATTGTC-CTTCTCATGATGCAGCGCTTTAATTCCCCG ATGCTC-CTGAGCACCTTTAACCCCAC-CTTTGCTTTCAGCTTGGAGGCCTTTGGTTCTG TAGGGCAGCAGAAATTCCTTTATATAT-CATTTATTACTGGTTATGCTCTTCTCCTTTC AGATCGTCAACTGCTCCTACAGCTACT-TCGCACTGCTGAAGCGCGTCAACAGTTAAAT TTC-GAAACACCGCAGCACCTAAA-GATTTTCAAGCCGATTTTTAAAAGCACTCAAAACG TTATGCACGTACAT

[**0232**] DOR20

[**0233**] MSKGVEIFYKGQKAFLNILSLWPQIER-RWRIIHQVNYVHVIVFWVLLFDLLLVLHVMA NLSYMSEVVKAIFILATSAGHTTKLLSI-KANNVQMEELFRRLDNEEFRPRGANEELIF AAAC-ERSRKLRDFYGALSFAALSMILIPQ-FALDWSHLPLKTYNPLGENTGSPAYWLLY CYQCLALSVSCITNIGFDSLCSS-LFIFLKCQLDILAVRLDKIGRLITTSGGTVEQQLK ENIRYHMTIVELSKTVERLLCKPISV-QIFCSVLVLTANFYAIAVWSCEFATRRLSVCD LSGVH-VDSDFYIVLLCRVGIPYPKCLPRPVMN-FIVSEVTQRSLDLPHELYKTSWVDWD YRSRRIALLFMQRLHSTLRIRTLNPSLG-FDLMLFSSVSSFRVLTFLCTVANFHNEAH

[**0234**] DOR20nt

[**0235**] ATGAGCAAAGGAGTAGAAATCTTTTA-CAAGGGCCAGAAGGCATTCTTGAACATCCTCT CGTTGTGGCCTCAGATAGAACGCCGGTG-GAGAATCATCCACCAGGTGAACTATGTCCA CGTAATTGTGTTTTGGGTGCT-GCTCTTTGATCTCCTCTTGGTGCTCCAT-GTGATGGCT AATTTGAGCTACATGTCCGAGGTTGT-GAAAGCCATCTTTATCCTGGCCACCAGTGCAG GGCACACCACCAAGCTGCTGTCCAT-AAAGGCGAACAATGTGCAGATGGAGGAGCTCTT TAGGAGATTGGATAACGAAGAGTTC-CGTCCTAGAGGCGCCAACGAAGAGTTGATCTTT GCAGCAGCCTGTGAAAGAAGTAG-GAAGCTTCGGGACTTCTATGGAGCGCTTTCGTTTG CCGCCTTGAGCATGATTCTCATAC-CCCAGTTCGCCTTGGACTGGTCCCACCTTCCGCT CAAAACATACAATCCGCTTGGC-GAGAATACCGGCTCACCTGCTTATTGGCTCCTCTAC TGCTATCAGTGTCTGGCCTTGTCCG-TATCCTGCATCACCAACATAGGATTCGACTCAC TCTGCTCCTCACTGTTCATCTTCCT-CAAGTGCCAGCTGGACATTCTGGCCGTGCGACT GGACAAGATCGGTCGGTTAATCACTACT-TCTGGTGGCACTGTGGAACAGCAACTTAAG GAAAATATCCGCTATCACATGAC-CATCGTTGAACTGTCGAAAACCGTGGAGCGTCTAC TTTGCAAGCCGATTTCGGTGCAGATCT-TCTGCTCGGTTTTGGTGCTGACTGCCAATTT CTAT-GCCATTGCTGTGGTGAGCTGTGAATTCG-CAACAAGAAGACTATCAGTATGTGAC CTATCAGGCGTGCATGTTGATTCA-GATTTTTATATTGTGCTACTATGCCGGGTGGGTA TTCCATATCCGAAATGCCTCCCCAGGC-CAGTAATGAATTTCATCGTCAGTGAGGTAAC CCAGCGCAGCCTGGACCTTCCGCAC-GAGCTGTACAAGACCTCCTGGGTGGACTGGGAC TACAGGAGCCGAAGGATTGCGCTC-CTCTTTATGCAACGCCTTCACTCGACCTTGAGGA TTAGGACACTTAATCCAAGTCTTG-GTTTTGACTTAATGCTCTTCAGCTCGGTGAGTTC TTTCCGTGTTTTGACTTTTTTGTGCACT-GTAGCCAATTTCCATAATGAGGCTCAT

[**0236**] DOR24

[**0237**] MDSFLQVQKSTIALLGFDLFSENREM-WKRPYRAMNVFSIAAIFPFILAAVLHNWKNVL LLADAMVALLITILGLFKFSMILYLRRD-FKRLIDKFRLLMSNEAEQGEEYAEILNAAN KQDQRMCTLFRTCFLLAWALNSVL-PLVRMGLSYWLAGHAEPELPFPCLFPWNIHIIRN YVLSFIWSAFASTGVVLPAVSLDTIFCS-FTSNLCAFFKIAQYKVVRFKGGSLKESQAT LNKVFA-LYQTSLDMCNDLNQCYQPIICAQFFISS-LQLCMLGYLFSITFAQTEGVYYAS FIATIIIQAYIYCYCGENLKTESASFEW-AIYDSPWHESLGAGGASTSICRSLLISMMR AHRG-FRITGYFFEANMEAFSSIVRTAMSYITMLRSFS

[**0238**] DOR24nt

[**0239**] GGCACGAGCCTTGTCGACATGGA-CAGTTTTCTGCAAGTACAGAAGAGCACCATTGCTC TTCTGGGCTTTGATCTCTTTAGT-GAAAATCGAGAAATGTGGAAACGCCCCTATAGAGC AATGAATGTGTTTAGCATAGCTGC-CATTTTTCCCTTTATCCTGGCAGCTGTGCTCCAT AATTGGAAGAATGTATTGCTGCTGGC-CGATGCCATGGTGGCCCTACTAATAACCATTC TGGGCCTATTCAAGTTTAGCAT-GATACTTTACTTACGTCGCGATTTCAAGCGACTGAT TGACAAATTTCGTTTGCTCATGTCGAAT-GAGGCGGAACAGGGCGAGGAATACGCCGAG ATTCTCAACGCAGCAAACAAGCAGGAT-CAACGAATGTGCACTCTGTTTAGGACTTGTT TCCTCCTCGCCTGGGCCTTGAATAGTGT-TCTGCCCCTCGTGAGAATGGGTCTCAGCTA TTGGT-TAGCAGGTCATGCAGAGCCCGAGTTGC-CTTTTCCCTGTCTTTTTCCCTGGAAT ATCCACATCATTCGCAATTAT-GTTTTGAGCTTCATCTG-GAGCGCTTTCGCCTCGACAG GTGTGGTTTTACCT-GCTGTCAGCTTGGATACCATATTCTGTTCCTTCAC CAGCAACCT GTGCGCCTTCTTCAAAATTGCGCAG-TACAAGGTGGTTAGATTTAAGGGCGGATCCCTT AAAGAATCACAGGCCACATTGAA-CAAAGTCTTTGCCCTGTACCAGACCAGCTTGGATA TGTGCAACGATCTGAATCAGTGCTAC-CAACCGATTATCTGCGCCCAGTTCTTCATTTC ATCTCTGCAACTCTGCATGCTGG-GATATCTGTTCTCCATTACTTTTGCCCAGACAGAG GGCGTGTACTATGCCTCTTTCATAGC-CACCATCATTATACAAGCCTATATCTACTGCT ACT-

GCGGGGAGAACCTGAAGACGGAGAGTGC-
CAGCTTCGAGTGGGCCATCTACGACAG
TCCGTGGCACGAGAGTTTGGGTGCTG-
GTGGAGCCTCTACCTCGATCTGCCGATCCTTG
CTGATCAGCATGATGCGGGCTCATCGGG-
GATTCCGCATTACGGGATACTTCTTCGAGG CAAA-
CATGGAGGCCTTCTCATCGATTGTTCG-
CACGGCTATGTCCTACATCACAATGCT
GAGATCATTCTCCTAAATGTGGTTTGAC-
CACAAGGCTTTGGATTGATTTTTGTGCAAT
TTTTGTTTTATTGCTGAGCATGCGTTGC-
CGTACGACATTTAACAATCGATCTTACGTA ATTTA-
CATATGATAATCTCACATATTGTTCGT-
TAAGCACTAAGTAGAATGTAGAATGT
GAATTGGCTGTAGAAATGCACAGAT-
GAAGCACGAAAAAAAAAAAAAAAAAAAAAAAA

[0240] DOR25

[0241] MNDSGYQSNLSLLRVFLDEFRSVL-
RQESPGLIPRLAFYYVRAFLSLPLYRWINLFIMC
NVMTIFWTMFVALPESKNVIEMGD-
DLVWISGMALVFTKIFYMHLRCDEIDELISDFEY
YNRELRPHNIDEEVLGWQRLCYVIESG-
LYINCFCLVNFFSAAIFLQPLLGEGKLPFHS
VYPFQWHRLDLHPYTFWFLYIWQS-
LTSQHNLMSILMVDMVGISTFLQTALNLKLLCIE
IRKLGDMEVSDKRFHEEFCRVVRFHQHI-
IKLVGKANRAFNGAFNAQLMASFSLISIST FET-
MAAAAvDPKMAAKFVLLMLVAFIQLSL-
WCVSGTLVYTQSVEVAQAAFDINDWHTK
SPGIQRDISFVILRAQKPLMYVAEP-
FLPFTLGTYMLVLKNCYRLLALMQESM

DOR25nt

[0242] ATGAACGACTCGGGTTATCAAT-
CAAATCTCAGCCTTCTGCGGGTTTTTCTCGACGAGT
TCCGATCGGTTCTGCGGCAGGAAAGTC-
CCGGTCTCATCCCACGCCTGGCTTTTTACTA TGT-
TCGCGCCTTTCTGAGCTTGCCCCTGTAC-
CGATGGATCAACTTGTTCATCATGTGC
AATGTGATGACCATTTTCTGGACCATGT-
TCGTGGCCCTGCCCGAGTCGAAGAACGTGA
TCGAAATGGGCGACGACTTGGTTTG-
GATTTCGGGGATGGCACTGGTGTTCACCAAGAT
CTTTTACATGCATTTGCGTTGCGAC-
GAGATCGATGAACTTATTTCGGATTTTGAATAC
TACAACCGGGAGCTGAGACCCCAT-
AATATCGATGAGGAGGTGTTGGGTTGGCAGAGAC
TGTGCTACGTGATAGAATCGGGTC-
TATATATCAACTGCTTTTGCCTGGTCAACTTCTT
CAGTGCCGCTATTTTCCTGCAACCTCT-
GTTGGGCGAGGGAAAGCTGCCCTTCCACAGC GTC-
TATCCGTTTCAATGGCATCGCTTG-
GATCTGCATCCCTACACGTTCTGGTTCCTCT
ACATCTGGCAGAGTCTGACCTCGCAGCA-
CAACCTAATGAGCATTCTAATGGTGGATAT GGTAG-
GCATTTCCACGTTCCTCCAGACGGCGCT-
CAATCTCAAGTTGCTTTGCATCGAG
ATAAGGAAACTGGGGGACATGGAGGT-
CAGTGATAAGAGGTTCCACGAGGAGTTTTGTC
GTGTGGTTCGCTTCCACCAGCACATTAT-
CAAGTTGGTGGGGAAAGCCAATAGAGCTTT
CAATGGCGCCTTCAATGCACAATTAATG-
GCCAGTTTCTCCCTGATTTCCATATCCACT TTC-
GAGACCATGGCTGCAGCGGCTGTGGATC-
CCAAAATGGCCGCCAAGTTCGTGCTTC
TCATGCTGGTGGCATTCATTCAACT-
GTCGCTTTGGTGCGTCTCTGGAACTTTGGTTTA
TACTCAGTCAGTGGAGGTGGCTCAGGCT-
GCTTTTGATATCAACGATTGGCACACCAAA TCGC-
CAGGCATCCAGAGGGATATATCCTTTGT-
GATACTACGAGCCCAGAAACCCCTGA
TGTATGTGGCCGAACCATTTCTGCCCT-
TCACCCTGGGAACCTATATGCTTGTACTGAA
GAACTGCTATCGTTTGCTGGCCCTGATG-
CAAGAATCGATGTAG

[0243] DOR28

[0244] MYSPEEAAELKRRNYRSIREMIRL-
SYTVGFNLLDPSRCGQVLRIWTIVLSVSSLASLY
GHWQMLARYIHDIPRIGETAGTALQFLT-
SIAKMWYFLFAHRQIYELLRKARCHELLQK CEL-
FERMSDLPVIKEIRQQVESTMNRYWAST-
RRQILIYLYSCICITTNYFINSFVINL
YRYFTKPKGSYDIMLPLPSLYPAWEHK-
GLEFPYYHIQMYLETCSLYICGMCAVSFDGV FIVL-
CLHSVGLMRSLNQMVEQATSELVPP-
DRRVEYLRCCIYQYQRVANFATEVNNCFR
HITFTQFLLSLFNWGLALFQMS-
VGLGNNSSITMIRMTMYLVAAGYQIVVYCYNGQRFA
TASEEIANAFYQVRWYGESREFRHLIRM-
MLMRTNRGFPRLDVSFMQMSLPTLMAVSSG AEQS-
RGPAGPAGPAGPPPRVPSYSQFHLID-
SQMVRTSGQYFLLLQNVNQK

[0245] DOR28nt

[0246] ATGTACTCACCGGAAGAGGCGGC-
CGAACTGAAGAGGCGCAACTATCGCAGCATCAGG
GAGATGATCCGACTCTCCTATACG-
GTGGGCTTCAACCTGTTGGATCCTTCCCGATGCG
GACAGGTGCTCAGAATCTGGACAAT-
TGTCCTTAGCGTGAGTAGCTTGGCATCGCTTTA
TGGGCACTGGCAAATGTTAGCCAGGTA-
CATTCATGATATTCCACGCATTGGAGAGACC GCTG-
GAACTGCCCTGCAGTTCCTAACATCGAT-
AGCAAAGATGTGGTACTTTCTGTTTG
CCCATAGACAGATATACGAATTGCTAC-
GAAAGGCGCGCTGCCATGAATTACTCCAAAA
GTGTGAGCTCTTTGAAAGGATGTCA-
GATCTACCTGTTATCAAAGAGATTCGCCAGCAG
GTTGAGTCCACGATGAATCGG-
TACTGGGCCAGCACTCGTCGGCAAAT-
TCTTATCTATT TGTACAGCTGTATTTGTATTACTA-
CAAACTACTTTATCAACTCCTTCGTAATCAACCT
CTATCGCTATTTCACTAAACCGAAAG-
GATCCTACGACATAATGTTACCTCTGCCATCT CTG-
TATCCCGCCTGGGAGCACAAGGGATTA-
GAGTTTCCCTACTATCATATACAGATGT
ACCTGGAAACCTGTTCTCTGTATATCT-
GCGGCATGTGTGCCGTTAGCTTTGATGGAGT CTT-
TATTGTCCTGTGCCTTCATAGCGTGG-
GACTTATGAGGTCACTTAACCAAATGGTG
GAACAAGCCACATCTGAGTTGGTTCCTC-
CAGATCGCAGGGTTGAATACTTGCGATGCT GTATT-
TATCAGTACCAACGAGTGGCGAACTTTG-
CAACCGAGGTTAACAACTGCTTTCG
GCACATCACTTTCACGCAGTTCCTGCT-
TAGCCTTTTCAACTGGGGCCTGGCCTTGTTC

CAAATGAGCGTCGGATTGGGCAACAA-CAGCAGCATCACCATGATCCGGATGACCATGT ACCTGGTGGCAGCCGGCTATCAGATAGT-TGTGTACTGCTACAATGGCCAGCGATTTGC GACT-GCTAGCGAGGAGATTGCCAACGCCTTT-TACCAGGTGCGATGGTACGGAGAGTCC AGGGAGTTCCGCCACCTCATCCGCAT-GATGCTGATGCGCACGAACCGGGGATTCAGGC TGGACGTGTCCTGGTTCATGCAAATGTC-CTTGCCCACACTCATGGCGGTGAGTAGCGG AGCA-GAGCAGAGCAGGGGTCCTGCAGGTCCTG-CAGGTCCTGCAGGTCCACCCCCAAGG GTCCCCTCCTACAGCCAGTTCCACT-TGATTGATTCGCAGATGGTCCGGACAAGTGGAC AGTACTTCCTGCTGCTGCAGAACGTCAACCAGAAA

[0247] DOR30

[0248] MAVSTRVATKQEVPESRRAFRNLFNCFY-ALGMQAPDGSRPTTSSTWQRIYACFSVVMY VWQLLLVPTFFVISYRYMGGMEITQVLT-SAQVAIDAVILPAKIVALAWNLPLLRRAEH HLAAL-DARCREQEEFQLILDAVRFCNYLVWFY-QICYAIYSSSTFVCAFLLGQPPYALY LPGLDWQRSQMQFCIQAWIEFLIMNWT-CLHQASDDVYAVIYLYVVRIQVQLLARRVEK LGT-DDSGQVEIYPDERRQEEHCAELQR-CIVDHQTMLQLLDCISPVISRTIFVQFLITA AIMGTTMINIFIFANTNTKIASIIYL-LAVTLQTAPCCYQATSLMLDNERLALAIFQCQ WLGQSARFRKMLLYYLHRAQQPITLTA-MKLFPINLATYFSIAKFSFSLYTLIKGMNLG ERFNRTN

[0249] DOR30nt

[0250] ATGGCGGTGAGCACTCGTGTGGCCA-CAAAGCAGGAAGTGCCCGAATCCCGGCGAGCGT TTAGGAATCTCTTCAATTGCTTCTATGC-CCTTGGCATGCAGGCACCGGATGGCAGTCG ACCGACCACGAGCAGCACATGGCAACG-CATCTACGCCTGCTTCTCGGTGGTCATGTAC GTGTGGCAACTGCTGCTGGTGCCCACAT-TCTTTGTGATCAGCTATCGGTACATGGGCG GCATG-GAGATTACCCAGGTGCTGACCTCCGC-CCAGGTGGCCATCGATGCGGTCATTCT GCCGGCCAAGATTGTGGCACTGGCGTG-GAATTTGCCATTGCTGCGCAGAGCAGAGCAT CATCTGGCCGCCTTGGATGCGCGGTG-CAGGGAACAGGAGGAGTTCCAATTGATCCTCG ATGCGGTGAGGTTTTGCAACTATCTGG-TATGGTTCTACCAGATCTGCTATGCCATCTA CTC-CTCGTCGACATTTGTGTGCGCCTTCCT-GCTGGGCCAACCGCCATATGCCCTCTAT TTGCCTGGCCTCGATTGGCAGCGTTC-CCAGATGCAGTTCTGCATCCAGGCCTGGATTG AGT-TCCTTATCATGAACTGGACGTGCCTG-CACCAAGCTAGCGATGATGTGTACGCCGT TATCTATCTGTATGTGGTCCGGAT-TCAAGTGCAATTGCTGGCCAGGCGGGTGGAGAAG CTGGGCACGGATGATAGTGGCCAGGTG-GAGATCTATCCCGATGAGCGGCGGCAGGAGG AGCATTGCGCGGAACTGCAGCGCTGCAT-TGTAGATCACCAGACGATGCTGCAGCTGCT CGACT-GCATTAGTCCCGTCATCTCGCGTAC-CATATTCGTTCAGTTCCTGATCACCGCC GCCATCATGGGCACCACCATGATCAA-CATTTTCATTTTCGCCAATACGAACACGAAGA TCG-CATCGATCATTTACCTGCTGGCGGTGAC-CCTGCAGACGGCTCCATGTTGCTATCA GGCCACCTCGCTGATGTTGCACAAC-GAGAGGCTGGCCCTGGCCATCTTCCAGTGCCAG TGGCTGGGCCAGAGTGCCCGGTTCCG-TAAGATGCTGCTCTACTATCTTCATCGCGCCC AGCAGCCCATCACGCTGACCGCCAT-GAAGCTGTTTCCCATCAATCTGGCCACGTACTT CAGTATAGCCAAGTTCTCGTTTTCGCTC-TACACGCTCATCAAGGGGATGAATCTCGGC GAGC-GATTCAACAGGACAAAT

[0251] DOR31

[0252] MIFKYIQEPVLGSLFRSRDSLIYLNR-SIDQMGWRLPPRTKPYWWLYYIWTLVVIVLVF IFIPYGLIMTGIKEFKN-FTTTDLFTYVQVPVNTNASIMKGIIV-LFMRRRFSRAQKMMD AMDIRCTKMEEKVQV HRAAALCNRVVVIYHCIYFGYLSMALT-GALVIGKTPFCLYNPL VNPDDHFYLATAIESVTMAGI-ILANLILDVYPIIYVVVLRIHMELLSERIKTLRTDVE KGDDQHYAELVECVKDHKLIVEYGNTL-RPMISATMFIQLLSVGLLLGLAAVSMQFYNT VMERV-VSGVYTIAILSQTFPFCYVCEQLSSD-CESLTNTLFHSKWIGAERRYRTTMLYF IHNVQQSILFTAGGIFPICLNTNIKMAK-FAFSVVTIVNEMDLAEKLRRE

[0253] DOR31nt

[0254] ATGATTTTTAAGTACATTCAAGAGC-CAGTCCTTGGATCCTTATTTCGATCCCGGGATT CGCTGATCTACTTAAACAGATCCATA-GATCAAATGGGATGGAGACTGCCGCCACGAAC TAAGCCGTACTGGTGGCTCTATTA-CATTTGGACATTGGTGGTCATAGTACTCGTCTTT ATCTTTATACCCTATGGACTGATAAT-GACTGGAATAAAGGAGTTCAAGAACTTCACGA CCACGGATCTGTTTACGTATGTCCAGGT-GCCGGTTAACACCAATGCTTCGATCATGAA GGGCATTATAGTGTTGTTTATGCGGCG-GCGATTTTCAAGGGCTCAGAAGATGATGGAC GCCATGGACATTCGATGCACCAAGATG-GAGGAGAAAGTCCAGGTGCACCGAGCAGCAG CCTTATGCAATCGTGTTGTTGTGATT-TACCATTGCATATACTTCGGCTATCTATCCAT GGC-CTTAACCGGAGCTCTGGTGATTGGGAA-GACTCCATTCTGTTTGTACAATCCACTG GTTAACCCCGACGATCATTTCTATCTG-GCCACTGCCATTGAATCGGTCACCATGGCTG GCAT-TATTCTGGCCAATCTCATTTTGGACG-TATATCCCATCATATATGTGGTCGTTCT GCGGATCCACATGGAGCTCTTGAGT-GAGCGAATCAAGACGCTGCGTACTGATGTGGAA AAAGGCGACGATCAACATTATGC-CGAGCTGGTGGAGTGTGTAAAGGATCACAAGCTAA TTGTCGAATATGGAAACACTCTGCGTC-CCATGATATCCGCCACGATGTTCATCCAACT ACT-ATCCGTTGGCTTACTTTTGGGTCTG-GCAGCGGTGTCCATGCAGTTCTATAACACC GTAATGGAGCGTGTTGTCTCCGGGGTC-TACACCATAGCCATTCTATCCCAGACCTTTC CATTTTGCTATGTCTGTGAGCAGCTGAG-CAGCGATTGCGAATCCCTGACCAACACACT GTTC-

CATTCCAAGTGGATTGGAGCTGAGCCAC-GATACAGAACCACGATGTTGTACTTC ATTCACAATGTTCAGCAGTCGATTTTGT-TCACTGCGGGCGGAATTTTCCCCATATGTC TAAA-CACCAATATAAAGATGGCCAAGT-TCGCTTTCTCAGTGGTGACCATTGTAAATGA GATGGACTTGGCCGAGAAATTGAGAAGGGAG

[0255] DOR32

[0256] MEPVQYSYEDFARLPTTVFWIMGYDM-LGVPKTRSRRILYWIYRFLCLASHGVCVGVMV FRM-VEAKTIDNVSLIMRYATLVTYIINSDTK-FATVLQRSAIQSLNSKLAELYPKrTLD RIYHRVNDHYWTKSFVYLVIIYIGSSIM-VVIGPIITSIIAYFTHNVFTYMHCYPYFLY DPEKD-PVWIYISIYALEWLHSTQMVISNIGADI-WLLYFQVQINLHFRGIIRSLADHKP SVKHDQEDRKFIAKIVDKQVHLVS-LQNDLNGIFGKSLLLSLLTTAAVICTVAVYTLIQ GPTLEGFTYVIFIGTSVMQVYLV-CYYGQQVLDLSGEVAHAVYNHDFHDASIAYKRYLL IIIIRAQQPVELNAMGYLSISLDT-FKQLMSVSYRVITMLMQMIQ

[0257] DOR32nt

[0258] ATGGAACCTGTGCAGTACAGCTACGAG-GATTTCGCTCGATTGCCCACGACGGTGTTCT GGAT-CATGGGCTACGACATGCTGGGCGTTC-CGAAGACCCGCTCTCGCAGGATACTATA CTGGATATATCGTTTCCTCTGTCTCGC-CAGCCATGGGGTCTGTGTAGGAGTCATGGTA TTTCGTATGGTGGAGGCAAAGACCAT-TGACAATGTTTCGCTGATCATGCGGTATGCCA CTCTGGTCACCTATATCATCAACTCG-GATACGAAATTCGCAACTGTCTTACAAAGGAG TGCAATTCAAACTCTAAACTCAAAACTG-GCCGAACTATATCCGAAGACCACGCTGGAC AGGATCTATCACCGGGTGAATGATCAC-TATTGGACCAAGTCATTTGTATATTTGGTTA TTATC-TACATTGGTTCGTCGATTATGGTTGT-TATTGGACCGATTATTACGTCGATTAT AGCTTACTTCACGCACAACGTTTTCAC-CTACATGCACTGCTATCCGTACTTTTTGTAT GATC-CTGAGAAGGATCCGGTTTGGATCTACAT-CAGCATCTATGCTCTGGAATGGTTGC ACAGCACACAGATGGTCATTTCGAACAT-TGGCGCGGATATCTGGCTGCTGTACTTTCA GGTG-CAGATAAATCTCCACTTCAGGGGCAT-TATACGATCACTGGCGGATCACAAGCCC AGTGTGAAGCACGACCAGGAGGACAG-GAAATTCATTGCGAAAATTGTCGACAAGCAGG TGCACCTGGTCAGTTTGCAAAACGATCT-GAATGGTATCTTTGGAAAATCGCTGCTTCT AAGC-CTGCTGACCACCGCAGCGGTTATCTG-CACGGTGGCGGTGTACACTCTGATTCAG GGTCCCACCTTGGAGGGCTTCACCTAT-GTGATCTTCATCGGGACTTCTGTGATGCAGG TCTACCTGGTGTGCTATTACGGTCAG-CAAGTTCTCGACTTGAGCGGCGAGGTGGCCCA CGCCGTGTACAATCATGATTTTCACGAT-GCTTCTATAGCGTACAAGAGGTACCTGCTC ATAAT-CATTATCAGGGCGCAGCAGCCCGTG-GAACTTAATGCCATGGGCTACCTGTCCA TTTCGCTGGACACCTTTAAACAGCTGAT-GAGCGTCTCCTACCGGGTTATAACCATGCT CATG-CAGATGATTCAG

[0259] DOR37

[0260] **protein sequence is incomplete and is in progress**

[0261] KVDSTRALVNHWRIFRIMGIHPPGKRTF-WGRHYTAYSMVWNVTFHICIWVSFSVNLLQ SNS-LETFCESLCVTMPHTLYMLKLINVRRM-RGQMISSHWLLRLLDKRLGCDDERQIIM AGIERAEFIFRTIFRGLACTVVLGIIYI-SASSEPTLMYPTWIPWNwRDsTSAYLATAM LHTTAL-MANATLVLNLSSYPGTYLILVSVHT-KALALRVSKLGYGAPLPAVRMQAILVG YIHDHQIILR*VSGNLISQCKNF*SISGVLTFIERRMY THFGVPNIFIVIEDYYILFL NYSLFKSLERSLSMTC-FLQFFSTACAQCTICYFLLFGNVGIMR-FMNMLFLLVILTTET LLLCYTAELPCKEGESLLTAVY-SCNWLSQSVNFRRLLLLMLARCQIPMILVSGVIVPI SMKTF

[0262] DOR37nt

[0263] **information on nucleotide sequence is in progress**

[0264] DOR38

[0265] MRLIKISYSALNEVCVWLKLNGSWPLT-ESSRPWRSQSLLATAYIVWAWYVIASVGITI SYQTAFLLNNLSDIIITTENCCTTFMGV-LNFVRLIHLRLNQRKFRQLIENFSYEIWIP NSSKN-NVAAECRRRMVTFSIMTSLLACLIIMY-CVLPLVEIFFGPAFDAQNKPFPYKMI FPYDAQSSWIRYVMTYIFTSYAGICVVT-TLFAEDTILGFFITYTCGQFHLLHQRIAGL FAGS-NAELAESIQLERLKRIVEKHNNIISANSV

[0266] DOR38nt

[0267] ATGCGTTTGATCAAAATTTCATATTCG-GCACTTAATGAGGTGTGCGTTTGGCTGAAAC TGAATGGTTCTTGGCCATTAACCGAAT-CATCGAGGCCATGGAGGAGCCAATCCTTATT GGC-CACCGCCTACATCGTGTGGGCGTGG-TACGTCATTGCATCTGTGGGCATAACAATC AGCTATCAGACGGCCTTTTTGCTGAA-CAACCTTTCGGACATTATTATCACCACGGAAA ATTGTTGCACCACCTTTATGGGTGTCCT-GAACTTTGTCCGACTCATCCATCTTCGCCT CAAT-CAGAGGAAATTCCGCCAGCTTAT-TGAGAACTTTTCCTACGAAATTTGGATACCT AATTCTTCCAAAAACAATGTTGCCGC-CGAGTGTCGCAGACGCATGGTTACCTTCAGCA TAATGACATCCTTGCTAGCGTGCCTGAT-CATAATGTATTGTGTCCTGCCGCTGGTGGA GATCT-TCTTTGGACCCGCCTTCGATGCACAGAA-CAAGCCGTTTCCCTACAAGATGATC TTTCCGTACGATGCCCAGAGCAGTTG-GATCCGATATGTGATGACCTACATCTTCACCT CCTACGCGGGAATCTGTGTGGTCACCAC-CTTGTTTGCAGAGGACACCATTCTTGGCTT CTTCATAACCTACACTTGTGGC-CAATTTCATTTGCTACACCAACGAATCGCAGGTTTA TTTGCGGGTTCCAATGCGGAATTGGC-CGAGAGCATTCAGCTGGAGCGACTCAAACGTA TTGTGGAAAAACACAACAATATTAT-CAGCGCAAATTCTGTA

[**0268**] DOR44

[**0269**] MKSTFKEERIKDDSKRRDLFVFVRQTM-
CIAAMYPFGYYVNGSGVLAVLVRFCDLTYEL FNY-
FVSVHIAGLYICTIYINYGQGDLDFFVN-
CLIQTIIYLWTIAMKLYFRRFRPGLLN
TILSNINDEYETRSAVGFSFVTMAGSYR-
MSKLWIKTYVYCCYIGTIFWLALPIAYRDR
SLPLACWYPFDYTQPGVYEVVFLLQAMG-
QIQVAASFASSSGLHMVLCVLISGQYDVLF CSLKNV-
LASSYVLMGANMTELNQLQAEQSAADVE-
PGQYAYSVEEETPLQELLKVGSSM
DFSSAFRLSFVRCIQHHRYIVAALK-
KIESFYSPIWFvKIGEVTFLMCLVAFvSTKSTA ANSFM-
RMVSLGQYLLLVLYELFIICYFADI-
VFQNSQRCGEALWRSPWQRHLKDVRSDY
MFFMLNSRRQFQLTAGKISNLNVDRFRGVGILT

[**0270**] DOR44nt

[**0271**] ATGAAGAGCACATTCAAGGAAGAAAG-
GATTAAGGACGACTCCAAGCGTCGCGACCTGT
TTGTATTCGTGAGGCAAACCATGTGTAT-
AGCGGCCATGTATCCCTTCGGTTACTACGT GAATG-
GATCTGGAGTCCTGGCCGTTCTGGTGC-
GATTCTGTGACTTGACCTACGAGCTC
TTTAACTACTTCGTTTCGGTACACAT-
AGCTGGCCTGTACATCTGCACCATCTACATCA ACT-
ATGGGCAAGGCGATTTGGACTTCTTCGT-
GAACTGTTTGATACAAACCATTATTTA
TCTGTGGACAATAGCGATGAAACTC-
TACTTTCGGAGCTTCAGACCTGGTTTGTTGAAT
ACCATTCTGTCCAACATCAATGATGAG-
TACGAGACACGTTCGGCTGTGGGATTCAGTT TCGT-
CACAATGGCGGGATCCTATCGGATGTC-
CAAGCTATGGATCAAAACCTATGTGTA
TTGCTGCTACATAGGCACCATTTTCTG-
GCTGGCTCTTCCCATTGCCTACCGGGATAGG
AGTCTTCCTCTTGCCTGCTGGTATC-
CCTTTGACTATACACAACCCGGTGTCTATGAGG
TAGTGTTCCTTCTCCAGGCGATGGGACA-
GATCCAAGTGGCCGCATCCTTTGCCTCCTC CAGTG-
GCCTGCATATGGTGCTTTGTGTGCT-
GATATCAGGGCAGTACGATGTCCTCTTT
TGCAGTCTCAAGAATGTATTAGCCAG-
CAGCTATGTCCTTATGGGAGCCAATATGACGG
AACTGAATCAATTGCAGGCTGAG-
CAATCTGCGGCCGATGTCGAGCCAGGTCAGTATGC
TTACTCCGTGGAGGAGGAGACACCTTTG-
CAAGAACTTCTAAAAGTTGGGAGCTCAATG GACT-
TCTCCTCCGCATTCAGGCTGTCTTTTGT-
GCGGTGCATTCAGCACCATCGATACA
TAGTGGCGGCACTGAAGAAAAT-
TGAGAGTTTCTACAGTCCCATATGGTTCGTGAAGAT
TGGCGAAGTCACCTTTCTTATGTGCCTG-
GTAGCCTTCGTCTCCACGAAGAGCACCGCG
GCCAACTCATTCATGCGAATGGTCTCCT-
TGGGCCAGTACCTGCTCTTAGTTCTCTACG AGCT-
GTTCATCATCTGCTACTTCGCGGA-
CATCGTTTTTCAGAACAGCCAGCGGTGCGG
TGAAGCCCTCTGGCGAAGTCCTTG-
GCAGCGACATTTGAAGGATGTTCGCAGTGATTAC
ATGTTCTTTATGCTGAATTCCCGCAG-
GCAGTTCCAACTTACGGCCGGAAAAATAAGCA
ATCTAAACGTGGATCGTTTCA-
GAGGGGTGGGTATCCTTACT

[**0272**] DOR46

[**0273**] MAEVRVDSLEFFKSHWTAWRYLGVAHFR-
VENWKNLYVFYSIVSNLLVTLCYPVHLGIS LFRNR-
TITEDILNLTTFATCTACSVK-
CLLYAYNIKDVLEMERLLRLLDERVVGPEQRS
IYGQVRVQLRNVLYVFIGIYMPCAL-
FAELSFLFKEERGLMYPAWFPFDWLHSTRNYYI
ANAYQIVGISFQLLQNYVSDCFPAVVL-
CLISSHIKMLYNRFEEVGLDPARDAEKDLEA CITDH-
KHILELFRRIEAFISLPMLIQFTVTALN-
VCIGLAALVFFVSEPMARMYFIFYS
LAMPLQIFPSCFFGTDNEYWFGRL-
HYAAFSCNWHTQNRSFKRKMMLFVEQSLKKSTAV
AGGMMRIHLDTFFSTLKGAYSLFTIIIRMRK

[**0274**] DOR46nt

[**0275**] ATGGCAGAGGTCAGAGTGGACAGTCTG-
GAGTTTTTCAAGAGCCATTGGACCGCCTGGC
GGTACTTGGGAGTGGCT-
CATTTTCGGGTCGAGAACTGGAAGAAC-
CTTTACGTGTTTTA CAGCATTGTGTCGAATCT-
TCTCGTGACCCTGTGCTACCCCGTTCACCTGGGA
ATATCC CTCTTTCGCAACCGCACCATCACCGAG-
GACATCCTCAACCTGACCACCTTTGCGACCT GCA-
CAGCCTGTTCGGTGAAGTGCCTGCTC-
TACGCCTACAACATCAAGGATGTGCTGGA
GATGGAGCGGCTGTTGAGGCTTTTGGAT-
GAACGCGTCGTGGGTCCGGAGCAACGCAGC ATC-
TACGGACAAGTGAGGGTCCAGCTGC-
GAAATGTGCTATACGTGTTCATCGGCATCT
ACATGCCGTGTGCCCTGTTCGCCGAGC-
TATCCTTTCTGTTCAAGGAGGAGCGCGGTCT GATG-
TATCCCGCCTGGTTTCCCTTCGACTG-
GCTGCACTCCACCAGGAACTATTACATA
GCGAACGCCTATCAGAT-
AGTGGGCATCTCGTTTCAGCTGCTG-
CAAAACTATGTTAGCG ACTGCTTTCCGGCGGTGGT-
GCTGTGCCTGATCTCATCCCACATCAAAATGTTGTACAA
CAGATTCGAGGAGGTGGGCCTGGATC-
CAGCCAGAGATGCGGAGAAGGACCTGGAGGCC
TGCATCACCGATCACAAGCATATTCTA-
GAGTGGGCAGGCGGCTCATTGGTTCGTGTTC TAT-
TCACTTTCCAACTTTTTTCCAGACTAT-
TCCGACGCATCGAGGCCTTCATTTCCCT
GCCCATGCTAATTCAGTTCACAGTGAC-
CGCCTTGAATGTGTGCATCGGTTTAGCAGCC CTG-
GTGTTTTTCGTCAGCGAGCCCATG-
GCACGGATGTACTTCATCTTCTACTCCCTGG
CCATGCCGCTGCAGATCTTTCCGTCCT-
GCTTTTTCGGCACCGACAACGAGTACTGGTT
CGGACGCCTCCACTACGCGGCCTTCAGT-
TGCAATTGGCACACACAGAACAGGAGCTTT
AAGCGGAAAATGATGCTGTTCGTTGAG-
CAATCGTTGAAGAAGAGCACCGCTGTGGCTG GCG-
GAATGATGCGTATCCACCTGGACACGT-
TCTTTTCCACCCTAAAGGGGGCCTACTC
CCTCTTTACCATCATTATTCGGATGAGAAAG

[**0276**] DOR48

[**0277**] MERHYFMVPKFALSLIGFYPEQKRTV-
LVKLWSFFNFFILTYGCYAEAYYGIHYIPINI
ATALDALCPVASSILSLVKKVAIWW-
YQDELRSLIERRFYTLATQLTFLLLCCGFCTST SYS-
VRHLIDNILRRTHGKDWIYETPFKMMFP-

DLLLRLPLYPITYILVHWHGYITVVCF VGADGFFLGFCLYFTVLLLCLQD-DVCDLLEVENIEKSPSEAEEARIVREMEKLVDRHN EVAELTERLSGVMVEITLAHFVTSSLI-IGTSVVDILLFSGLGIIVYVVYTCAVGVEIF LYCLGGSHIMEACSNLARSTFSSHW-YGHSVRVQKMTLLMVARAQRVLTIKIPFFSPSL ETLTSILRFTGSLIALAKSVI

[0278] DOR48nt

[0279] ATGGAGCGCCATTATTTCATGGTGC-CAAAGTTTGCATTATCGCTGATTGGTTTTTATC CCGAACAGAAGCGAACGGTTTTGGT-GAAACTTTGGAGTTTCTTCAACTTTTTCATCCT CACCTACGGCTGTTATGCAGAGGCTTAC-TATGGCATACACTATATACCGATTAACATA GCCACT-GCATTGGATGCCCTTTGTCCTGTGGC-CTCCAGCATTTTGTCGCTGGTGAAAA TGGTCGCCATTTGGTGGTATCAAGAT-GAATTAAGGAGTTTGATAGAGCGGGTAAGATT TTTAACAGAGCAACAGAAGTCCAAGAG-GAAACTGGGCTATAAGAAGAGGTTCTATACA CTG-GCAACGCAACTAACATTCCTGCTACTAT-GCTGTGGATTTTGCACCAGTACTTCCT ATTCCGTCAGACATTTGAT-TGATAATATCCTGAGACGCACCCATG-GCAAGGACTGGAT CTACGAGACTCCGTTCAAGAT-GATGTAAGGAAAGGGAAGAATGGTTTATATATACT TT TGGAACGAAATAATGATGTGATCTAAA-CAAGATGCACTTTTTTTTAGGTTCCCCGATC TTCTC-CTGCGTTTGCCACTCTATCCCATCAC-CTATATACTCGTGCATTGGCATGGCTA CATTACTGTGGTTTGTTTTGTCGGCGCG-GATGGTTTCTTCCTGGGGTTCTGTTTGTAC TTCACT-GTTTTGCTGCTCTGTCTGCAGGACGAT-GTTTGTGATTTACTAGAGGTTGAAA ACATCGAGAAGAGTCCCTCCGAAGCG-GAGGAAGCTCGCATAGTTCGGGAAATGGAAAA ACTGGTGGACCGGCATAACGAGGTGGC-CGAGCTGACAGAAAGATTGTCGGGTGTTATG GTG-GAAATAACACTGGCCCACTTTGTTACT-TCGAGTTTGATAATCGGAACCAGCGTGG TGGATATTTTATTAGTGGGTATTTA-CATTTGATTAGATCCTTTCGATATATGTTCTTA AAT-TCTAGTTTTCCGGCCTGGGAATCATTGT-GTATGTGGTCTACACTTGTGCCGTAGG TGTGGAAATATTTCTATACTGTTTAG-GAGGATCTCATATTATGGAAGCGGTATATTCA TAA-GAAACTACTATAAAGTTACTTTTAAAT-TCATTGCATTTCTTAGTGTTCCAATCTA GCGCGCTCCACATTTTCCAGCCACTGG-TATGGCCACAGTGTTCGGGTCCAAAAGATGA CCCTTTTGATGGTAGCTCGTGCTCAAC-GAGTTCTCACAATTAAAATTCCTTTCTTTTC CCCAT-CATTAGAGACTCTAACTTCGGTAAGCT-TATGCGAAAATGTTATGGTACACACA AGTCTACATTTCTATGAGGTCTTGTA-GATTTTGCGCTTCACTGGATCTCTGATTGCCC TGGCAAAGTCGGTTATA

[0280] DOR53

[0281] MLSKFFPHIKEKPLSERVK-SRDAFIYLDRVMWSFGWTEPEN-KRWILPYKLWLAFVNIV MLILLPISISIEYLHRFKTF-SAGEFLSSLEIGVNMYGSSFKCAFTLIGFKKRQEAK VL LDQLDKRCLSDKERSTVHRYVAMGN-FFDILYHIFYSTFVVMNFPYFLLERRHAWRMYF PYIDSDEQFYISSIAECFLMTEAIYM-DLCTDVCPLISMLMARCHISLLKQRLRNLRSK PGRT-EDEYLEELTECIRDHRLLLDYVDALR-PVFSGTIFVQFLLIGTVLGLSMINLMFF STFWTGVATCLFMFDVSMETFrFCYLCN-MIIDDCQEMSNCLFQSDWTSADRRYKSTLV YFLHNLQQPITLTAGGVFPISMQTNLAM-VKLAFSVVTVIKQFNLAERFQ

[0282] DOR53nt

[0283] TCAAACAAAGCCACGGACAAGATGT-TAAGCAAGTTTTTCCCCACATAAAAGAAAAGC CATTGAGCGAGCGGGTTAAGTC-CCGAGATGCCTTCATTTACTTGGATCGGGTGATGTG GTCCTTTGGCTGGACAGAGCCTGAAAA-CAAAAGGTGGATCCTTCCTTATAAACTGTGG TTAGCGTTCGTGAACATAGTAATGCT-CATCCTTCTGCCGATCTCGATAAGCATCGAGT ACCTCCACCGATTTAAAACCTTCTCG-GCGGGGGAGTTCCTTAGTTCCCTCGAGATTGG AGT-CAACATGTACGGAAGCTCTTTTAAGT-GCGCCTTCACCTTGATTGGATTCAAGAAA AGACAGGAAGCTAAGGTTTTACTGGAT-CAGCTGGACAAGAGATGCCTTAGCGATAAGG AGAGGTCCACTGTTCATCGCTATGTCGC-CATGGGAAACTTTTTCGATATTTTGTATCA CATTTTTTACTCCACCTTCGTGGTAAT-GAACTTCCCGTATTTTCTGCTTGAGAGACGC CAT-GCTTGGCGCATGTACTTTCCATATATC-GATTCCGACGAACAGTTTTACATCTCCA GCATCGCCGAGTGTTTTCTGATGACG-GAGGCCATCTACATGGATCTCTGTACGGACGT GTGTCCCTTGATCTCCATGCTTATG-GCTCGATGCCACATCAGCCTCCTGAAACAGCGA CTGAGAAATCTCCGATCGAAGCCAG-GAAGGACCGAAGATGAGTACTTGGAGGAGCTCA CCGAGTGCATTCGGGATCATCGATTGC-TATTGGACTATGTTGACGCATTGCGACCCGT CTTTTCGGGAACCATTTTTGTGCAGTTC-CTCCTGATCGGTACTGTACTGGGTCTCTCA ATGATAAATCTAATGTTCTTCTCGA-CATTTTGGACTGGTGTCGCCACTTGCCTTTTTA TGT-TCGACGTGTCCATGGAGACGTTC-CCCTTTTGCTATTTGTGCAACATGATTATCGA TGACTGCCAGGAAATGTCCAATTGC-CTCTTTCAATCGGACTGGACCTCTGCCGATCGT CGCTACAAATCCACTTTGG-TATACTTTCTTCACAATCTTCAGCAAC-CCATTACTCTCA CGGCTGGTGGAGTGTTTC-CTATTTCCATGCAAACAAATTTGGCTATGGTGAA GCTGGC ATTTTCTGTGGTTACGGTAATTAAG-CAATTTAACTTGGCCGAAAGGTTTCAATAAGTT GAGAGGGACGAGCTCTGCTACTAT-TATATTATATATTATATTATATTATATATATATT ATTT-TATATTATATATTGCTGTAC-CCTAATAAATATTTAGTAATAAAAAAAAAAAAAA AAAA

[0284] DOR56

[0285] MDPVEMPIFGSTLKLMKFWSYLFVHNWR-RYVAMTPYIIINCTQYVDIYLSTESLDFII RNVYLAV-

LFTNTVVRGVLLCVQRFSYERFINILKS-FYIELLVSTERLSQKCILHKWAV LPYGMYLPTIDEYKYASPYYE-IFFVIQAIMAPMGCCMYIPYTNMVVTFTLFAILMCRV LQHKLRSLEKLKNEQVRGEIAQ-TIAQTVIVIAYMVMIFANSVVLYYVANELYFQSFDI AIAAYESNWMDFDVDTQKTLKFLIMR-SQKPLASLVGGTYPMNLKMLQSLINAIYSFFT LLR-RVYG

[0286] DOR56nt

[0287] ATGGATCCGGTGGAGATGCCCATTTTTG-GTAGCACTCTGAAGCTAATGAAGTTCTGGT CATATCTGTTTGTTCACAACTGGCGC-CGCTATGTCGCAATGACTCCGTACATCATTAT CAACTGTACTCAGTATGTG-GATATATATCTGAGCACCGAATCCTTG-GACTTTATCATC AGAAATGTATACCTGGCTGTAT-TGTTTACCAACACGGTGGTCAGAGGTGTATTGTTAT GCGTACAGCGGTTTAGCTAC-GAGCGTTTCAT-TAATATTTTGAAAAGCTTTTACATTGA GTTGTTGGT-GAGTACCGAAAGATTATCTCAAAAATGCATATTG CATAAATGGGCAGTT CTGCCATATGGCATG-TATTTGCCCACTATTGATGAATA-CAAATACGCATCACCTTACT ACGAGATTTTCTTTGT-GATTCAAGCCATTATGGCTCCAATGGGGTGTTGC ATGTACAT ACCATACACAAACATGGTAGTGACATT-TACCCTTTTCGCCATTCTCATGTGTCGAGTG TTG-CAACATAAGTTGAGAAGCCTA-GAAAAGCTGAAAAATGAACAAGTACGTGGTGAAA TCGCTCAAACAATTGCTCAGACCGTCAT-AGTCATCGCATACATGGTAATGATATTTGC CAA-CAGTGTAGTCCTTTACTACGTGGCCAAT-GAGCTATACTTTCAAAGCTTTGATATT GCCATTGCTGCCTATGAGAGCAATTG-CATGGACTTTGATGTGGACACACAAAAGACTT TGAAGTTCCTCATCATGCGCTCG-CAAAAGCCCTTGGCGAGTCTGGTGGGTGGCACATA TCCCATGAACTTGAAAATGCTTCAGT-CACTACTAAATGCCATTTACTCCTTCTTCACC CTTCTGCGTCGCGTTTACGGC

[0288] DOR58

[0289] MDASYFAVQRRALEIVGFDPST-PQLSLKHPIWAGILILSLISHNWPMVVYALQDLSDL TRLTDNFAVFMQGSQSTFKFLVM-MAKRRRIGSLIHRLHKLNQAASATPNHLEKIEREN QLDRYVARSFRNAAYGVICASAIAPM-LLGLWGYVETGVFTPTTPMEFNFWLDERKPHF YWPIYVWGVLGVAAAAWLAIATDTLF-SWLTHNVVIQFQLLELVLEEKDLNGGDSPLTG FVS-RHRIALDLAKELSSIFGEIVFVKYML-SYLQLCMLAFRFSRSGWSAQVPFRATFLV AIIIQLSSYCYGGEYIKQQSLA-IAQAVYGQINWPEMTPKKRRLWQMVIMRAQRPAKIF GFMFVVDLPLLLWVIRTAGSFLAMLRTFER

[0290] DOR58nt

[0291] ATGGACGCCAGCTACTTTGCCGTCCA-GAGAAGAGCTCTGGAAATAGTTGGATTCGATC CCAGTACTCCGCAACTGAGTCTGAAA-CATCCCATCTGGGCCGGGATTCTCATCCTGTC CTTGATCTCTCACAACTGGCCCATGG-TAGTCTATGCCCTGCAGGATCTCTCCGACTTG ACCCGTCTGACGGACAACTTTGCGGT-GTTTATGCAAGGATCACAGAGCACCTTCAAGT TCCTGGTCATGATGGCGAAACGAAGGCG-CATTGGATCGTTGATTCACCGTTTGCATAA GCTAAACCAGGCGGCCAGTGCCACGC-CCAATCACCTGGAGAAGATCGAGAGGGAAAAC CAACTGGATAGGTATGTCGCCAGGTC-CTTTAGAAATGCCGCCTACGGAGTGATTTGTG CCTCGGCCATAGCGCCCATGTTGCTTG-GCCTGTGGGGATATGTGGAGACGGGTGTATT TAC-CCCCACCACACCCATGGAGTTCAACT-TCTGGCTGGACGAGCGAAAGCCTCACTTT TATTGGCCCATCTACGTTTGGGGCG-TACTGGGCGTGGCAGCTGCCGCCTGGTTGGCCA TTGCAACGGACACCCTGTTCTCCTGGCT-GACTCACAATGTGGTGATTCAGTTCCAACT ACTG-GAGCTTGLTCTCGAAGAGAAGGATCT-GAATGGCGGAGACTCTCGCCTGACCGGG TTTGTTAGTCGTCATCGTATAGCTCTG-GATTTGGCCAAGGAACTAAGTTCGATTTTCG GGGAGATCGTCTTTGTGAAATACATGCT-CAGTTACCTGCAACTCTGCATGTTGGCCTT TCGCT-TCAGCCGCAGTGGCTGGAGTGCCCAGGT-GCCATTTAGAGCCACCTTCCTAGTG GCCATCATCATCCAACTGAGTTCGTAT-TGCTATGGAGGCGAGTATATAAAGCAGCAAA GTTTGGCCATCGCACAAGCCGTTTATG-GTCAAATCAATTGGCCAGAAATGACGCCAAA GAAAAGAAGACTCTGGCAAATGGTGAT-CATGAGGGCGCAGCGACCGGCTAAGATTTTT GGATTCATGTTCGTTGTGGACTTGC-CACTGCTGCTTTGGGTCATCAGAACTGCGGGCT CATTTCTGGCCATGCTTAGGACTTTCGAGCGT

[0292] DOR59

[0293] MHEADNREMELLVATQAYTRTITLLI-WIPSVIAGLMAYSDCIYRSLFLPKSVFNVPAV RRGEE-HPILLFQLFPFGELCDNFVVGYLGPWY-ALGLGITAIPLWHTFITCLMKYVNLK LQILNKRVEEMDITRLNSKLVIGRLTA-SELTFWQMQLFKEFVKEQLRIRKFVQELQYL ICVPV-MADFIIFSVLICFLFFALTVGH-DELSLAYFSCGWYNFEMPLQKMLVFMMMHAQ RPMKMRALLVDLNLRTFIDIGRGAYSYFNLLRSSHLY

[0294] DOR59nt

[0295] ATGCACGAAGCAGATAATCGGGAGATG-GAACTTTTGGTCGCCACTCAGGCTTATACAC GAAC-CATTACCCTGTTGATCTGGATACCATCG-GTTATTGCTGGCCTAATGGCCTATTC AGACTGCATCTACAGGAGTCTGTTTCT-GCCGAAATCGGTTTTCAATGTGCCAGCTGTG CGACGTGGTGAGGAGCATCCCATTCTGC-TATTTCAGCTGTTTCCCTTCGGAGAACTTT GCGATAACTTCGTTGTTGGATACTTGG-GACCTTGGTATGCTCTGGGCCTGGGAATCAC GGC-TATCCCATTGTGGCACACCTTTATCACT-TGCCTCATGAAGTACGTAAATCTCAAG CTGCAAATACTCAACAAGCGAGTGGAG-GAGATGGATATTACCCGACTTAATTCCAAAT TGG-TAATTGGTCGCCTAACTGCCAGTGAGT-TAACCTTCTGGCAAATGCAACTCTTCAA GGAATTTGTAAAGGAACAGCTGAGGAT-

TCGAAAATTTGTCCAGGAACTACAGTATCTG
ATTTGCGTGCCTGTGATGGCA-
GATTTCATTATCTTCTCGGTTCTCATTTGCTTTCTCT
TTTTTGCCTTGACAGTTGGCCACGAT-
GAACTGAGCCTTGCTTACTTTTCTTGCGGATG GTA-
CAACTTCGAAATGCCTTTGCAGAAAAT-
GCTGGTTTTTATGATGATGCATGCCCAA
AGGCCGATGAAGATGCGCGCCCTGCTG-
GTCGATTTGAATCTGAGGACCTTCATAGACA TTG-
GCCGTGGAGCCTACAGCTACT-
TCAATTTGCTGCGTAGCTCCCACTTGTAT

[0296] DOR61

[0297] MGHKDDMDSTDSTALSLKHISS-
LIFVISAQYPLISYVAYNRNDMEKVTACLSVVFTNM
LTVIKISTFLANRKDFWEMIHRFRKM-
HEQCKYREGLDYVAEANKLASFLGRAYCVSCG LTG-
LYFMLGPIVKIGVCRWHGTTCDKELPMP-
MKFPFNDLESPGYEVCFLYTVLVTVVV
VAYASAVDGLFISFAINLRAHFQTLQR-
QIENWEFPSSEPDTQIRLKSIVEYHVLLLSL SRKLR-
SIYTPTVMGQFVITSLQVGVIIYQLVT-
NMDSVMDLLLYASFFGSIMLQLFIYC
YGGEIIKAESLQVDTAVRLSNWHLASPK-
TRTSLSLIILQSQKEVLIRAGFFVASLANF PYRLITLIK-
SIDSIC

[0298] DOR61nt

[0299] **information on nucleotide sequence is in progress**

[0300] DOR62

[0301] MEKQEDFKLNTHSAVYYHWRVWELTGLM-
RPPGVSSLLYVVYSITVNLVVTVLFPLSLL ARLLFTT-
NMAGLCENLTITITDIVANLKFANVYM-
VRKQLHEIRSLLRLMDARARLVGD
PEEISALRKEVNIAQGTFRTFASIFVF-
GTTLSCVRVVVRPDRELLYPAWFGVDWMHST
RNYVLINIYQLFGLIVQAIQNCASDSYP-
PAFLCLLTGHMRALELRVRRIGCRTEKSNK GQT-
YEAWREEVYQELIECIRDLARVHRLREI-
IQRVLSVPCMAQFVCSAAVQCTVAMHF
LYVADDHDHTAMIISIVFF-
SAVTLEVFVICYFGDRMRTQSEAL-
CDAFYDCNWIEQLPK FKRELLFTLARTQRPSLIYAG-
NYIALSLETFEQVMRFTYSVFTLLLRAK

[0302] DOR62nt

[0303] ATGGAGAAGCAAGAGGATTTCAAACT-
GAACACCCACAGTGCTGTGTACTACCACTGGC
GCGTTTGGGAGCTCACTGGCCTGAT-
GCGTCCTCCGGGCGTTTCAAGCCTGCTTTACGT
GGTATACTCCATTACGGTCAACTTGGTG-
GTCACCGTGCTGTTTCCCTTGAGCTTGCTG GCCAG-
GCTGCTGTTCACCACCAACATGGCCG-
GATTGTGCGAGAACCTGACCATAACTA
TTACCGATATTGTGGC-
CAATTTGAAGTTTGCGAATGTGTACATG-
GTGAGGAAGCAGCT CCATGAGATTCGCTCTCTC-
CTAAGGCTCATGGACGCTAGAGCCCGGCTGGTGG
GCGAT CCCGAGGAGATTTCTGCCTTGAGGAAG-
GAAGTGAATATCGCACAGGGCACTTTCCGCA
CCTTTGCCAGTATTTTCGTATTTGGCAC-
TACTTTGAGTTGCGTCCGCGTGGTCGTTCG CCCG-
GATCGAGAGCTCCTGTATCCGGCCTGGT-
TCGGCGTTGACTGGATGCACTCCACC
AGAAACTATGTGCTCATCAATATCTAC-
CAGCTCTTCGGCTTGATAGTGCAGGCTATAC
AGAACTGCGCTAGTGACTCCTATCCGC-
CTGCGTTTCTCTGCCTGCTCACGGGTCATAT GCGT-
GCTTTGGAGCTGAGGGTGCGGCGGATTG-
GCTGCAGGACGGAAAAGTCCAATAAA
GGGCAGACATATGAAGCCTGGCGGGAG-
GAGGTGTACCAGGAACTCATCGAGTGCATCC
GCGATCTGGCGCGGGTCCATCGGCT-
GAGGGAGATCATTCAGCGGGTCCTTTCAGTGCC
CTGCATGGCCCAGTTCGTCTGCTCCGC-
CGCCGTCCAGTGTACCGTCGCCATGCACTTC CTG-
TACGTAGCGGATGACCACGACCACAC-
CGCCATGATCATCTCGATTGTATTTTTCT
CGGCCGTCACCTTGGAGGTGTTTG-
TAATCTGCTATTTTGGGGACAGGATGCGGACACA
GAGCGAGGCGCTGTGCGATGCCTTCTAC-
GATTGCAACTGGATAGAACAGCTGCCCAAG
TTCAAGCGCGAACTGCTCTTCACCCTG-
GCCAGGACGCAGCGGCCTTCTCTTATTTACG CAG-
GCAACTACATCGCACTCTCGCTGGAGAC-
CTTCGAGCAGGTCATGAGGTTCACATA
CTCTGTTTTCACACTCTTGCTGAGGGC-
CAAGTAAGAACTTTATAATCTCTTTTTGGGG
AGAAAAATTTTAAAGCACAATAGCA-
GAAAAATATATCAGATAATATAACAAA

[0304] DOR64

[0305] MKLSETLKIDYFRVQLNAWRICGALDL-
SEGRYWSWSMLLCILVYLPTPMLLRGVYSFE
DPVENNFSLSLTVTSLSNLMKFCMYVA-
QLTKMVEVQSLIGQLDARVSGESQSERHRNM
TEHLLRMSKLFQITYAVWFI-
IAAVPFVFETELSLPMPMWFPFDWKNSM-
VAYIGALVFQ EIGYVFQIMQCFAADSFPPLVLYLISE-
QCQLLILRISEIGYGYKTLEENEQDLVNCIR
DQNALYRLLDVTKSLVSYPMMVQFM-
VIGINIAITLFVLIFYVETLYDRIYYLCFLLGI TVQTY-
PLCYYGTMVQESFAELHYAVFCSNWVDQ-
SASYRGHMLILAERTKRMQLLLAGN
LVPIHLSTYVACWKGAYSFFTLMADRDGLGS

[0306] DOR64nt

[0307] GGCACGAGCCAAGAATTCAAAAT-
GAAACTCAGCGAAACCCTAAAAATCGACTATTTTC
GAGTCCAGTTGAATGCCTGGC-
GAATTTGTGGTGCCTTGGATCTCAGC-
GAGGGTAGGTA CTGGAGTTGGTCGATGCTATTGTG-
CATCTTGGTGTACCTGCCGACACCCATGCTACTG
AGAGGAGTATACAGTTTCGAGGATCCG-
GTGGAAAATAATTTCAGCTTGAGCCTGACGG TCA-
CATCGCTGTCCAATCTCATGAAGTTCTG-
CATGTACGTGGCCCAACTAACAAAGAT
GGTCGAGGTCCAGAGTCTTATTGGT-
CAGCTGGATGCCCGGGTTTCTGGCGAGAGCCAG
TCTGAGCGTCATAGAAATATGACCGAG-
CACCTGCTAAGGATGTCCAAGCTGTTCCAGA
TCACCTACGCTGTAGTCTTCATCAT-
TGCTGCAGTTCCCTTCGTTTTCGAAACTGAGCT
AAGCTTACCCATGCCCATGTGGTTTC-
CCTTCGACTGGAAGAACTCGATGGTGGCCTAC
ATCGGAGCTCTGGTTTTCCAGGAGATTG-

GCTATGTCTTTCAAATTATGCAATGCTTTG CAGCT-GACTCGTTTCCCCCGCTCGTACTGTAC-CTGATCTCCGAGCAATGTCAATTGCT GATCCTGAGAATCTCTGAAATCG-GATATGGTTACAAGACTCTGGAGGAGAACGAACAG GATCTGGTCAACTGCATCAGGGAT-CAAAACGCGCTGTATAGATTACTCGATGTGACCA AGAGTCTCGTTTCGTATCCCATGATGGT-GCAGTTTATGGTTATTGGCATCAACATCGC CAT-CACCCTATTTGTCCTGATATTTTACGTG-GAGACCTTGTACGATCGCATCTATTAT CTTTGCTTTCTCTTGGGCATCACCGTG-CAGACATATCCATTGTGCTACTATGGAACCA TGGT-GCAGGAGAGTTTTGCTGAGCTTCACTAT-GCGGTATTCTGCAGCAACTGGGTGGA TCAAAGTGCCAGCTATCGTGGGCACAT-GCTCATCCTGGCGGAGCGCACTAAGCGGATG CAGCTTCTCCTCGCCGGCAACCTGGTGC-CCATCCACCTGAGCACCTACGTGGCCTGTT GGAAGGGAGCCTACTCCTTCTTCACCCCT-GATGGCCGATCGAGATGGCCTGGGTTCTTA GTAGC-CCAGTCATTTCACTCACATTCTACAT-CAAGTAGTACTACCACTGAACACGAAC ACGAATATTTCAAAAGTAAACACAT-AATATTCACAATAGTGTATCACTTTAATAAAAT TTTTGGTTACCATGAAAAAAAAAAAAAAAAAA

[**0308**] DOR67

[**0309**] MLSQFFPHIKEKPLSERVK-SRDAFVYLDRVMWSFGWTVPENKRWDL-HYKLWSTFVTLV IFILLPISVSVEYIQRFKTFSAGE-FLSSIQIGVNMYGSSFKSYLTMMGYKKRQEAKMS LDELDKRCVCDEERTIVHRHVALGNF-CYIFYHIAYTSFLISNFLSFIMKRIHAWRMYF PYVD-PEKQFYISSIAEVILRGWAVFMDLCTD-VCPLISMVIARCHITLLKQRLRNLRSE PGRTEDEYLKELADCVRDHR-LILDYVDALRSVFSGTIFVQFLLIGIVLGLSMINIMFF STLSTGVAVVLFMSCVSMQTFPFCYLCN-MIMDDCQEMADSLFQSDWTSADRRYKSTLV YFLHNLQQPIILTAGGVFPISMQTNLNM-VKLAFTVVTIVKQFNLAEKFQ

[**0310**] DOR67nt

[**0311**] GGCACGAGGAAATGTTAAGCCAGT-TCTTTCCCCACATTAAAGAAAAGCCATTGAGCGA GCGGGTTAAGTCCCGAGATGCCTTCGTT-TACTTAGATCGGGTGATGTGGTCCTTTGGC TGGA-CAGTGCCTGAAAACAAAAGGTGGGATC-TACATTACAAACTGTGGTCAACTTTCG TGACATTGGTGATATTTATCCTTCTGC-CGATATCGGTAAGCGTTGAGTATATTCAGCG GTTCAAGACCTTCTCGGCGGGT-GAGTTTCTTAGCTCAATCCAGATTGGCGTTAACATG TACGGAAGCAGCTTTAAAAGT-TATTTGACCATGATGGGATATAAGAA-GAGACAGGAGG CTAAGATGTCACTGGATGAGCTG-GACAAGAGATGCGTTTGTGATGAGGAGAGGACCAT TGTACATCGACATGTCGCCCTGG-GAAACTTTTGCTATATTTTCTATCACATTGCGTAC ACTAGCTTTTTGATTTCAAACTTTTTGT-CATTTATAATGAAGAGAATCCATGCCTGGC GCATG-TACTTTCCCTACGTCGACCCCGAAAAG-CAATTTTACATCTCTAGCATCGCCGA AGTCATTCTTAGGGGGTGGGCCGTCT-TCATGGATCTCTGCACGGATGTGTGTCCTTTG ATCTCCATGGTAATAGCACGATGCCA-CATCACCCTTCTGAAACAGCGCCTGCGAAATC TAC-GATCGGAACCAGGAAGGACGGAAGAT-GAGTACTTGAAGGAGCTCGCCGACTGCGT TCGAGATCACCGCTTGATATTGGACTAT-GTCGACGCATTGCGATCCGTCTTTTCGGGG ACAATTTTTGTGCAGTTCCTCTTGATCG-GTATTGTACTGGGTCTGTCAATGATAAATA TAAT-GTTTTTCTCAACACTTTCGACTGGT-GTCGCCGTTGTCCTTTTTATGTCCTGCGT ATCTATGCAGACGTTCCCCTTTTGC-TATTTGTGTAACATGATTATGGATGACTGCCAA GAGATGGCCGACTCCCTTTTTCAATCG-GACTGGACATCTGCCGATCGTCGCTACAAAT CCACTTTGGTATACTTTCTTCACAATCT-TCAGCAGCCCATTATTCTTACGGCTGGTGG AGTCTTTCCTATTTCCATGCAAA-CAAATTTAAATATGGTGAAGCTGGCCTTTACTGTG GTTACAATAGTGAAACAATTTAACTTG-GCAGAAAAGTTTCAATAAGTTAAGATATGCA AGCTCTGCTATTATAAACCTACACTC-GAGAAAATATTTCTTCACATTAATAAACCTTC AGTACTTACTGCTTGTGGCGCCCCCG-GAAAAAAAAAAAAAAAAAA

[**0312**] DOR68

[**0313**] MSKLIEVFLGNLWTQRFTFARMGLDLQP-DKKGNVLRSPLLYCIMCLTTSFELCTVCAF MVQN-RNQIVLCSEALMHGLQMVSSLLKMAI-FLAKSHDLVDLIQQIQSPFTEEDLVGTE WRSQNQRGOLMAAIYFMMCAGTSVSFLL-MPVALTMLKYHSTGEFAPVSSFRVLLPYDV TQPH-VYAMDCCLMVFVLSFFCCSTTGVDTLYG-WCALGVSLQYRRLGQQLKRIPSCFNP SRSDFGLSGIFVEHARLLKIVQHFNYS-FMEIAFVEVVIICGLYCSVICQYIMPHTNQN FAFLG-FFSLVVTTQLCIYLFGAEQVRLEAERFS-RLLYEVIPWQNLPPKHRKLFLFPIE RAQRETVLGAYFFELGRPLLVWVSIFLFIVLLF

[**0314**] DOR68nt

[**0315**] ATGTCAAAGCTAATCGAGGT-GTTTCTGGGTAATCTGTGGAC-CCAGCGTTTTACCTTCG CCCGAATGGGTTTG-GATTTGCAGCCCGATAAAAAGGGCAATGTTTTGC GATCTCCGCT TCTTTATTGTATTATGTGTCTGACAA-CAAGCTTTGAGCTCTGCACCGTGTGCGCCTTT ATG-GTCCAAAATCGCAACCAAATCGT-GCTTTGTTCCGAGGCCCTGATGCACGGACTAC AGATGGTCTCCTCGCTACTGAAGATGGC-TATATTCTTGGCCAAATCTCACGACCTGGT GGAC-CTAATTCAACAGATTCAGTCGCCTTTTA-CAGAGGAGGATCTTGTAGGTACAGAG TGGAGATCCCAAAATCAAAGGGGACAAC-TAATGGCTGCCATTTACTTTATGATGTGTG CCGG-TACGAGTGTGTCATTTCTGTTGATGC-CAGTGGCTTTGACCATGCTTAAGTACCA TTCCACTGGGGAATTCGCGCCTGT-CAGCTCGTTCCGGGTTCTGCTTCCATACGATGTG ACACAACCGCATGTTTATGCCATGGACT-GCTGCTTGATGGTATTTGTGTTAAGTTTTT TTTGCT-GCTCCACCACCGGAGTGGATACCT-

TATATGGATGGTGTGCTTTAGGCGTGAG
TTTACAATACCGTCGCCTCGGTCAA-
CAACTTAAAAGGATACCCTCCTGTTTCAATCCA
TCTCGGTCTGACTTTGGATTAAGTGG-
GATTTTTGTGGAGCATGCTCGTCTGCTTAAAA
TAGTCcAACATTTTAATTATAGTTT-
TATGGAGATCGCATTTGTGGAGGTTGTTATAAT
CTGTGGACTCTATTGCTCAGTAATTTGT-
CAGTATATAATGCCACACACCAACCAAAAC TTCGC-
CTTTCTGGGTTTCTTTTCATTGGTAGT-
TACCACACAGCTGTGCATCTATCTTT
TCGGTGCCGAACAGGTCCGTTTGGAG-
GCTGAGCGATTTTCCCGGCTGCTATACGAAGT AAT-
TCCTTGGCAAAACCTTCCTCCTAAACAC-
CGGAAACTTTTCCTTTTTCCAATTGAG
CGCGCCCAACGAGAAACTGTTCTCGGT-
GCTTATTTCTTCGAACTAGGCAGACCTCTTC
TTGTTTGGGTAAGCATATTCCTTTTTAT-
TGTATTATTATTT

[0316] DOR71

[0317] MVIIDSLSFYRPFWICMRLLVPT-
FFKDSSRPVQLYVVLLHILVTLWFPLHLLLHLLLL
PSTAEFFKNLTMSLTCVACSLKHVAHL-
YHLPQIVEIESLIEQLDTFIASEQEHRYYRD HVH-
CHARRFTRCLYISFGMIYALFLF-
GVFVQVISGNWELLYPAYFPFDLESNRFLGAV
ALGYQVFSMLVEGFQGLGNDTYTPLTL-
CLLAGHVHLWSIRMGQLGYFDDETVVNHQRL
LDYIEQHKLLVRFHNLVSR-
TISEVQLVQLGGCGATLCIIVSYM-
LFFVGDTISLVYYLV FFGVVCVQLFPSCYFASE-
VAEELERLPYAIFSSRWYDQSRDHRFDLLIFTQLTL
GNRG WIIKAGGLIELNLNAFFATLKMAY-
SLFAVVHRETGNPLQREH

[0318] DOR71nt

[0319] ATGGTCATTATCGACAGTCTTAGTTTT-
TATCGTCCATTCTGGATCTGCATGCGATTGC TGG-
TACCGACTTTCTTCAAGGATTCCT-
CACGTCCTGTCCAGCTGTACGTGGTGTTGCT
GCACATCCTGGTCACCTTGTGGTTTC-
CACTGCATCTGCTGCTGCATCTTCTGCTACTT
CCATCTACCGCTGAGTTCTTTAAGAAC-
CTGACCATGTCTCTGACTTGTGTGGCCTGCA GTCT-
GAAGCATGTGGCCCACTTGTATCACT-
TGCCGCAGATTGTGGAAATCGAATCACT
GATCGAGCAATTAGACACATTTATTGC-
CAGCGAACAGGAGCATCGTTACTATCGGGAT
CACGTACATTGCCATGCTAGGCGCTTTA-
CAAGATGTCTCTATATTAGCTTTGGCATGA TCTAT-
GCGCTTTTCCTGTTCGGCGTCTTCGT-
TCAGGTTATTAGCGGAAATTGGGAACT
TCTCTATCCAGCCTATTTCCCATTC-
GACTTGGAGAGCAATCGCTTTCTCGGCGCAGTA
GCCTTGGGCTATCAGGTATTCAGCATGT-
TAGTTGAAGGCTTCCAGGGGCTGGGCAACG ATAC-
CTATACCCCACTGACCCTATGCCTTCTG-
GCCGGACATGTCCATTTGTGGTCCAT
ACGAATGGGTCAACTGGGATACTTCGAT-
GACGAGACGGTGGTGAATCATCAGCGTTTG CTG-
GATTACATTGAGCAGCATAAACTCTTG-
GTGCGGTTCCACAACCTGGTGAGCCGGA
CCATCAGCGAAGTGCAACTGGTG-
CAGCTGGGCGGATGTGGAGCCACTCTGTGCATCAT
TGTCTCCTACATGCTCTTCTTTGTGGGC-
GACACAATCTCGCTGGTCTACTACTTGGTG
TTCTTTGGAGTGGTCTGCGTG-
CAGCTCTTTCCCAGCTGCTATTTTGC-
CAGCGAAGTAG CCGAGGAGTTGGAACGGCTGC-
CATATGCGATCTTCTCCAGCAGATGGTACGATCA
ATC GCGGGATCATCGATTCGATTTGCT-
CATCTTTACACAATTAACACTGGGAAACCGGGGG
TGGATCATCAAGGCAGGAGGTCTTATC-
GAGCTGAATTTGAATGCCTTTTTCGCCACCC TGAA-
GATGGCCTATTCCCTTTTTGCAGTTGTG-
GTGCGGGCAAAGGGTATA

[0320] DOR72

[0321] MDLKPRVIRSEDIYRTYWLY-
WHLLGLESNFFLNRLLDLVITIFVTIWYPIHLILGLFM
ERSLGDVCKGLPITAACFFASFKFICFR-
FKLSEIKEIEILFKELDQRALSREECEFFN QNTRRE-
ANFIWKSFIVAYGLSNISAIASV-
LFGGGHKLLYPAWFPYDVQATELIFWLSV
TYQIAGVSLAILQNLANDBYPPMTFCV-
VAGHVRLLAMRLSRIGQGPEETIYLTGKQLI
ESIEDHRKLMKIVELLRSTM-
NISQLGQFISSGVNISITLVNILFFADNNFAITYYGVY
FLSMVLELFPCCYYGTLISVEMN-
QLTYAIYSSNWMSMNRSYSRILLIFMQLTLAEVQI
KAGGMIGIGMNAFFATVRLAYSFFTLAMSLR

[0322] DOR72nt

[0323] ATGGACTTAAAACCGCGAGTCATTC-
GAAGTGAAGATATCTACAGAACCTATTGGTTAT
ATTGGCATCTTTTGGGCCTGGAAAG-
CAATTTCTTTCTGAATCGCTTGTTGGATTTGGT GAT-
TACAATTTTCGTAACCATTTGGTATC-
CAATTCACCTGATTCTGGGACTGTTTATG
GAAAGATCTTTGGGGGATGTCTG-
CAAGGGTCTACCAATTACGGCAGCATGCTTTTTCG
CCAGCTTTAAATTTATTTGTTTTCGCT-
TCAAGCTATCTGAAATTAAAGAAATCGAAAT
ATTATTTAAAGAGCTGGATCAGC-
GAGCTTTAAGTCGAGAGGAATGCGAGTTTTTCAAT
CAAAATACGAGACGTGAGGC-
GAATTTCATTTGGAAAAGTTTCATTGTG-
GCCTATGGAC TGTCGAATATCTCGGCTATTGCAT-
CAGTTCTTTTCGGCGGTGGACATAAGCTATTATA
TCCCGCCTGGTTTCCATACGATGTGCAG-
GCCACGGAACTAATATTTTGGCTAAGTGTA ACAT-
ACCAAATTGCCGGAGTAAGTTTGGCCAT-
ACTTCAGAATTTGGCCAATGATTCCT
ATCCACCGATGACATTTTGCGTGGTTGC-
CGGTCATGTAAGACTTTTGGCGATGCGCTT GAGTA-
GAATTGGCCAAGGTCCAGAGGAAA-
CAATATACTTAACCGGAAAGCAATTAATC
GAAAGCATCGAGGATCACCGAAAAC-
TAATGAAGATAGTGGAATTACTGCGCAGCACCA
TGAATATTTCGCAGCTCGGCCAGTT-
TATTTCAAGTGGTGTTAATATTTCCATAACACT AGT-
CAACATTCTCTTCTTTGCG-
GATAATAATTTCGCTATAACCTACTACGGAGTGTAC
TTCCTATCGATGGTGTTGGAATTATTC-
CCGTGCTGCTATTACGGCACCCTGATATCCG
TGGAGATGAACCAGCTGACCTATGC-
GATTTACTCAAGTAACTGGATGAGTATGAATCG

GAGCTACAGCCGCATCCTACTGATCT-
TCATGCAACTCACCCTGGCGGAAGTGCAGATC
AAGGCCGGTGGGATGATTGGCATCG-
GAATGAACGCCTTCTTTGCCACCGTGCGATTGG
CCTACTCCTTCTTCACTTTGGCCATGTCGCTGCGT

[0324] DOR73

[0325] MDSRRKVRSENLYKTYWLYWRLLGVEG-
DYPFRRLVDFTITSFITILFPVHLILGMYKK PQIQV-
FRSLHFTSECLFCSYKFFCFRWKLKEIK-
TIEGLLQDLDSRVESEEERNYFNQN
PSRVARMLSKSYLVAAISAIITATVA-
GLFSTGRNLMYLGWFPYDFQATAAIYWISFSY
QAIGSSLLILENLANDSYPPITFCVWS-
GHVRLLIMRLSRIGHDVKLSSSENTRKLIEG
IQDHRKLMKIIRLLRSTLHLSQLGQ-
FLSSGINISITLINILFFAENNFAMLYYAVFFA
AMLIELFPSCYYGILMTMEFDKLPYAIF-
SSNWLKMDKRYNRSLIILMQLTLVPVNIKA
GGIVGIDMSAFFATVRMAYSFYTLALSFRV

[0326] DOR73nt

[0327] ATGGATTCAAGAAGGAAAGTCCGAAGT-
GAAAATCTTTACAAAACCTATTGGCTTTACT GGC-
GACTTCTGGGAGTCGAGGGCGATTATC-
CTTTTCGACGGCTAGTGGATTTTACAAT
CACGTCTTTCATTACGATTTTATTTC-
CCGTGCATCTTATACTGGGAATGTATAAAAAG
CCCCAGATTCAAGTCTTCAGGAGTCTG-
CATTTCACATCGGAATGCCTTTTCTGCAGCT
ATAAGTTTTTCTGTTTTCGTTGGAAACT-
TAAAGAAATAAAGACCATCGAAGGATTGCT CCAG-
GATCTCGATAGTCGAGTTGAAAGTGAA-
GAAGAACGCAACTACTTTAATCAAAAT
CCAAGTCGTGTGGCTCGAATGCTTTC-
GAAAAGTTACTTGGTAGCTGCTATATCGGCCA
TAATCACTGCAACTGTAGCTGGTTTATT-
TAGTACTGGTCGAAATTTAATGTATCTGGG TTG-
GTTTCCCTACGATTTTCAAGCAACCGC-
CGCAATCTATTGGATTAGTTTTTCCTAT
CAGGCGATTGGCTCTAGTCTGTTGAT-
TCTGGAAAATCTGGCCAACGATTCATATCCGC
CGATTACATTTTGTGTGGTCTCTGGA-
CATGTGAGACTATTGATAATGCGTTTAAGTCG AAT-
TGGTCACGATGTAAAATTATCAAGTTCG-
GAAAATACCAGAAAACTCATCGAAGGT
ATCCAGGATCACAGGAAACTAATGAA-
GATAATACGCCTACTTCGCAGCACTTTACATC
TTAGCCAACTGGGCCAGTTC-
CTTTCTAGTGGAATCAACATTTCCATAA-
CACTCATCAA CATCCTGTTCTTTGCGGAAAA-
CAACTTTGCAATGCTTTATTATGCGGTGTTCTTTGCT
GCAATGTTAATAGAACTATTTCCAAGT-
TGTTACTATGGAATTCTGATGACAATGGAGT
TTGATAAGCTACCATATGCCATCTTCTC-
CAGCAACTGGCTTAAAATGGATAAAAGATA CAATC-
GATCCTTGATAATTCTGATGCAACTAA-
CACTGGTTCCAGTGAATATAAAAGCA
GGTGGTATTGTTGGCATCGATATGAGTG-
CATTTTTTGCCACAGTTCGGATGGCATATT CCTTT-
TACACTTTAGCCTTGTCATTTCGAGTA

[0328] DOR77

[0329] MELMRVPVQFYRTIGEDIYAHRSTNPLK-
SLLFKIYLYAGFINFNLLVIGELVFFYNSI QDFETIRLA-
IAVAPCIGFSLVADFKQAAMIRGKK-
TLIMLLDDLENMHPKTLAKQMEYK
LPDFEKTMKRVINIFTFLCLAYTTTFS-
FYPAIKASVKFNFLGYDTFDRNFGFLIWFPF
DATRNNLIYWIMYWDIAHGAY-
LAAFQVTESTVEVIIIYCIFLMTSMVQVFMVCYYGDT
LIAASLKVGDAAYNQKWFQCSKSYCTM-
LKLLIMRSQKPASIRPPTFPPISLVTYMKNP FNNLP-
KHSSSLQINANRYI

[0330] DOR77nt

[0331] ATGGAATTGATGCGAGTGCCAGTA-
CAGTTTTACAGAACGATTGGAGAGGATATCTACG
CCCATCGATCCACGAATC-
CCCTAAAATCGCTTCTCTTCAAGATC-
TATCTATATGCGGG ATTCATAAATTTTAATCTGTTGG-
TAATCGGTGAACTGGTGTTCTTCTACAACTCAATT
CAGGACTTTGAAACCATTCGATTGGC-
CATCGCGGTGGCTCCATGTATCGGATTTTCTC TGGT-
TGCTGATTTTAAACAAGCTGCCAT-
GATTAGAGGCAAGAAAACACTAATTATGCT
ACTCGATGATTTGGAGAACATGCATC-
CGAAAACCCTGGCAAAGCAAATGGAATACAAA
TTGCCGGACTTTGAAAAGACCAT-
GAAACGTGTGATCAATATATTCACCTTTCTCTGCT
TGGCCTATACGACTACGTTCTCCTTT-
TATCCGGCCATCAAGGCATCCGTGAAATTTAA
TTTCTTGGGCTACGACACCTTTGATC-
GAAATTTTGGTTTCCTCATCTGGTTTCCCTTC GATG-
CAACAAGGAATAATTTGATATACTGGAT-
CATGTACTGGGACATAGCCCATGGGG
CCTATCTAGCGGCCTTTCAGGTCAC-
CGAATCAACAGTGGAAGTGATTATTATTTACTG
CATTTTTTTGATGACCTCGATGGTTCAG-
GTATTTATGGTGTGCTACTATGGGGATACT TTAAT-
TGCCGCGAGCTTGAAAGTGGGCGATGC-
CGCTTACAACCAAAAGTGGTTTCAGT
GCAGCAAATCCTATTGCACCATGT-
TGAAGTTGCTAATCATGAGGAGTCAGAAACCAGC
TTCAATAAGACCGCCGACTTTTC-
CCCCCATATCCTTGGTTACCTATATGAAGAATCCC
TTCAACAATCTACCCAAACACAGCTCT-
TCCCTGCAAATCAACGCCAATCGCTATATC

[0332] DOR78

[0333] MKFMKYAVFFYTSVGIEPYTIDSR-
SKKASLWSHLLFWANVINLSVIVFGEILYLGVAY
SDGKFIDAVTVLSYIGFVIVGMSKMFFI-
WWKKTDLSDLVKELEHIYPNGKAEEEMYRL DRYL-
RSCSRISITYALLYSVLIWTFNLFSIMQ-
FLVYEKLLKIRVVGQTLPYLMYFPWN
WHENWTYYVLLFCQNFAGHTSASGQIST-
DLLLCAVATQVVMHFDYLARVVEKQVLDRD WSEN-
SRFLAKTVQYHQRILRLMDVLNDIFGI-
PLLLNFMVSTFVICFVGFQMTVGVPPD
IMIKLFLFLFSSLSQVYLICHYGQLIA-
DAVRDFRSSSLSISAYKQNWQNADIRYRRAL VFFI-
ARPQRTTYLKATIFMNITRATMTDVRYNLKCH

[0334] DOR78nt

[0335] ATGAAGTTCATGAAGTACG-
CAGTTTTCTTTTACACATCGGTGGGCAT-
TGAGCCGTATA CGATTGACTCGCGGTC-
CAAAAAAGCGAGCCTATGGTCACATCTTCTCTTC

TGGGCCAA TGTGATCAATTTAAGTGTCATTGTTTTCGGAGAGATCCTCTATCTGGGAGTGGCCTAT TCCGATGGAAAGTTCATTGATGCCGTCACTGTACTGTCATATATCGGATTCGTAATCG TGGGCATGAGCAAGATGTTCTTCATATGGTGGAAGAAGACCGATCTAAGCGATTTGGT TAAGGAATTGGAGCACATCTATCCAAATGGCAAAGCTGAGGAGGAGATGTATCGGTTG GATAGGTATCTGCGATCTTGTTCACGAATTAGCATTACCTATGCACTACTCTACTCCG TACTCATCTGGACCTTCAATCTGTTCAGTATCATGCAATTCCTTGTCTATGAAAAGTT GCTTAAAATCCGAGTGGTCGGCCAAACGCTGCCATATTTGATGTACTTTCCCTGGAAC TGGCATGAAAACTGGACGTATTATGTGCTGCTGTTCTGTCAAAACTTCGCAGGACATA CTTCGGCATCGGGACAGATCTCTACGGATCTTTTGCTTTGTGCTGTTGCTACCCAGGT GGTAATGCACTTCGATTACTTGGCCAGAGTGGTGGAAAAACAAGTGTTAGATCGCGAT TGGAGCGAAAACTCCAGATTTTTGGCAAAAACTGTACAATATCATCAGCGCATTCTTC GGCTAATGGACGTTCTCAACGATATATTCGGGATACCGCTACTGCTTAACTTTATGGT CTCCACATTTGTCATCTGCTTTGTGGGATTCCAAATGACCGTGGGTGTCCCGCCGGAC ATCATGATTAAGCTCTTCTTGTTCCTGTTCTCGTCCTTGTCGCAAGTGTACTTGATAT GCCACTACGGCCAGCTGATTGCCGATGCGGTAAGAGACTTTCGAAGCTCTAGCTTATC GATTTCTGCATATAAGCAGAATTGGCAAAATGCTGACATTCGCTATCGTCGGGCTCTG GTATTCTTTATAGCTCGACCTCAGAGGACAACTTATCTAAAAGCTACAATTTTCATGA ATATAACAAGGGCCACCATGACGGACGTAAGATACAATTTGAAATGTCAT

[**0336**] DOR81

[**0337**] MMETLRNSGLNLKNDFGIGRKIWRVFSFTYNMVILPVSFPINYVIHLAEFPPELLLQS LQLCLNTWCFALKFFTLIVYTHRLELANKHFDELDKYCVKPAEKRKVRDMVATITRLY LTFVVVYVLYATSTLLDGLLHHRVPYNTYYPFINWRVDRTQMYIQSFLEYFTVGYAIY VATATDSYPVIYVAALRTHILLLKDRIIYLGDPSNEGSSDPSYMFKSLVDCIKAHRTM LNFCDAIQPIISGTIFAQFIICGSILGIIMINMVLFADQSTRFGIVIYVMAVLLQTFP LCFYCNAIVDDCKELAHALFHSAWWVQDKRYQRTVIQFLQKLQQPMTFTAMNIFNINL ATNINVSPLLSVRTGKEAKSELQSLQVAKFAFTVYAIASGMNLDQKLSIKE

[**0338**] DOR81nt

[**0339**] ATGATGGAGACGCTGCGAAATTCGGGCTTGAATTTGAAGAACGATTTCGGTATAGGCC GCAAGATTTGGAGGGTGTTTTCGTTCACCTACAATATGGTGATACTTCCCGTAAGTTT CCCAATCAACTATGTGATACATCTGGCGGAGTTCCCGCCGGAGCTGCTGCTGCAATCC CTGCAACTGTGCCTCAACACTTGGTGCTTCGCTCTGAAGTTCTTCACTCTGATCGTCT ATACGCACCGCTTGGAGCTGGCCAACAAGCACTTTGACGAATTGGATAAGTACTGCGT GAAGCCGGCGGAGAAGCGCAAGGTTCGCGACATGGTGGCCACTATTACAAGACTGTAC CTGACCTTCGTCGTGGTCTACGTCCTCTACGCCACCTCCACGCTACTGGACGGACTAC TGCACCACCGTGTTCCCTACAATACGTACTATCCGTTCATAAACTGGCGAGTCGATCG GACCCAGATGTACATCCAGAGTTTTCTGGAGTACTTCACCGTGGGTTATGCCATATAT GTGGCCACCGCCACCGATTCCTACCCTGTGATTTACGTGGCAGCCCTGCGAACTCATA TTCTCTTGCTCAAGGACCGTATCATTTACTTGGGCGATCCCAGCAACGAGGGTAGCAG CGACCCGAGCTACATGTTTAAATCGTTGGTGGATTGTATCAAGGCACACAGAACCATG CTAAAGT0CAGTTTTTGTGATGCCATTCAACCAATCATCTCTGGCACGATATTTGCCC AATTCATCATATGCGGATCGATCCTGGGCATAATTATGATCAACATGGTATTGTTCGC TGATCAATCGACCCGATTCGGCATAGTCATCTACGTTATGGCCGTCCTTCTGCAGACT TTTCCGCTTTGCTTCTACTGCAACGCCATCGTGGACGACTGCAAAGAACTGGCCCACG CACTTTTCCATTCCGCCTGGTGGGTGCAGGACAAGCGATACCAGCGGACTGTCATCCA GTTCCTGCAGAAACTGCAGCAGCCCATGACCTTCACCGCCATGAACATATTTAACATT AATTTGGCCACTAACATCAATGTAAGTCCACTGCTCTCGGTTAGAACGGGGAAGGAAG CAAAGTCCGAACTTCAATCCTTGCAGGTAGCCAAGTTCGCCTTCACCGTGTACGCCAT CGCGAGCGGTATGAACCTGGACCAAAAGTTAAGCATTAAGGAA

[**0340**] DOR82

[**0341**] MACIPRYQWKGRPTERQFYASEQRIVFLLGTICQIFQITGVLIYWYCNGRLATETGTP VAQLSEMCSSFCLTFVGFCNVYAISTNRNQIETLLEELHQIYPRYRKNHYRcQHYFDM AMTIMRIEFLFYMILYVYYNSAPLWVLLWEHLHEEYDLSFKTQTNTWFPWKVHGSALG FGMAVLSITVGSFVGVGFSIVTQNLICLLTFQLKLHYDGISSQLVSLDCRRPGAHKEL SILIAHHSRILQLGDQVNDIMNFVFGSSLVGATIAICMSSVSIMLLDLASAFKYASGL VAFVLYNFVICYMGTEVTLAVKIGSYMDGRRWIPKDSLLRSQRLQVLVAVGFFNICVL SNRRPKIEILLRYYYHIMFYSFKLYFSLRKGSLWKILSSFTLLRI

[**0342**] DOR82nt

[**0343**] ATGGCATGCATACCAAGATATCAATGGAAAGGACGCCCTACTGAAAGACAGTTCTACG CTTCGGAGCAAAGGATAGTGTTCCTTCTTGGAACCATTTGCCAGATATTCCAGATTAC TGGAGTGCTTATCTATTGGTATTGCAATGGCCGTCTTGCCACGGAAACGGGCACCTTT GTGGCACAATTATCTGAAATGTGCAGTTCTTTTTGTCTAACATTTGTGGGATTCTGTA ACGTTTATGCGATCTCTACAAACCGCAATCAAATTGAAACATTACTCGAGGAGCTTCA TCAGATATATCCGAGATACAGGAAAAATCACTATCGCTGCCAGCATTATTTTGACATG GCCATGACAATAATGAGAATTGAGTTTCTTTTCTATATGATCTTGTACGTGTACTACA

ATAGTGCACCATTATGGGTGCT-TCTTTGGGAACACTTGCACGAGGAATATGATCTTAG CTTCAAGACGCAGACCAACACTTG-GTTTCCATGGAAAGTCCATGGGTCGGCACTTGGA TTTGGTATGGCTGTACTAAGCATAAC-CGTGGGATCCTTTGTGGGCGTAGGTTTCAGTA TTGTCACCCAGAATCTTATCTGTTTGT-TAACCTTCCAACTAAAGTTGCACTACGATGG AATATCCAGTCAGTTAGTATCTCTCGAT-TGCCGTCGTCCTGGAGCTCATAAGGAGTTG AGCATCCTCATCGCCCACCACAGC-CGAATCCTTCAGCTGGGCGACUAAGTCAATGACA TAATGAACTTTGTATTCGGCTCTAGC-CTAGTAGGTGCCACTATTGCCATTTGTATGTC AAGT-GTTTCTATAATGCTACTGGACTTAG-CATCTGCCTTCAAATATGCCAGTGGTCTA GTGGCATTCGTCCTCTACAACTTTGT-CATCTGCTACATGGGAACCGAGGTCACTTTAG CTGTGAAGATTGGTTCATATATGGACG-GAAGGCGGTGGATACCCAAAGATTCGTTGCT GAGATCTCAGAGGCTACAGGT-GCTCGTCGCAGTTGGATTTTTTAATATATGTGTCCTC TCGAATCGTCGTCCTAAAAT-TGAAATTTTGCTTAGATATTATTACCATATTATGTTTT ATTCATTTAAATTATATTTTTCTTTAAG-GAAAGGTAGCCTTTGGAAAATCTTcTCTTC TTTCACCTTATTGAGGATC

[0344] DOR83

[0345] MQLEDFMRYPDLVCQAAQLPRYTWN-GRRSLEVKRNLAKRIIFWLGAVNLVYHNIGCVM YGYFGDGRTKDPIAYLAELASVASMLGF-TIVGTLNLWKMLSLKTHFENLLNEFEELFQ LIKHRAYRIHHYQEKYTRHIRNTFIFHT-SAVVYYNSLPILLMIREHFSNSQQLGYRIQ SNTWYP-WQVQGSIPGFFAAVACQIFSCQTNMCVN-MFIQFLINFFGIQLEIHFDGLARQ LETIDARNPHAKDQLKYLIVYHTKLLN-LADRVNRSFNFTFLISLSVSMISNCFLAFSM TMFDF-GTSLKHLLGLLLFITYNFSMCRSGTH-LILTSGKVLPAAFYNNWYEGDLVYRRM LLILMMRATKPYMWKTYKLAPVSITTY-MAECKTKEAHEQRHFRRHERQKPRVARI

[0346] DOR83nt

[0347] ATGCAGTTGGAGGACTTTATGCGGTAC-CCGGACCTCGTGTGTCAAGCGGCCCAACTTC CCA-GATACACGTGGAATGGCAGACGATCCT-TGGAAGTTAAACGCAACTTGGCAAAACG CATTATCTTCTGGCTTGGAGCAG-TAAATTTGGTTTATCACAATATTGGCTGCGTCATG TATGGCTATTTCGGTGATGGAAGAA-CAAAGGATCCAATTGCGTATTTAGCTGAATTGG CATCTGTGGCCAGCATGCTTGGTTTCAC-CATTGTGGGCACCCTCAACTTGTGGAAGAT GCT-GAGCCTTAAGACCCATTTTGAGAAC-CTACTAAATGAATTCGAGGAATTATTTCAA CTAATCAAGCACAGGGCGTATCGCATA-CACCACTATCAAGAAAAGTATACGCGTCATA TAC-GAAATACATTTATTTTCCATACCTCTGC-CGTTGTCTACTACAACTCACTACCAAT TCTTCTAATGATTCGGGAACATTTCTC-GAACTCACAGCAGTTGGGCTATAGAATTCAG AGTAATACCTGGTATCCCTGGCAGGT-TCAGGGATCAATTCCTGGATTTTTTGCTGCAG TCGCCTGTCAAATCTTTTCGTGCCAAAC-CAATATGTGCGTCAATATGTTTATCCAGTT TCTGAT-CAACTTTTTTGGTATCCAGCTAGAAATA-CACTTCGATGGTTTGGCCAGGCAG CTGGAGACCATCGATGCCCGCAATC-CCCATGCCAAGGATCAATTGAAGTATCTGATTG TATATCACACAAAATTGCTTAATCTAGC-CGACAGAGTTAATCGATCGTTTAACTTTAC GTTTCTCATAAGTCTGTCGGTATCCAT-GATATCCAACTGTTTTCTGGCATTTTCCATG ACCAT-GTTCGACTTTGGCACCTCTCTAAAA-CATTTACTCGGACTTTTGCTATTCATCA CATATAATTTTTCAATGTGCCGCAGTGG-TACGCACTTGATTTTAACGAGTGGCAAAGT ATTGC-CAGCGGCCTTTTATAACAATTGGTAT-GAAGGCGATCTTGTTTATCGAAGGATG CTCCTCATCCTGATGATGCGTGCTAC-GAAACCTTATATGTGGAAAACCTACAAGCTGG CACCTGTATCCATAACTACATATATG-GCAGAATGCAAAACAAAAGAAGCCCATGAACA ACGCCATTTTAGACGCCATGAAAGA-CAAAAACCTCGGGTTGCACGAATA

[0348] DOR84

[0349] MVFSFYAEVATLVDRLRDNEN-FLESCILLSYVSFVVMGLSKI-GAVMKKKPKMTALVRQ LETCFPSPSAKVQEEYAVK-SWLKRCHIYTKGFGGLFMIMYFAHALIPLFIYFIQR VLL HYPDAKQIMPFYQLEPWEFRDSWL-FYPSYFHQSSAGYTATCGSIAGDLMIFAVVLQVI MHYERLAKVLREFKIQAHNAPN-GAKEDIRKLQSLVANHIDILRLTDLMNEVFGIPLLL NFIASALLVCLVGVQLTIALSPEYFCK-QMLFLISVLLEVYLLCSFSQRLIDAVC

[0350] DOR84nt

[0351] ATGGTGTTTAGTTTTTATGCCGAGG-TAGCGACTCTGGTGGACAGGTTACGCGATAATG AAAATTTTCTCGAGAGCTGCATCTTACT-GAGCTACGTGTCCTTTGTGGTCATGGGCCT CTC-CAAGATAGGTGCTGTAAT-GAAAAAAAAGCCAAAAATGACAGCTTTGGTCA GGCAA TTGGAGACCTGCTTTCCGTCGCCAAGTG-CAAAGGTTCAAGAGGAATATGCTGTGAAGT CCTG-GCTGAAACGCTGCCATATATACA-CAAAGGGATTTGGTGGTCTCTTCATGATCAT GTATTTCGCTCACGCTCTGATTCCCT-TATTCATATACTTCATTCAAAGAGTGCTGCTC CAC-TATCCGGATGCCAAGCAGATTATGC-CGTTTTACCAACTCGAACCTTGGGAATTTC GCGACTCCTGGTTGTTTTATCCAAGC-TATTTTCACCAGTCGTCGGCCGGATATACGGC TACATGTGGATCCATTGCCGGTGAC-CTAATGATCTTCGCTGTGGTCCTGCAGGTCATC ATGCACTACCAAAGACTGGCCAAGGT-TCTTAGGGAGTTTAAGATTCAAGCCCATAACG CAC-CCAATGGAGCTAAGGAGGATATAAG-GAAGTTGCAGTCCCTAGTCGCCAATCACAT TGATATACTTCGACTCACTGATCTGAT-GAACGAGGTCTTTGGAATTCCCTTGTTGCTA AACTTTATTGCATCTGCGCTGCTGGTCT-GCCTGGTGGGAGTTCAATTAACCATCGCTT TAAGTCCAGAGTATTTTTGCAAGCAGAT-

GCTATTTCTGATTTCCGTACTGCTTGAGGT CTATCTCCTTTGCTCCTTCAGCCAGAG-GTTAATAGATGCTGTATGT

[0352] DOR87

[0353] MTIEDIGLVGINVRMWRHLAVLYPT-PGSSWRKFAFVLPVTAMNLMQFVYLLRMWGDLP AFILNMFFFSAIFNALMRTWLVIIKRRQ-FEEFLGQLATLFHSILDSTDEWGRGILRRA EREARN-LAILNLSASFLDIVGALVSPLFREERAH-PFGVALPGVSMTSSPVYEVIYLAQ LPTPLLLSMMYMPFVSLFAGLAIFGKAM-LQILVHRLGQIGGEEQSEEERFQRLASCIA YHTQVM-RYVWQLNKLVANIVAVEAIIFGSIICS-LLFCLNIITSPTQVISIVMYILTML YVLFTYYNRANEICLENNRVAEAVYNVP-WYEAGTRFRKTLLIFLMQTQHPMEIRVGNV YPMT-LAMFQSLLNASYSYFTMLRGVTGK

[0354] DOR87nt

[0355] GGCACGAGGCTTATAGAAAGTGCCGAG-CAATGACAATCGAGGATATCGGCCTGGTGGG CAT-CAACGTGCGGATGTGGCGACACTTGGC-CGTGCTGTACCCCACTCCGGGCTCCAGC TGGCGCAAGTTCGCCTTCGTGCTGCCG-GTGACTGCGATGAATCTGATGCAGTTCGTCT ACCT-GCTGCGGATGTGGGGCGACCTGCCCGC-CTTCATTCTGAACATGTTCTTCTTCTC GGCCATTTTCAACGCCCTGATGCG-CACGTGGCTGGTCATAATCAAGCGGCGCCAGTTC GAGGAGTTTCTCGGCCAACTGGC-CACTCTGTTCCATTCGATTCTCGACTCCACCGACG AGTGGGGGCGTGGCATCCTGCG-GAGGGCGGAACGGGAGGCTCGGAACCTG-GCCATCCT TAATTTGAGTGCCTCCTTCCTGGACAT-TGTCGGTGCTCTGGTATCGCCGCTTTTCAGG GAGGAGAGAGCTCATCCCTTCGGCG-TAGCTCTACCAGGAGTGAGCATGACCAGTTCAC CCGTCTACGAGGTTATCTACTTGGC-CCAACTGCCTACGCCCCTGCTGCTGTCCATGAT GTACATGCCTTTCGTCAGCCTTTTTGC-CGGCCTGGCCATCTTTGGGAAGGCCATGCTG CAGATCCTGGTACACAGGCTGGGCCA-GATTGGCGGAGAAGAGCAGTCGGAGGAGGAGC GCTTCCAAAGGCTGGCCTCCTGCAT-TGCGTACCACACGCAGGTGATGCGCTATGTGTG GCAGCTCAACAAACTGGTGGCCAACAT-TGTGGCGGTGGAAGCAATTATTTTTGGCTCG ATAATCTGCTCACTGCTCTTCTGTCT-GAATATTATAACCTCACCCACCCAGGTGATCT CGATAGTGATGTACATTCTGACCATGCT-GTACGTTCTCTTCACCTACTACAATCGGGC CAAT-GAAATATGCCTCGAGAACAACCGGGTG-GCGGAGGCTGTTTACAATGTGCCCTGG TACGAGGCAGGAACTCGGTTTCG-CAAAACCCTCCTGATCTTCTTGATGCAAACACAAC ACCCGATGGAGATAAGAGTCG-GCAACGTTTACCCCATGACATTGGCCAT-GTTCCAGAG TCTGTTGAATGCGTCCTACTC-CTACTTTACCATGCTGCGTGGCGTCACCGGCAAA TGA GCTGAAAGACCGAAAAAACCGGAGTATC-CCCTTCCATATTCCCCCTGCTCCTTTATTT TCCTTTC-CTTTTCCCTTTCCGTTTTCCCAT-TCGCTTTTCCAGCAATCCGGGTAATGCA AAAAGTTGTTGCTGGCTGTGGTCCTG-GCTGCTTGTTTGGCATTTGCATATGCTTGTCG TTTGAAAGGATTTAATCGGACTGCTG-GCACGGAGTCGGCATCCTGGCTCCTGGATCCT GGCATGCAAATAGTTGGCTTCTTAGAT-TGTTACACAAAATAGATTGTAGATTGCAGCT GAAT-GTTGTGCTTGGAATAAAGTCAAAAGGAT-GTGGAGTCGGCCCAAGGCTCTGCCCA TTCTGTTTGCTCGGGATGCCCGAAAG-TATGAAAAAAAAAAAAAAAAAA

[0356] DOR91

[0357] MVRYVPRFADGQKVKLAWPLAVFRLN-HIFWPLDPSTGKWGRYLDKVLAVAMSLVFMQH NDAELRYLRFEASNRNLDAFLTGMPTYL-ILVEAQFRSLHILLHFEKLQKFLEIFYANI YID-PRKEPEMFRKVDGKMIINRLVSAMYGA-VISLYLIAPVFSIINQSKDFLYSMIFPF DSDPLYIFVPLLLTNVWVGIVIDTMMF-GETNLLCELIVHLNGSYMLLKRDLQLAIEKI LVARD-RPHMAKQLKVLITKTLRKNVALNQF-GQQLEAQYTVRVFIMFAFAAGLLCALSF KAYTTDSLSTMYYLTHWEQILQYST-NPSENLRLLKLINLAIEMNSKPFYVTGLKYFRV SLQAGLKRQKFLRSASSSTLSTADVLAFAFAFTRWLL

[0358] DOR91nt

[0359] ATGGTTCGTTACGTGCCCCGGTTCGCT-GATGGTCAGAAAGTAAAGTTGGCTTGGCCCT TGGCGGTTTTTCGGTTAAATCACATAT-TCTGGCCATTGGATCCGAGCACAGGGAAATG GGGCCGATATCTGGACAAGGTTCTAGCT-GTTGCGATGTCCTTGGTTTTTATGCAACAC AAC-GATGCAGAGCTGAGGTACTTGCGCTTC-GAGGCAAGTAATCGGAATTTGGATGCCT TTCTCACAGGAATGCCAACGTATT-TAATCCTCGTGGAGGCTCAATTTAGAAGTCTTCA CATTCTACTGCACTTCGAGAAGCTTCA-GAAGTTTTTAGAAATATTCTACGCAAATATT TATAT-TGATCCCCGTAAGGAACCCGAAAT-GTTTCGAAAAGTGGATGGAAAGATGATAA TTAACAGATTAGTTTCGGCCATGTACG-GTGCAGTTATCTCTCTGTATCTAATCGCACC CGTTTTTTCCATCATTAACCAAAGCAAA-GATTTTCTATACTCTATGATCTTTCCGTTC GATTCG-GATCCCTTGTACATATTTGTGCCACT-GCTTTTGACAAACGTATGGGTTGGCA TTGTAATAGATACCATGATGTTCGGG-GAGACGAATTTGTTGTGTGAACTAATTGTCCA CCTAAATGGTAGTTATATGTTGCTCAA-GAGGGACTTGCAGTTGGCCATTGAAAAGATA TTAGTTGCAAGGGACCGTCCGCATATG-GCCAAACAGCTAAAGGTTTTAATTACAAAAA CTCTCCGAAAGAATGTGGCTCTAAAT-CAGTTTGGCCAGCAGCTGGAGGCTCAGTATAC TGT-GCGGGTTTTTATTATGTTTGCATTCGCT-GCGGGCCTTTTATGTGCTCTTTCTTTT AAGGCTTATACGACGGATTCCCTCAGCA-CAATGTACTACCTTACCCATTGGGAGCAAA TCCTG-CAGTACTCTACAAATCCCAGC-GAAAATCTGCGATTACTAAAGCTCATTAACTT GGCCATTGAGATGAACAGCAAGCCCTTC-TATGTGACAGGGCTAAAATATTTTCGCGTT AGTCT-GCAGGCTGGCTTAAAACGT-

CAAAAGTTTCTGCGGTCTGCCAGCTCATCCACCC TTAGCACCGCTGATGTGTTG-GCATTTGCTTTTGCTTTTACTCGCTGGCTGCTT

[0360] DOR92

[0361] MSEWLRFLKRDQQLDVYF-FAVPRLSLDIMGYWPGKTGDTWPWRSLI-HFAILAIGVATE LHAGMCFLDRQQITLALETLCPAGT-SAVTLLKMFLMLRFRQDLSIMWNRLRGLLFDPN WERPEQRDIRLKHSAMAARINFWPLSAG-FFTCTTYNLKPILIAMILYLQNRYEDFVWF TPFNMT-MPKVLLNYPFFPLTYIFIAYTGYVTIFM-FGGCDGFYFEFCAHLSALFEVLQA EIESMFRPYTDHLELSPVQLYILEQK-MRSVIIRHNAIIDLTRFFRDRYTIITLAHFVS AAMVIG-FSMVNLLTLGNNGLGAMLYVAY-TVAALSQLLVYCYGGTLVAESSTGLCRAMF SCPWQLFKPKQRRLVQLLILRSQRPVS-MAVPFFSPSLATFAAILQTSGSIIALVKSFQ

[0362] DOR92nt

[0363] ATGTCCGAGTGGTTACGCTTTCT-GAAACGCGATCAACAGCTGGATGTGTACTTTTTTG CAGTGCCCCGCTTGAGTTTAGACAT-AATGGGCTATTGGCCGGGCAAAACTGGTGATAC ATGGCCCTGGAGATCCCTGATTCACT-TCGCAATCCTGGCCATTGGCGTGGCCACCGAA CTGCATGCTGGCATGTGTTTTCTAGAC-CGACAGCAGATTACCTTGGCACTGGAGACCC TCT-GTCCAGCTGGCACATCGGCGGTCACGCT-GCTCAAGATGTTCCTAATGCTGCGCTT TCGTCAGGATCTCTCCATTATGTGGAAC-CGCCTGAGGGGCCTGCTCTTCGATCCCAAC TGG-GAGCGACCCGAGCAGCGGGACATCCG-GCTAAAGCACTCGGCCATGGCGGCTCGCA TCAATTTCTGGCCCCTGTCAGCCGGAT-TCTTCACATGCACCACCTACAACCTAAAGCC GATACTGATCGCAATGATATTGTATCTC-CAGAATCGTTACGAGGACTTCGTTTGGTTT ACAC-CCTTCAATATGACTATGCCCAAAGTTCT-GCTAAACTATCCATTTTTTCCCCTGA CCTACATATTTATTGCCTATACGGGC-TATGTGACCATCTTTATGTTCGGCGGCTGTGA TGGTTTTTATTTCGAGTTCTGTGCCCAC-CTATCAGCTCTTTTCGAAGTGCTCCAGGCG GAGATAGAATCAATGTTTAGACCCTA-CACTGATCACTTGGAACTGTCGCCAGTGCAGC TTTACATTTTAGAGCAAAAGATGCGAT-CAGTAATCATTAGGCACAATGCCATCATCGA TTTGACCAGATTTTTTCGTGATCGC-TATACCATTATTACCCTGGCCCATTTTGTGTCC GCCGCCATGGTGATTGGATTCAGCATG-GTTAATCTCCTGACATTGGGCAATAATGGTC TGGGCGCAATGCTCTATGTGGCCTA-CACGGTTGCCGCTTTGAGCCAACTGCTGGTTTA TTGCTATGGCGGAACTCTGGTGGC-CGAAAGTAGCACTGGTCTGTGCCGAGCCATGTTC TCCTGTCCGTGGCAGCTTTTTAAGC-CTAAACAACGTCGACTCGTTCAGCTTTTGATTC TCAGATCGCAGCGTCCTGTTTCCATG-GCAGTGCCATTCTTTTCGCCATCGTTGGCTAC CTTTGCTGCGATTCTTCAAACTTCGGGT-TCCATAATTGCGCTGGTTAAGTCCTTTCAG

[0364] DOR95

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[0366] DOR95nt

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[0368] DOR99

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[0370] DOR99nt

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[0376] Genbank Accession Numbers

[0377] The accession numbers for the sequences reported in this paper are AF127921-AF127926.

[0378] References

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    130                 135                 140

Thr Thr Leu Ser Cys Val Arg Val Val Val Arg Pro Asp Arg Glu Leu
145                 150                 155                 160

Leu Tyr Pro Ala Trp Phe Gly Val Asp Trp Met His Ser Thr Arg Asn
                165                 170                 175

Tyr Val Leu Ile Asn Ile Tyr Gln Leu Phe Gly Leu Ile Val Gln Ala
            180                 185                 190

Ile Gln Asn Cys Ala Ser Asp Ser Tyr Pro Pro Ala Phe Leu Cys Leu
        195                 200                 205

Leu Thr Gly His Met Arg Ala Leu Glu Leu Arg Val Arg Arg Ile Gly
    210                 215                 220

Cys Arg Thr Glu Lys Ser Asn Lys Gly Gln Thr Tyr Glu Ala Trp Arg
225                 230                 235                 240

Glu Glu Val Tyr Gln Glu Leu Ile Glu Cys Ile Arg Asp Leu Ala Arg
                245                 250                 255

Val His Arg Leu Arg Glu Ile Ile Gln Arg Val Leu Ser Val Pro Cys
            260                 265                 270

Met Ala Gln Phe Val Cys Ser Ala Ala Val Gln Cys Thr Val Ala Met
        275                 280                 285
```

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```
His Phe Leu Tyr Val Ala Asp Asp His Asp His Thr Ala Met Ile Ile
    290                 295                 300

Ser Ile Val Phe Phe Ser Ala Val Thr Leu Glu Val Phe Val Ile Cys
305                 310                 315                 320

Tyr Phe Gly Asp Arg Met Arg Thr Gln Ser Glu Ala Leu Cys Asp Ala
                325                 330                 335

Phe Tyr Asp Cys Asn Trp Ile Glu Gln Leu Pro Lys Phe Lys Arg Glu
            340                 345                 350

Leu Leu Phe Thr Leu Ala Arg Thr Gln Arg Pro Ser Leu Ile Tyr Ala
        355                 360                 365

Gly Asn Tyr Ile Ala Leu Ser Leu Glu Thr Phe Glu Gln Val Met Arg
    370                 375                 380

Phe Thr Tyr Ser Val Phe Thr Leu Leu Leu Arg Ala Lys
385                 390                 395


<210> SEQ ID NO 3
<211> LENGTH: 1499
<212> TYPE: DNA
<213> ORGANISM: DROSOPHILA MELANOGASTER  DOR104

<400> SEQUENCE: 3

gaattcggca cgagcagtcg atggccagtc ttcagttcca cggcaacgtc gatgcggaca     60

tcaggtatga tattagcctg gatccggcta gggaatcgaa tctcttccgt ctgctaatgg    120

gactccagtt ggcgaatggc acgaagccat cgccgcggtt acccaaatgg tggccaaagc    180

ggctggaaat gattggtaaa gtgctgccca aagcctattg ttccatggtg attttcacct    240

ccctgcattt gggtgtcctg ttcacgaaaa ccacactgga tgtcctgccg acgggggagc    300

tgcaggccat aacggatgcc ctcaccatga ccataatata ctttttcacg ggctacggca    360

ccatctactg gtgcctgcgc tcccggcgcc tcttggccta catggagcac atgaaccggg    420

agtatcgcca tcattcgctg gccggggtga cctttgtgag tagccatgcg gcctttagga    480

tgtccagaaa cttcacggtg gtgtggataa tgtcctgcct gctgggcgtg atttcctggg    540

gcgtttcgcc actgatgctg ggcatccgga tgctgccgct ccaatgttgg tatcccttcg    600

acgccctggg tcccggcaca tatacggcgg tctatgctac acaacttttc ggtcagatca    660

tggtgggcat gacctttgga ttcgggggat cactgtttgt caccctgagc ctgctactcc    720

tgggacaatt cgatgtgctc tactgcagcc tgaagaacct ggatgcccat accaagttgc    780

tgggcgggga gtctgtaaat ggcctgagtt cgctgcaaga ggagttgctg ctgggggact    840

cgaagaggga attaaatcag tacgttttgc tccaggagca tccgacggat ctgctgagat    900

tgtcggcagg acgaaaatgt cctgaccaag gaaatgcgtt tcacaacgcc ttggtggaat    960

gcattcgctt gcatcgcttc attctgcact gctcacagga gttggagaat ctattcagtc   1020

catattgtct ggtcaagtca ctgcagatca cctttcagct ttgcctgctg gtctttgtgg   1080

gcgtttcggg tactcgagag gtcctgcgga ttgtcaacca gctacagtac ttgggactga   1140

ccatcttcga gctcctaatg ttcacctatt gtggcgaact cctcagtcgg catagtattc   1200

gatctggcga cgccttttgg agggtgcgt ggtggaagca cgcccatttc atccgccagg   1260

acatcctcat ctttctggtc aatagtagac gtgcagttca cgtgactgcc ggcaagtttt   1320

atgtgatgga tgtgaatcgt ctaagatcgg ttataacgca ggcgttcagc ttcttgactt   1380

tgctgcaaaa gttggctgcc aagaagacgg aatcggagct ctaaactggt accacgcatc   1440
```

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```
gatatttatt tagcgcatta aaaaaaagtc gagtaaaagc aaaaaaaaaa aaaaaaaaa     1499


<210> SEQ ID NO 4
<211> LENGTH: 467
<212> TYPE: PRT
<213> ORGANISM: DROSOPHILA MELANOGASTER  DOR104

<400> SEQUENCE: 4

Met Ala Ser Leu Gln Phe His Gly Asn Val Asp Ala Asp Ile Arg Tyr
1               5                   10                  15

Asp Ile Ser Leu Asp Pro Ala Arg Glu Ser Asn Leu Phe Arg Leu Leu
            20                  25                  30

Met Gly Leu Gln Leu Ala Asn Gly Thr Lys Pro Ser Pro Arg Leu Pro
        35                  40                  45

Lys Trp Trp Pro Lys Arg Leu Glu Met Ile Gly Lys Val Leu Pro Lys
    50                  55                  60

Ala Tyr Cys Ser Met Val Ile Phe Thr Ser Leu His Leu Gly Val Leu
65                  70                  75                  80

Phe Thr Lys Thr Thr Leu Asp Val Leu Pro Thr Gly Glu Leu Gln Ala
                85                  90                  95

Ile Thr Asp Ala Leu Thr Met Thr Ile Ile Tyr Phe Phe Thr Gly Tyr
            100                 105                 110

Gly Thr Ile Tyr Trp Cys Leu Arg Ser Arg Arg Leu Leu Ala Tyr Met
        115                 120                 125

Glu His Met Asn Arg Glu Tyr Arg His His Ser Leu Ala Gly Val Thr
    130                 135                 140

Phe Val Ser Ser His Ala Ala Phe Arg Met Ser Arg Asn Phe Thr Val
145                 150                 155                 160

Val Trp Ile Met Ser Cys Leu Leu Gly Val Ile Ser Trp Gly Val Ser
                165                 170                 175

Pro Leu Met Leu Gly Ile Arg Met Leu Pro Leu Gln Cys Trp Tyr Pro
            180                 185                 190

Phe Asp Ala Leu Gly Pro Gly Thr Tyr Thr Ala Val Tyr Ala Thr Gln
        195                 200                 205

Leu Phe Gly Gln Ile Met Val Gly Met Thr Phe Gly Phe Gly Gly Ser
    210                 215                 220

Leu Phe Val Thr Leu Ser Leu Leu Leu Leu Gly Gln Phe Asp Val Leu
225                 230                 235                 240

Tyr Cys Ser Leu Lys Asn Leu Asp Ala His Thr Lys Leu Leu Gly Gly
                245                 250                 255

Glu Ser Val Asn Gly Leu Ser Ser Leu Gln Glu Glu Leu Leu Leu Gly
            260                 265                 270

Asp Ser Lys Arg Glu Leu Asn Gln Tyr Val Leu Leu Gln Glu His Pro
        275                 280                 285

Thr Asp Leu Leu Arg Leu Ser Ala Gly Arg Lys Cys Pro Asp Gln Gly
    290                 295                 300

Asn Ala Phe His Asn Ala Leu Val Glu Cys Ile Arg Leu His Arg Phe
305                 310                 315                 320

Ile Leu His Cys Ser Gln Glu Leu Glu Asn Leu Phe Ser Pro Tyr Cys
                325                 330                 335

Leu Val Lys Ser Leu Gln Ile Thr Phe Gln Leu Cys Leu Leu Val Phe
            340                 345                 350
```

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```
Val Gly Val Ser Gly Thr Arg Glu Val Leu Arg Ile Val Asn Gln Leu
        355                 360                 365

Gln Tyr Leu Gly Leu Thr Ile Phe Glu Leu Leu Met Phe Thr Tyr Cys
    370                 375                 380

Gly Glu Leu Leu Ser Arg His Ser Ile Arg Ser Gly Asp Ala Phe Trp
385                 390                 395                 400

Arg Gly Ala Trp Trp Lys His Ala His Phe Ile Arg Gln Asp Ile Leu
                405                 410                 415

Ile Phe Leu Val Asn Ser Arg Arg Ala Val His Val Thr Ala Gly Lys
            420                 425                 430

Phe Tyr Val Met Asp Val Asn Arg Leu Arg Ser Val Ile Thr Gln Ala
        435                 440                 445

Phe Ser Phe Leu Thr Leu Leu Gln Lys Leu Ala Ala Lys Lys Thr Glu
    450                 455                 460

Ser Glu Leu
465
```

```
<210> SEQ ID NO 5
<211> LENGTH: 1556
<212> TYPE: DNA
<213> ORGANISM: DROSOPHILA MELANOGASTER  DOR87

<400> SEQUENCE: 5

ggcacgaggc ttatagaaag tgccgagcaa tgacaatcga ggatatcggc ctggtgggca     60

tcaacgtgcg gatgtggcga cacttggccg tgctgtaccc cactccgggc tccagctggc    120

gcaagttcgc cttcgtgctg ccggtgactg cgatgaatct gatgcagttc gtctacctgc    180

tgcggatgtg ggcgacctg cccgccttca ttctgaacat gttcttcttc tcggccattt    240

tcaacgccct gatgcgcacg tggctggtca taatcaagcg gcgccagttc gaggagtttc    300

tcggccaact ggccactctg ttccattcga ttctcgactc caccgacgag tgggggcgtg    360

gcatcctgcg gagggcggaa cgggaggctc ggaacctggc catccttaat ttgagtgcct    420

ccttcctgga cattgtcggt gctctggtat cgccgctttt cagggaggag agagctcatc    480

ccttcggcgt agctctacca ggagtgagca tgaccagttc acccgtctac gaggttatct    540

acttggccca actgcctacg cccctgctgc tgtccatgat gtacatgcct ttcgtcagcc    600

tttttgccgg cctggccatc tttgggaagg ccatgctgca gatcctggta cacaggctgg    660

gccagattgg cggagaagag cagtcggagg aggagcgctt ccaaaggctg gcctcctgca    720

ttgcgtacca cacgcaggtg atgcgctatg tgtggcagct caacaaactg gtggccaaca    780

ttgtggcggt ggaagcaatt atttttggct cgataatctg ctcactgctc ttctgtctga    840

atattataac ctcacccacc caggtgatct cgatagtgat gtacattctg accatgctgt    900

acgttctctt cacctactac aatcgggcca atgaaatatg cctcgagaac aaccgggtgg    960

cggaggctgt ttacaatgtg ccctggtacg aggcaggaac tcggtttcgc aaaaccctcc   1020

tgatcttctt gatgcaaaca caacacccga tggagataag agtcggcaac gtttacccca   1080

tgacattggc catgttccag agtctgttga atgcgtccta ctcctacttt accatgctgc   1140

gtggcgtcac cggcaaatga gctgaaagac cgaaaaaacc ggagtatccc cttccatatt   1200

ccccctgctc ctttattttc ctttcctttt ccctttccgt tttcccattc gcttttccag   1260

caatccgggt aatgcaaaaa gttgttgctg gctgtggtcc tggctgcttg tttggcattt   1320
```

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gcatatgctt gtcgtttgaa aggatttaat cggactgctg gcacggagtc ggcatcctgg 1380

ctcctggatc ctggcatgca aatagttggc ttcttagatt gttacacaaa atagattgta 1440

gattgcagct gaatgttgtg cttggaataa agtcaaaagg atgtggagtc ggcccaaggc 1500

tctgcccatt ctgtttgctc gggatgcccg aaagtatgaa aaaaaaaaaa aaaaaa 1556

<210> SEQ ID NO 6
<211> LENGTH: 376
<212> TYPE: PRT
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR87

<400> SEQUENCE: 6

Met Thr Ile Glu Asp Ile Gly Leu Val Gly Ile Asn Val Arg Met Trp
1 5 10 15

Arg His Leu Ala Val Leu Tyr Pro Thr Pro Gly Ser Ser Trp Arg Lys
20 25 30

Phe Ala Phe Val Leu Pro Val Thr Ala Met Asn Leu Met Gln Phe Val
35 40 45

Tyr Leu Leu Arg Met Trp Gly Asp Leu Pro Ala Phe Ile Leu Asn Met
50 55 60

Phe Phe Phe Ser Ala Ile Phe Asn Ala Leu Met Arg Thr Trp Leu Val
65 70 75 80

Ile Ile Lys Arg Arg Gln Phe Glu Glu Phe Leu Gly Gln Leu Ala Thr
85 90 95

Leu Phe His Ser Ile Leu Asp Ser Thr Asp Glu Trp Gly Arg Gly Ile
100 105 110

Leu Arg Arg Ala Glu Arg Glu Ala Arg Asn Leu Ala Ile Leu Asn Leu
115 120 125

Ser Ala Ser Phe Leu Asp Ile Val Gly Ala Leu Val Ser Pro Leu Phe
130 135 140

Arg Glu Glu Arg Ala His Pro Phe Gly Val Ala Leu Pro Gly Val Ser
145 150 155 160

Met Thr Ser Ser Pro Val Tyr Glu Val Ile Tyr Leu Ala Gln Leu Pro
165 170 175

Thr Pro Leu Leu Leu Ser Met Met Tyr Met Pro Phe Val Ser Leu Phe
180 185 190

Ala Gly Leu Ala Ile Phe Gly Lys Ala Met Leu Gln Ile Leu Val His
195 200 205

Arg Leu Gly Gln Ile Gly Gly Glu Glu Gln Ser Glu Glu Glu Arg Phe
210 215 220

Gln Arg Leu Ala Ser Cys Ile Ala Tyr His Thr Gln Val Met Arg Tyr
225 230 235 240

Val Trp Gln Leu Asn Lys Leu Val Ala Asn Ile Val Ala Val Glu Ala
245 250 255

Ile Ile Phe Gly Ser Ile Ile Cys Ser Leu Leu Phe Cys Leu Asn Ile
260 265 270

Ile Thr Ser Pro Thr Gln Val Ile Ser Ile Val Met Tyr Ile Leu Thr
275 280 285

Met Leu Tyr Val Leu Phe Thr Tyr Tyr Asn Arg Ala Asn Glu Ile Cys
290 295 300

Leu Glu Asn Asn Arg Val Ala Glu Ala Val Tyr Asn Val Pro Trp Tyr
305 310 315 320

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```
Glu Ala Gly Thr Arg Phe Arg Lys Thr Leu Leu Ile Phe Leu Met Gln
                325                 330                 335

Thr Gln His Pro Met Glu Ile Arg Val Gly Asn Val Tyr Pro Met Thr
            340                 345                 350

Leu Ala Met Phe Gln Ser Leu Leu Asn Ala Ser Tyr Ser Tyr Phe Thr
        355                 360                 365

Met Leu Arg Gly Val Thr Gly Lys
    370                 375
```

<210> SEQ ID NO 7
<211> LENGTH: 1338
<212> TYPE: DNA
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR53

<400> SEQUENCE: 7

```
tcaaacaaag ccacggacaa gatgttaagc aagtttttc cccacataaa agaaaagcca     60

ttgagcgagc gggttaagtc ccgagatgcc ttcatttact tggatcgggt gatgtggtcc    120

tttggctgga cagagcctga aaacaaaagg tggatccttc cttataaact gtggttagcg    180

ttcgtgaaca tagtaatgct catccttctg ccgatctcga taagcatcga gtacctccac    240

cgatttaaaa ccttctcggc gggggagttc cttagttccc tcgagattgg agtcaacatg    300

tacggaagct cttttaagtg cgccttcacc ttgattggat tcaagaaaag acaggaagct    360

aaggttttac tggatcagct ggacaagaga tgccttagcg ataaggagag gtccactgtt    420

catcgctatg tcgccatggg aaactttttc gatattttgt atcacatttt ttactccacc    480

ttcgtggtaa tgaacttccc gtattttctg cttgagagac gccatgcttg gcgcatgtac    540

tttccatata tcgattccga cgaacagttt tacatctcca gcatcgccga gtgttttctg    600

atgacggagg ccatctacat ggatctctgt acggacgtgt gtcccttgat ctccatgctt    660

atggctcgat gccacatcag cctcctgaaa cagcgactga gaaatctccg atcgaagcca    720

ggaaggaccg aagatgagta cttggaggag ctcaccgagt gcattcggga tcatcgattg    780

ctattggact atgttgacgc attgcgaccc gtcttttcgg gaaccatttt tgtgcagttc    840

ctcctgatcg gtactgtact gggtctctca atgataaatc taatgttctt ctcgacattt    900

tggactggtg tcgccacttg cctttttatg ttcgacgtgt ccatggagac gttccccttt    960

tgctatttgt gcaacatgat tatcgatgac tgccaggaaa tgtccaattg cctctttcaa   1020

tcggactgga cctctgccga tcgtcgctac aaatccactt tggtatactt tcttcacaat   1080

cttcagcaac ccattactct cacggctggt ggagtgtttc ctatttccat gcaaacaaat   1140

ttggctatgg tgaagctggc attttctgtg gttacggtaa ttaagcaatt taacttggcc   1200

gaaaggtttc aataagttga gagggacgag ctctgctact attatattat atattatatt   1260

atattatata tatattattt tatattatat attgctgtac cctaataaat atttagtaat   1320

aaaaaaaaaa aaaaaaa                                                  1338
```

<210> SEQ ID NO 8
<211> LENGTH: 397
<212> TYPE: PRT
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR53

<400> SEQUENCE: 8

```
Met Leu Ser Lys Phe Phe Pro His Ile Lys Glu Lys Pro Leu Ser Glu
```

-continued

```
1               5                   10                  15

Arg Val Lys Ser Arg Asp Ala Phe Ile Tyr Leu Asp Arg Val Met Trp
            20                  25                  30

Ser Phe Gly Trp Thr Glu Pro Glu Asn Lys Arg Trp Ile Leu Pro Tyr
        35                  40                  45

Lys Leu Trp Leu Ala Phe Val Asn Ile Val Met Leu Ile Leu Leu Pro
    50                  55                  60

Ile Ser Ile Ser Ile Glu Tyr Leu His Arg Phe Lys Thr Phe Ser Ala
65                  70                  75                  80

Gly Glu Phe Leu Ser Ser Leu Glu Ile Gly Val Asn Met Tyr Gly Ser
                85                  90                  95

Ser Phe Lys Cys Ala Phe Thr Leu Ile Gly Phe Lys Lys Arg Gln Glu
            100                 105                 110

Ala Lys Val Leu Leu Asp Gln Leu Asp Lys Arg Cys Leu Ser Asp Lys
        115                 120                 125

Glu Arg Ser Thr Val His Arg Tyr Val Ala Met Gly Asn Phe Phe Asp
    130                 135                 140

Ile Leu Tyr His Ile Phe Tyr Ser Thr Phe Val Val Met Asn Phe Pro
145                 150                 155                 160

Tyr Phe Leu Leu Glu Arg Arg His Ala Trp Arg Met Tyr Phe Pro Tyr
                165                 170                 175

Ile Asp Ser Asp Glu Gln Phe Tyr Ile Ser Ser Ile Ala Glu Cys Phe
            180                 185                 190

Leu Met Thr Glu Ala Ile Tyr Met Asp Leu Cys Thr Asp Val Cys Pro
        195                 200                 205

Leu Ile Ser Met Leu Met Ala Arg Cys His Ile Ser Leu Leu Lys Gln
    210                 215                 220

Arg Leu Arg Asn Leu Arg Ser Lys Pro Gly Arg Thr Glu Asp Glu Tyr
225                 230                 235                 240

Leu Glu Glu Leu Thr Glu Cys Ile Arg Asp His Arg Leu Leu Leu Asp
                245                 250                 255

Tyr Val Asp Ala Leu Arg Pro Val Phe Ser Gly Thr Ile Phe Val Gln
            260                 265                 270

Phe Leu Leu Ile Gly Thr Val Leu Gly Leu Ser Met Ile Asn Leu Met
        275                 280                 285

Phe Phe Ser Thr Phe Trp Thr Gly Val Ala Thr Cys Leu Phe Met Phe
    290                 295                 300

Asp Val Ser Met Glu Thr Phe Pro Phe Cys Tyr Leu Cys Asn Met Ile
305                 310                 315                 320

Ile Asp Asp Cys Gln Glu Met Ser Asn Cys Leu Phe Gln Ser Asp Trp
                325                 330                 335

Thr Ser Ala Asp Arg Arg Tyr Lys Ser Thr Leu Val Tyr Phe Leu His
            340                 345                 350

Asn Leu Gln Gln Pro Ile Thr Leu Thr Ala Gly Gly Val Phe Pro Ile
        355                 360                 365

Ser Met Gln Thr Asn Leu Ala Met Val Lys Leu Ala Phe Ser Val Val
    370                 375                 380

Thr Val Ile Lys Gln Phe Asn Leu Ala Glu Arg Phe Gln
385                 390                 395
```

<210> SEQ ID NO 9

-continued

<211> LENGTH: 1321
<212> TYPE: DNA
<213> ORGANISM: DROSOPHILA MELANOGASTER   DOR67

<400> SEQUENCE: 9

```
ggcacgagga aatgttaagc cagttctttc cccacattaa agaaaagcca ttgagcgagc     60

gggttaagtc ccgagatgcc ttcgtttact tagatcgggt gatgtggtcc tttggctgga    120

cagtgcctga aaacaaaagg tgggatctac attacaaact gtggtcaact ttcgtgacat    180

tggtgatatt tatccttctg ccgatatcgg taagcgttga gtatattcag cggttcaaga    240

ccttctcggc gggtgagttt cttagctcaa tccagattgg cgttaacatg tacggaagca    300

gctttaaaag ttatttgacc atgatgggat ataagaagag acaggaggct aagatgtcac    360

tggatgagct ggacaagaga tgcgtttgtg atgaggagag gaccattgta catcgacatg    420

tcgccctggg aaacttttgc tatattttct atcacattgc gtacactagc tttttgattt    480

caaacttttt gtcatttata atgaagagaa tccatgcctg gcgcatgtac tttccctacg    540

tcgaccccga aaagcaattt tacatctcta gcatcgccga agtcattctt agggggtggg    600

ccgtcttcat ggatctctgc acggatgtgt gtcctttgat ctccatggta atagcacgat    660

gccacatcac ccttctgaaa cagcgcctgc gaaatctacg atcggaacca ggaaggacgg    720

aagatgagta cttgaaggag ctcgccgact gcgttcgaga tcaccgcttg atattggact    780

atgtcgacgc attgcgatcc gtcttttcgg ggacaatttt tgtgcagttc ctcttgatcg    840

gtattgtact gggtctgtca atgataaata taatgttttt ctcaacactt tcgactggtg    900

tcgccgttgt cctttttatg tcctgcgtat ctatgcagac gttccccttt tgctatttgt    960

gtaacatgat tatggatgac tgccaagaga tggccgactc ccttttttcaa tcggactgga   1020

catctgccga tcgtcgctac aaatccactt tggtatactt tcttcacaat cttcagcagc   1080

ccattattct tacggctggt ggagtctttc ctatttccat gcaaacaaat ttaaatatgg   1140

tgaagctggc ctttactgtg gttacaatag tgaaacaatt taacttggca gaaaagtttc   1200

aataagttaa gatatgcaag ctctgctatt ataaacctac actcgagaaa atatttcttc   1260

acattaataa accttcagta cttactgctt gtggcgcccc cggaaaaaaa aaaaaaaaaa   1320

a                                                                    1321
```

<210> SEQ ID NO 10
<211> LENGTH: 397
<212> TYPE: PRT
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR67

<400> SEQUENCE: 10

```
Met Leu Ser Gln Phe Phe Pro His Ile Lys Glu Lys Pro Leu Ser Glu
1               5                   10                  15

Arg Val Lys Ser Arg Asp Ala Phe Val Tyr Leu Asp Arg Val Met Trp
            20                  25                  30

Ser Phe Gly Trp Thr Val Pro Glu Asn Lys Arg Trp Asp Leu His Tyr
        35                  40                  45

Lys Leu Trp Ser Thr Phe Val Thr Leu Val Ile Phe Ile Leu Leu Pro
    50                  55                  60

Ile Ser Val Ser Val Glu Tyr Ile Gln Arg Phe Lys Thr Phe Ser Ala
65                  70                  75                  80

Gly Glu Phe Leu Ser Ser Ile Gln Ile Gly Val Asn Met Tyr Gly Ser
```

-continued

```
                85                  90                  95

Ser Phe Lys Ser Tyr Leu Thr Met Met Gly Tyr Lys Lys Arg Gln Glu
            100                 105                 110

Ala Lys Met Ser Leu Asp Glu Leu Asp Lys Arg Cys Val Cys Asp Glu
        115                 120                 125

Glu Arg Thr Ile Val His Arg His Val Ala Leu Gly Asn Phe Cys Tyr
    130                 135                 140

Ile Phe Tyr His Ile Ala Tyr Thr Ser Phe Leu Ile Ser Asn Phe Leu
145                 150                 155                 160

Ser Phe Ile Met Lys Arg Ile His Ala Trp Arg Met Tyr Phe Pro Tyr
                165                 170                 175

Val Asp Pro Glu Lys Gln Phe Tyr Ile Ser Ser Ile Ala Glu Val Ile
            180                 185                 190

Leu Arg Gly Trp Ala Val Phe Met Asp Leu Cys Thr Asp Val Cys Pro
        195                 200                 205

Leu Ile Ser Met Val Ile Ala Arg Cys His Ile Thr Leu Leu Lys Gln
    210                 215                 220

Arg Leu Arg Asn Leu Arg Ser Glu Pro Gly Arg Thr Glu Asp Glu Tyr
225                 230                 235                 240

Leu Lys Glu Leu Ala Asp Cys Val Arg Asp His Arg Leu Ile Leu Asp
                245                 250                 255

Tyr Val Asp Ala Leu Arg Ser Val Phe Ser Gly Thr Ile Phe Val Gln
            260                 265                 270

Phe Leu Leu Ile Gly Ile Val Leu Gly Leu Ser Met Ile Asn Ile Met
        275                 280                 285

Phe Phe Ser Thr Leu Ser Thr Gly Val Ala Val Val Leu Phe Met Ser
    290                 295                 300

Cys Val Ser Met Gln Thr Phe Pro Phe Cys Tyr Leu Cys Asn Met Ile
305                 310                 315                 320

Met Asp Asp Cys Gln Glu Met Ala Asp Ser Leu Phe Gln Ser Asp Trp
                325                 330                 335

Thr Ser Ala Asp Arg Arg Tyr Lys Ser Thr Leu Val Tyr Phe Leu His
            340                 345                 350

Asn Leu Gln Gln Pro Ile Ile Leu Thr Ala Gly Gly Val Phe Pro Ile
        355                 360                 365

Ser Met Gln Thr Asn Leu Asn Met Val Lys Leu Ala Phe Thr Val Val
    370                 375                 380

Thr Ile Val Lys Gln Phe Asn Leu Ala Glu Lys Phe Gln
385                 390                 395
```

<210> SEQ ID NO 11
<211> LENGTH: 1308
<212> TYPE: DNA
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR64

<400> SEQUENCE: 11

```
ggcacgagcc aagaattcaa aatgaaactc agcgaaaccc taaaaatcga ctattttcga      60

gtccagttga atgcctggcg aatttgtggt gccttggatc tcagcgaggg taggtactgg     120

agttggtcga tgctattgtg catcttggtg tacctgccga cacccatgct actgagagga     180

gtatacagtt tcgaggatcc ggtggaaaat aatttcagct tgagcctgac ggtcacatcg     240

ctgtccaatc tcatgaagtt ctgcatgtac gtggcccaac taacaaagat ggtcgaggtc     300
```

-continued

```
cagagtctta ttggtcagct ggatgcccgg gtttctggcg agagccagtc tgagcgtcat    360

agaaatatga ccgagcacct gctaaggatg tccaagctgt tccagatcac ctacgctgta    420

gtcttcatca ttgctgcagt tcccttcgtt ttcgaaactg agctaagctt acccatgccc    480

atgtggtttc ccttcgactg gaagaactcg atggtggcct acatcggagc tctggttttc    540

caggagattg gctatgtctt tcaaattatg caatgctttg cagctgactc gtttccccg     600

ctcgtactgt acctgatctc cgagcaatgt caattgctga tcctgagaat ctctgaaatc    660

ggatatggtt acaagactct ggaggagaac gaacaggatc tggtcaactg catcagggat    720

caaaacgcgc tgtatagatt actcgatgtg accaagagtc tcgtttcgta tcccatgatg    780

gtgcagttta tggttattgg catcaacatc gccatcaccc tatttgtcct gatattttac    840

gtggagacct tgtacgatcg catctattat ctttgctttc tcttgggcat caccgtgcag    900

acatatccat tgtgctacta tggaaccatg gtgcaggaga gttttgctga gcttcactat    960

gcggtattct gcagcaactg ggtggatcaa agtgccagct atcgtgggca catgctcatc   1020

ctggcggagc gcactaagcg gatgcagctt ctcctcgccg gcaacctggt gcccatccac   1080

ctgagcacct acgtggcctg ttggaaggga gcctactcct tcttcaccct gatggccgat   1140

cgagatggcc tgggttctta gtagcccagt catttcactc acattctaca tcaagtagta   1200

ctaccactga acacgaacac gaatatttca aaagtaaaca cataatattc acaatagtgt   1260

atcactttaa taaaattttt ggttaccatg aaaaaaaaaa aaaaaaaa                1308
```

```
<210> SEQ ID NO 12
<211> LENGTH: 379
<212> TYPE: PRT
<213> ORGANISM: DROSOPHILA MELANOGASTER  DOR64

<400> SEQUENCE: 12

Met Lys Leu Ser Glu Thr Leu Lys Ile Asp Tyr Phe Arg Val Gln Leu
1               5                   10                  15

Asn Ala Trp Arg Ile Cys Gly Ala Leu Asp Leu Ser Glu Gly Arg Tyr
            20                  25                  30

Trp Ser Trp Ser Met Leu Leu Cys Ile Leu Val Tyr Leu Pro Thr Pro
        35                  40                  45

Met Leu Leu Arg Gly Val Tyr Ser Phe Glu Asp Pro Val Glu Asn Asn
    50                  55                  60

Phe Ser Leu Ser Leu Thr Val Thr Ser Leu Ser Asn Leu Met Lys Phe
65                  70                  75                  80

Cys Met Tyr Val Ala Gln Leu Thr Lys Met Val Glu Val Gln Ser Leu
                85                  90                  95

Ile Gly Gln Leu Asp Ala Arg Val Ser Gly Glu Ser Gln Ser Glu Arg
            100                 105                 110

His Arg Asn Met Thr Glu His Leu Leu Arg Met Ser Lys Leu Phe Gln
        115                 120                 125

Ile Thr Tyr Ala Val Val Phe Ile Ile Ala Ala Val Pro Phe Val Phe
    130                 135                 140

Glu Thr Glu Leu Ser Leu Pro Met Pro Met Trp Phe Pro Phe Asp Trp
145                 150                 155                 160

Lys Asn Ser Met Val Ala Tyr Ile Gly Ala Leu Val Phe Gln Glu Ile
                165                 170                 175
```

-continued

```
Gly Tyr Val Phe Gln Ile Met Gln Cys Phe Ala Ala Asp Ser Phe Pro
            180                 185                 190

Pro Leu Val Leu Tyr Leu Ile Ser Glu Gln Cys Gln Leu Leu Ile Leu
        195                 200                 205

Arg Ile Ser Glu Ile Gly Tyr Gly Tyr Lys Thr Leu Glu Glu Asn Glu
    210                 215                 220

Gln Asp Leu Val Asn Cys Ile Arg Asp Gln Asn Ala Leu Tyr Arg Leu
225                 230                 235                 240

Leu Asp Val Thr Lys Ser Leu Val Ser Tyr Pro Met Met Val Gln Phe
                245                 250                 255

Met Val Ile Gly Ile Asn Ile Ala Ile Thr Leu Phe Val Leu Ile Phe
            260                 265                 270

Tyr Val Glu Thr Leu Tyr Asp Arg Ile Tyr Tyr Leu Cys Phe Leu Leu
        275                 280                 285

Gly Ile Thr Val Gln Thr Tyr Pro Leu Cys Tyr Tyr Gly Thr Met Val
    290                 295                 300

Gln Glu Ser Phe Ala Glu Leu His Tyr Ala Val Phe Cys Ser Asn Trp
305                 310                 315                 320

Val Asp Gln Ser Ala Ser Tyr Arg Gly His Met Leu Ile Leu Ala Glu
                325                 330                 335

Arg Thr Lys Arg Met Gln Leu Leu Leu Ala Gly Asn Leu Val Pro Ile
            340                 345                 350

His Leu Ser Thr Tyr Val Ala Cys Trp Lys Gly Ala Tyr Ser Phe Phe
        355                 360                 365

Thr Leu Met Ala Asp Arg Asp Gly Leu Gly Ser
    370                 375
```

<210> SEQ ID NO 13
<211> LENGTH: 1152
<212> TYPE: DNA
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR71g

<400> SEQUENCE: 13

```
atggtcatta tcgacagtct tagtttttat cgtccattct ggatctgcat gcgattgctg     60

gtaccgactt tcttcaagga ttcctcacgt cctgtccagc tgtacgtggt gttgctgcac    120

atcctggtca ccttgtggtt tccactgcat ctgctgctgc atcttctgct acttccatct    180

accgctgagt tctttaagaa cctgaccatg tctctgactt gtgtggcctg cagtctgaag    240

catgtggccc acttgtatca cttgccgcag attgtggaaa tcgaatcact gatcgagcaa    300

ttagacacat ttattgccag cgaacaggag catcgttact atcgggatca cgtacattgc    360

catgctaggc gctttacaag atgtctctat attagctttg gcatgatcta tgcgcttttc    420

ctgttcggcg tcttcgttca ggttattagc ggaaattggg aacttctcta tccagcctat    480

ttcccattcg acttggagag caatcgcttt ctcggcgcag tagccttggg ctatcaggta    540

ttcagcatgt tagttgaagg cttccagggg ctgggcaacg atacctatac ccactgacc    600

ctatgccttc tggccggaca tgtccatttg tggtccatac gaatgggtca actgggatac    660

ttcgatgacg agacggtggt gaatcatcag cgtttgctgg attacattga gcagcataaa    720

ctcttggtgc ggttccacaa cctggtgagc cggaccatca gcgaagtgca actggtgcag    780

ctgggcggat gtggagccac tctgtgcatc attgtctcct acatgctctt ctttgtgggc    840

gacacaatct cgctggtcta ctacttggtg ttctttggag tggtctgcgt gcagctcttt    900
```

-continued

```
cccagctgct attttgccag cgaagtagcc gaggagttgg aacggctgcc atatgcgatc    960

ttctccagca gatggtacga tcaatcgcgg gatcatcgat tcgatttgct catctttaca   1020

caattaacac tgggaaaccg gggtggatc atcaaggcag gaggtcttat cgagctgaat   1080

ttgaatgcct ttttcgccac cctgaagatg gcctattccc tttttgcagt tgtggtgcgg   1140

gcaaagggta ta                                                         1152


<210> SEQ ID NO 14
<211> LENGTH: 390
<212> TYPE: PRT
<213> ORGANISM: DROSOPHILA MELANOGASTER  DOR71g

<400> SEQUENCE: 14

Met Val Ile Ile Asp Ser Leu Ser Phe Tyr Arg Pro Phe Trp Ile Cys
1               5                   10                  15

Met Arg Leu Leu Val Pro Thr Phe Phe Lys Asp Ser Ser Arg Pro Val
            20                  25                  30

Gln Leu Tyr Val Val Leu Leu His Ile Leu Val Thr Leu Trp Phe Pro
        35                  40                  45

Leu His Leu Leu Leu His Leu Leu Leu Leu Pro Ser Thr Ala Glu Phe
    50                  55                  60

Phe Lys Asn Leu Thr Met Ser Leu Thr Cys Val Ala Cys Ser Leu Lys
65                  70                  75                  80

His Val Ala His Leu Tyr His Leu Pro Gln Ile Val Glu Ile Glu Ser
                85                  90                  95

Leu Ile Glu Gln Leu Asp Thr Phe Ile Ala Ser Glu Gln Glu His Arg
            100                 105                 110

Tyr Tyr Arg Asp His Val His Cys His Ala Arg Arg Phe Thr Arg Cys
        115                 120                 125

Leu Tyr Ile Ser Phe Gly Met Ile Tyr Ala Leu Phe Leu Phe Gly Val
    130                 135                 140

Phe Val Gln Val Ile Ser Gly Asn Trp Glu Leu Leu Tyr Pro Ala Tyr
145                 150                 155                 160

Phe Pro Phe Asp Leu Glu Ser Asn Arg Phe Leu Gly Ala Val Ala Leu
                165                 170                 175

Gly Tyr Gln Val Phe Ser Met Leu Val Glu Gly Phe Gln Gly Leu Gly
            180                 185                 190

Asn Asp Thr Tyr Thr Pro Leu Thr Leu Cys Leu Leu Ala Gly His Val
        195                 200                 205

His Leu Trp Ser Ile Arg Met Gly Gln Leu Gly Tyr Phe Asp Asp Glu
    210                 215                 220

Thr Val Val Asn His Gln Arg Leu Leu Asp Tyr Ile Glu Gln His Lys
225                 230                 235                 240

Leu Leu Val Arg Phe His Asn Leu Val Ser Arg Thr Ile Ser Glu Val
                245                 250                 255

Gln Leu Val Gln Leu Gly Gly Cys Gly Ala Thr Leu Cys Ile Ile Val
            260                 265                 270

Ser Tyr Met Leu Phe Phe Val Gly Asp Thr Ile Ser Leu Val Tyr Tyr
        275                 280                 285

Leu Val Phe Phe Gly Val Val Cys Val Gln Leu Phe Pro Ser Cys Tyr
    290                 295                 300
```

-continued

```
Phe Ala Ser Glu Val Ala Glu Glu Leu Glu Arg Leu Pro Tyr Ala Ile
305                 310                 315                 320

Phe Ser Ser Arg Trp Tyr Asp Gln Ser Arg Asp His Arg Phe Asp Leu
                325                 330                 335

Leu Ile Phe Thr Gln Leu Thr Leu Gly Asn Arg Gly Trp Ile Ile Lys
            340                 345                 350

Ala Gly Gly Leu Ile Glu Leu Asn Leu Asn Ala Phe Phe Ala Thr Leu
        355                 360                 365

Lys Met Ala Tyr Ser Leu Phe Ala Val Val His Arg Glu Thr Gly Asn
    370                 375                 380

Pro Leu Gln Arg Glu His
385                 390
```

<210> SEQ ID NO 15
<211> LENGTH: 1137
<212> TYPE: DNA
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR72g

<400> SEQUENCE: 15

```
atggacttaa aaccgcgagt cattcgaagt gaagatatct acagaaccta ttggttatat      60

tggcatcttt tgggcctgga aagcaatttc tttctgaatc gcttgttgga tttggtgatt     120

acaattttcg taaccatttg gtatccaatt cacctgattc tgggactgtt tatggaaaga     180

tctttggggg atgtctgcaa gggtctacca attacggcag catgcttttt cgccagcttt     240

aaatttattt gttttcgctt caagctatct gaaattaaag aaatcgaaat attatttaaa     300

gagctggatc agcgagcttt aagtcgagag gaatgcgagt ttttcaatca aaatacgaga     360

cgtgaggcga atttcatttg gaaaagtttc attgtggcct atggactgtc gaatatctcg     420

gctattgcat cagttctttt cggcggtgga cataagctat tatatcccgc ctggtttcca     480

tacgatgtgc aggccacgga actaatattt tggctaagtg taacatacca aattgccgga     540

gtaagtttgg ccatacttca gaatttggcc aatgattcct atccaccgat gacattttgc     600

gtggttgccg gtcatgtaag acttttggcg atgcgcttga gtagaattgg ccaaggtcca     660

gaggaaacaa tatacttaac cggaaagcaa ttaatcgaaa gcatcgagga tcaccgaaaa     720

ctaatgaaga tagtggaatt actgcgcagc accatgaata tttcgcagct cggccagttt     780

atttcaagtg gtgttaatat ttccataaca ctagtcaaca ttctcttctt tgcggataat     840

aatttcgcta taacctacta cggagtgtac ttcctatcga tggtgttgga attattcccg     900

tgctgctatt acggcaccct gatatccgtg gagatgaacc agctgaccta tgcgatttac     960

tcaagtaact ggatgagtat gaatcggagc tacagccgca tcctactgat cttcatgcaa    1020

ctcaccctgg cggaagtgca gatcaaggcc ggtgggatga ttggcatcgg aatgaacgcc    1080

ttctttgcca ccgtgcgatt ggcctactcc ttcttcactt tggccatgtc gctgcgt       1137
```

<210> SEQ ID NO 16
<211> LENGTH: 379
<212> TYPE: PRT
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR72g

<400> SEQUENCE: 16

```
Met Asp Leu Lys Pro Arg Val Ile Arg Ser Glu Asp Ile Tyr Arg Thr
1               5                   10                  15

Tyr Trp Leu Tyr Trp His Leu Leu Gly Leu Glu Ser Asn Phe Phe Leu
```

-continued

```
            20                  25                  30

Asn Arg Leu Leu Asp Leu Val Ile Thr Ile Phe Val Thr Ile Trp Tyr
        35                  40                  45

Pro Ile His Leu Ile Leu Gly Leu Phe Met Glu Arg Ser Leu Gly Asp
    50                  55                  60

Val Cys Lys Gly Leu Pro Ile Thr Ala Ala Cys Phe Phe Ala Ser Phe
65                  70                  75                  80

Lys Phe Ile Cys Phe Arg Phe Lys Leu Ser Glu Ile Lys Glu Ile Glu
                85                  90                  95

Ile Leu Phe Lys Glu Leu Asp Gln Arg Ala Leu Ser Arg Glu Glu Cys
            100                 105                 110

Glu Phe Phe Asn Gln Asn Thr Arg Arg Glu Ala Asn Phe Ile Trp Lys
        115                 120                 125

Ser Phe Ile Val Ala Tyr Gly Leu Ser Asn Ile Ser Ala Ile Ala Ser
    130                 135                 140

Val Leu Phe Gly Gly Gly His Lys Leu Leu Tyr Pro Ala Trp Phe Pro
145                 150                 155                 160

Tyr Asp Val Gln Ala Thr Glu Leu Ile Phe Trp Leu Ser Val Thr Tyr
                165                 170                 175

Gln Ile Ala Gly Val Ser Leu Ala Ile Leu Gln Asn Leu Ala Asn Asp
            180                 185                 190

Ser Tyr Pro Pro Met Thr Phe Cys Val Val Ala Gly His Val Arg Leu
        195                 200                 205

Leu Ala Met Arg Leu Ser Arg Ile Gly Gln Gly Pro Glu Glu Thr Ile
    210                 215                 220

Tyr Leu Thr Gly Lys Gln Leu Ile Glu Ser Ile Glu Asp His Arg Lys
225                 230                 235                 240

Leu Met Lys Ile Val Glu Leu Leu Arg Ser Thr Met Asn Ile Ser Gln
                245                 250                 255

Leu Gly Gln Phe Ile Ser Ser Gly Val Asn Ile Ser Ile Thr Leu Val
            260                 265                 270

Asn Ile Leu Phe Phe Ala Asp Asn Asn Phe Ala Ile Thr Tyr Tyr Gly
        275                 280                 285

Val Tyr Phe Leu Ser Met Val Leu Glu Leu Phe Pro Cys Cys Tyr Tyr
    290                 295                 300

Gly Thr Leu Ile Ser Val Glu Met Asn Gln Leu Thr Tyr Ala Ile Tyr
305                 310                 315                 320

Ser Ser Asn Trp Met Ser Met Asn Arg Ser Tyr Ser Arg Ile Leu Leu
                325                 330                 335

Ile Phe Met Gln Leu Thr Leu Ala Glu Val Gln Ile Lys Ala Gly Gly
            340                 345                 350

Met Ile Gly Ile Gly Met Asn Ala Phe Phe Ala Thr Val Arg Leu Ala
        355                 360                 365

Tyr Ser Phe Phe Thr Leu Ala Met Ser Leu Arg
    370                 375
```

<210> SEQ ID NO 17
<211> LENGTH: 1134
<212> TYPE: DNA
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR73g

<400> SEQUENCE: 17

-continued

```
atggattcaa gaaggaaagt ccgaagtgaa aatctttaca aaacctattg gctttactgg     60

cgacttctgg gagtcgaggg cgattatcct tttcgacggc tagtggattt tacaatcacg    120

tctttcatta cgattttatt tcccgtgcat cttatactgg gaatgtataa aaagccccag    180

attcaagtct tcaggagtct gcatttcaca tcggaatgcc ttttctgcag ctataagttt    240

ttctgttttc gttggaaact taaagaaata aagaccatcg aaggattgct ccaggatctc    300

gatagtcgag ttgaaagtga agaagaacgc aactacttta atcaaaatcc aagtcgtgtg    360

gctcgaatgc tttcgaaaag ttacttggta gctgctatat cggccataat cactgcaact    420

gtagctggtt tatttagtac tggtcgaaat ttaatgtatc tgggttggtt tccctacgat    480

tttcaagcaa ccgccgcaat ctattggatt agtttttcct atcaggcgat tggctctagt    540

ctgttgattc tggaaaatct ggccaacgat tcatatccgc cgattacatt ttgtgtggtc    600

tctggacatg tgagactatt gataatgcgt ttaagtcgaa ttggtcacga tgtaaaatta    660

tcaagttcgg aaaataccag aaaactcatc gaaggtatcc aggatcacag gaaactaatg    720

aagataatac gcctacttcg cagcacttta catcttagcc aactgggcca gttcctttct    780

agtggaatca acatttccat aacactcatc aacatcctgt tctttgcgga aaacaacttt    840

gcaatgcttt attatgcggt gttctttgct gcaatgttaa tagaactatt tccaagttgt    900

tactatggaa ttctgatgac aatggagttt gataagctac catatgccat cttctccagc    960

aactggctta aaatggataa aagatacaat cgatccttga taattctgat gcaactaaca   1020

ctggttccag tgaatataaa agcaggtggt attgttggca tcgatatgag tgcatttttt   1080

gccacagttc ggatggcata ttccttttac actttagcct tgtcatttcg agta          1134
```

```
<210> SEQ ID NO 18
<211> LENGTH: 378
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR73g

<400> SEQUENCE: 18

Met Asp Ser Arg Arg Lys Val Arg Ser Glu Asn Leu Tyr Lys Thr Tyr
1               5                   10                  15

Trp Leu Tyr Trp Arg Leu Leu Gly Val Glu Gly Asp Tyr Pro Phe Arg
            20                  25                  30

Arg Leu Val Asp Phe Thr Ile Thr Ser Phe Ile Thr Ile Leu Phe Pro
        35                  40                  45

Val His Leu Ile Leu Gly Met Tyr Lys Lys Pro Gln Ile Gln Val Phe
    50                  55                  60

Arg Ser Leu His Phe Thr Ser Glu Cys Leu Phe Cys Ser Tyr Lys Phe
65                  70                  75                  80

Phe Cys Phe Arg Trp Lys Leu Lys Glu Ile Lys Thr Ile Glu Gly Leu
                85                  90                  95

Leu Gln Asp Leu Asp Ser Arg Val Glu Ser Glu Glu Glu Arg Asn Tyr
            100                 105                 110

Phe Asn Gln Asn Pro Ser Arg Val Ala Arg Met Leu Ser Lys Ser Tyr
        115                 120                 125

Leu Val Ala Ala Ile Ser Ala Ile Ile Thr Ala Thr Val Ala Gly Leu
    130                 135                 140

Phe Ser Thr Gly Arg Asn Leu Met Tyr Leu Gly Trp Phe Pro Tyr Asp
145                 150                 155                 160
```

-continued

```
Phe Gln Ala Thr Ala Ala Ile Tyr Trp Ile Ser Phe Ser Tyr Gln Ala
                165                 170                 175

Ile Gly Ser Ser Leu Leu Ile Leu Glu Asn Leu Ala Asn Asp Ser Tyr
            180                 185                 190

Pro Pro Ile Thr Phe Cys Val Val Ser Gly His Val Arg Leu Leu Ile
        195                 200                 205

Met Arg Leu Ser Arg Ile Gly His Asp Val Lys Leu Ser Ser Ser Glu
    210                 215                 220

Asn Thr Arg Lys Leu Ile Glu Gly Ile Gln Asp His Arg Lys Leu Met
225                 230                 235                 240

Lys Ile Ile Arg Leu Leu Arg Ser Thr Leu His Leu Ser Gln Leu Gly
                245                 250                 255

Gln Phe Leu Ser Ser Gly Ile Asn Ile Ser Ile Thr Leu Ile Asn Ile
            260                 265                 270

Leu Phe Phe Ala Glu Asn Asn Phe Ala Met Leu Tyr Tyr Ala Val Phe
        275                 280                 285

Phe Ala Ala Met Leu Ile Glu Leu Phe Pro Ser Cys Tyr Tyr Gly Ile
    290                 295                 300

Leu Met Thr Met Glu Phe Asp Lys Leu Pro Tyr Ala Ile Phe Ser Ser
305                 310                 315                 320

Asn Trp Leu Lys Met Asp Lys Arg Tyr Asn Arg Ser Leu Ile Ile Leu
                325                 330                 335

Met Gln Leu Thr Leu Val Pro Val Asn Ile Lys Ala Gly Gly Ile Val
            340                 345                 350

Gly Ile Asp Met Ser Ala Phe Phe Ala Thr Val Arg Met Ala Tyr Ser
        355                 360                 365

Phe Tyr Thr Leu Ala Leu Ser Phe Arg Val
    370                 375
```

<210> SEQ ID NO 19
<211> LENGTH: 1191
<212> TYPE: DNA
<213> ORGANISM: DROSOPHILA MELANOGASTER   DOR46

<400> SEQUENCE: 19

```
atggcagagg tcagagtgga cagtctggag tttttcaaga gccattggac cgcctggcgg      60

tacttgggag tggctcattt tcgggtcgag aactggaaga acctttacgt gttttacagc     120

attgtgtcga atcttctcgt gaccctgtgc taccccgttc acctgggaat atccctcttt     180

cgcaaccgca ccatcaccga ggacatcctc aacctgacca cctttgcgac ctgcacagcc     240

tgttcggtga agtgcctgct ctacgcctac aacatcaagg atgtgctgga gatggagcgg     300

ctgttgaggc ttttggatga acgcgtcgtg ggtccggagc aacgcagcat ctacggacaa     360

gtgagggtcc agctgcgaaa tgtgctatac gtgttcatcg gcatctacat gccgtgtgcc     420

ctgttcgccg agctatcctt tctgttcaag gaggagcgcg gtctgatgta tcccgcctgg     480

tttcccttcg actggctgca ctccaccagg aactattaca tagcgaacgc ctatcagata     540

gtgggcatct cgtttcagct gctgcaaaac tatgttagcg actgctttcc ggcggtggtg     600

ctgtgcctga tctcatccca catcaaaatg ttgtacaaca gattcgagga ggtgggcctg     660

gatccagcca gagatgcgga gaaggacctg gaggcctgca tcaccgatca caagcatatt     720

ctagagtggg caggcggctc attggttcgt gttctattca ctttccaact tttttccaga     780
```

-continued

```
ctattccgac gcatcgaggc cttcatttcc ctgcccatgc taattcagtt cacagtgacc    840

gccttgaatg tgtgcatcgg tttagcagcc ctggtgtttt tcgtcagcga gcccatggca    900

cggatgtact tcatcttcta ctccctggcc atgccgctgc agatctttcc gtcctgcttt    960

ttcggcaccg acaacgagta ctggttcgga cgcctccact acgcggcctt cagttgcaat   1020

tggcacacac agaacaggag ctttaagcgg aaaatgatgc tgttcgttga gcaatcgttg   1080

aagaagagca ccgctgtggc tggcggaatg atgcgtatcc acctggacac gttcttttcc   1140

accctaaagg gggcctactc cctctttacc atcattattc ggatgagaaa g            1191


<210> SEQ ID NO 20
<211> LENGTH: 379
<212> TYPE: PRT
<213> ORGANISM: DROSOPHILA MELANOGASTER  DOR46

<400> SEQUENCE: 20

Met Ala Glu Val Arg Val Asp Ser Leu Glu Phe Phe Lys Ser His Trp
1               5                   10                  15

Thr Ala Trp Arg Tyr Leu Gly Val Ala His Phe Arg Val Glu Asn Trp
            20                  25                  30

Lys Asn Leu Tyr Val Phe Tyr Ser Ile Val Ser Asn Leu Leu Val Thr
        35                  40                  45

Leu Cys Tyr Pro Val His Leu Gly Ile Ser Leu Phe Arg Asn Arg Thr
    50                  55                  60

Ile Thr Glu Asp Ile Leu Asn Leu Thr Thr Phe Ala Thr Cys Thr Ala
65                  70                  75                  80

Cys Ser Val Lys Cys Leu Leu Tyr Ala Tyr Asn Ile Lys Asp Val Leu
                85                  90                  95

Glu Met Glu Arg Leu Leu Arg Leu Leu Asp Glu Arg Val Val Gly Pro
            100                 105                 110

Glu Gln Arg Ser Ile Tyr Gly Gln Val Arg Val Gln Leu Arg Asn Val
        115                 120                 125

Leu Tyr Val Phe Ile Gly Ile Tyr Met Pro Cys Ala Leu Phe Ala Glu
    130                 135                 140

Leu Ser Phe Leu Phe Lys Glu Glu Arg Gly Leu Met Tyr Pro Ala Trp
145                 150                 155                 160

Phe Pro Phe Asp Trp Leu His Ser Thr Arg Asn Tyr Tyr Ile Ala Asn
                165                 170                 175

Ala Tyr Gln Ile Val Gly Ile Ser Phe Gln Leu Leu Gln Asn Tyr Val
            180                 185                 190

Ser Asp Cys Phe Pro Ala Val Val Leu Cys Leu Ile Ser Ser His Ile
        195                 200                 205

Lys Met Leu Tyr Asn Arg Phe Glu Glu Val Gly Leu Asp Pro Ala Arg
    210                 215                 220

Asp Ala Glu Lys Asp Leu Glu Ala Cys Ile Thr Asp His Lys His Ile
225                 230                 235                 240

Leu Glu Leu Phe Arg Arg Ile Glu Ala Phe Ile Ser Leu Pro Met Leu
                245                 250                 255

Ile Gln Phe Thr Val Thr Ala Leu Asn Val Cys Ile Gly Leu Ala Ala
            260                 265                 270

Leu Val Phe Phe Val Ser Glu Pro Met Ala Arg Met Tyr Phe Ile Phe
        275                 280                 285
```

-continued

```
Tyr Ser Leu Ala Met Pro Leu Gln Ile Phe Pro Ser Cys Phe Phe Gly
    290                 295                 300

Thr Asp Asn Glu Tyr Trp Phe Gly Arg Leu His Tyr Ala Ala Phe Ser
305                 310                 315                 320

Cys Asn Trp His Thr Gln Asn Arg Ser Phe Lys Arg Lys Met Met Leu
                325                 330                 335

Phe Val Glu Gln Ser Leu Lys Lys Ser Thr Ala Val Ala Gly Gly Met
            340                 345                 350

Met Arg Ile His Leu Asp Thr Phe Phe Ser Thr Leu Lys Gly Ala Tyr
        355                 360                 365

Ser Leu Phe Thr Ile Ile Ile Arg Met Arg Lys
    370                 375
```

<210> SEQ ID NO 21
<211> LENGTH: 1290
<212> TYPE: DNA
<213> ORGANISM: DROSOPHILA MELANOGASTER   DOR19g

<400> SEQUENCE: 21

```
atggttacgg aggactttta taagtaccag gtgtggtact tccaaatcct tggtgtttgg      60

cagctcccca cttgggccgc agaccaccag cgtcgttttc agtccatgag gtttggcttc     120

atcctggtca tcctgttcat catgctgctg cttttctcct tcgaaatgtt gaacaacatt     180

tcccaagtta gggagatcct aaaggtattc ttcatgttcg ccacggaaat atcctgcatg     240

gccaaattat tgcatttgaa gttgaagagc cgcaaactcg ctggcttggt tgatgcgatg     300

ttgtccccag agttcggcgt taaaagtgaa caggaaatgc agatgctgga attggataga     360

gtggcggttg tccgcatgag gaactcctac ggcatcatgt ccctgggcgc ggcttccctg     420

atccttatag ttccctgttt cgacaacttt ggcgagctac cactggccat gttggaggta     480

tgcagcatcg agggatggat ctgctattgg tcgcagtacc ttttccactc gatttgcctg     540

ctgcccactt gtgtgctgaa tataacctac gactcggtgg cctactcgtt gctctgtttc     600

ttgaaggttc agctacaaat gctggtcctg cgattagaaa agttgggtcc tgtgatcgaa     660

ccccaggata atgagaaaat cgcaatggaa ctgcgtgagt gtgccgccta ctacaacagg     720

attgttcgtt tcaaggacct ggtggagctg ttcataaagg ggccaggatc tgtgcagctc     780

atgtgttctg ttctggtgct ggtgtccaac ctgtacgaca tgtccaccat gtccattgca     840

aacggcgatg ccatctttat gctcaagacc tgtatctatc agctggtgat gctctggcag     900

atcttcatca tttgctacgc ctccaacgag gtaactgtcc agagctctag gttgtgtcac     960

agcatctaca gctcccaatg gacgggatgg aacagggcaa accgccggat tgtccttctc    1020

atgatgcagc gctttaattc cccgatgctc ctgagcacct ttaaccccac ctttgctttc    1080

agcttggagg cctttggttc tgtagggcag cagaaattcc tttatatatc atttattact    1140

ggttatgctc ttctcctttc agatcgtcaa ctgctcctac agctacttcg cactgctgaa    1200

gcgcgtcaac agttaaattt cgaaacaccg cagcacctaa agattttcaa gccgattttt    1260

aaaagcactc aaaacgttat gcacgtacat                                     1290
```

<210> SEQ ID NO 22
<211> LENGTH: 430
<212> TYPE: PRT
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR19g

-continued

<400> SEQUENCE: 22

```
Met Val Thr Glu Asp Phe Tyr Lys Tyr Gln Val Trp Tyr Phe Gln Ile
1               5                   10                  15

Leu Gly Val Trp Gln Leu Pro Thr Trp Ala Ala Asp His Gln Arg Arg
            20                  25                  30

Phe Gln Ser Met Arg Phe Gly Phe Ile Leu Val Ile Leu Phe Ile Met
        35                  40                  45

Leu Leu Leu Phe Ser Phe Glu Met Leu Asn Asn Ile Ser Gln Val Arg
    50                  55                  60

Glu Ile Leu Lys Val Phe Phe Met Phe Ala Thr Glu Ile Ser Cys Met
65                  70                  75                  80

Ala Lys Leu Leu His Leu Lys Leu Lys Ser Arg Lys Leu Ala Gly Leu
                85                  90                  95

Val Asp Ala Met Leu Ser Pro Glu Phe Gly Val Lys Ser Glu Gln Glu
            100                 105                 110

Met Gln Met Leu Glu Leu Asp Arg Val Ala Val Val Arg Met Arg Asn
        115                 120                 125

Ser Tyr Gly Ile Met Ser Leu Gly Ala Ala Ser Leu Ile Leu Ile Val
    130                 135                 140

Pro Cys Phe Asp Asn Phe Gly Glu Leu Pro Leu Ala Met Leu Glu Val
145                 150                 155                 160

Cys Ser Ile Glu Gly Trp Ile Cys Tyr Trp Ser Gln Tyr Leu Phe His
                165                 170                 175

Ser Ile Cys Leu Leu Pro Thr Cys Val Leu Asn Ile Thr Tyr Asp Ser
            180                 185                 190

Val Ala Tyr Ser Leu Leu Cys Phe Leu Lys Val Gln Leu Gln Met Leu
        195                 200                 205

Val Leu Arg Leu Glu Lys Leu Gly Pro Val Ile Glu Pro Gln Asp Asn
    210                 215                 220

Glu Lys Ile Ala Met Glu Leu Arg Glu Cys Ala Ala Tyr Tyr Asn Arg
225                 230                 235                 240

Ile Val Arg Phe Lys Asp Leu Val Glu Leu Phe Ile Lys Gly Pro Gly
                245                 250                 255

Ser Val Gln Leu Met Cys Ser Val Leu Val Leu Val Ser Asn Leu Tyr
            260                 265                 270

Asp Met Ser Thr Met Ser Ile Ala Asn Gly Asp Ala Ile Phe Met Leu
        275                 280                 285

Lys Thr Cys Ile Tyr Gln Leu Val Met Leu Trp Gln Ile Phe Ile Ile
    290                 295                 300

Cys Tyr Ala Ser Asn Glu Val Thr Val Gln Ser Ser Arg Leu Cys His
305                 310                 315                 320

Ser Ile Tyr Ser Ser Gln Trp Thr Gly Trp Asn Arg Ala Asn Arg Arg
                325                 330                 335

Ile Val Leu Leu Met Met Gln Arg Phe Asn Ser Pro Met Leu Leu Ser
            340                 345                 350

Thr Phe Asn Pro Thr Phe Ala Phe Ser Leu Glu Ala Phe Gly Ser Val
        355                 360                 365

Gly Gln Gln Lys Phe Leu Tyr Ile Ser Phe Ile Thr Gly Tyr Ala Leu
    370                 375                 380

Leu Leu Ser Asp Arg Gln Leu Leu Leu Gln Leu Leu Arg Thr Ala Glu
385                 390                 395                 400
```

-continued

Ala Arg Gln Gln Leu Asn Phe Glu Thr Pro Gln His Leu Lys Ile Phe
405 410 415

Lys Pro Ile Phe Lys Ser Thr Gln Asn Val Met His Val His
420 425 430

<210> SEQ ID NO 23
<211> LENGTH: 1391
<212> TYPE: DNA
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR24

<400> SEQUENCE: 23

ggcacgagcc ttgtcgacat ggacagtttt ctgcaagtac agaagagcac cattgctctt 60

ctgggctttg atctctttag tgaaaatcga gaaatgtgga aacgccccta tagagcaatg 120

aatgtgttta gcatagctgc catttttccc tttatcctgg cagctgtgct ccataattgg 180

aagaatgtat tgctgctggc cgatgccatg gtggccctac taataaccat tctgggccta 240

ttcaagttta gcatgatact ttacttacgt cgcgatttca agcgactgat tgacaaattt 300

cgtttgctca tgtcgaatga ggcggaacag ggcgaggaat acgccgagat tctcaacgca 360

gcaaacaagc aggatcaacg aatgtgcact ctgtttagga cttgtttcct cctcgcctgg 420

gccttgaata gtgttctgcc cctcgtgaga atgggtctca gctattggtt agcaggtcat 480

gcagagcccg agttgccttt tccctgtctt tttccctgga atatccacat cattcgcaat 540

tatgttttga gcttcatctg gagcgctttc gcctcgacag gtgtggtttt acctgctgtc 600

agcttggata ccatattctg ttccttcacc agcaacctgt gcgccttctt caaaattgcg 660

cagtacaagg tggttagatt taagggcgga tcccttaaag aatcacaggc cacattgaac 720

aaagtctttg ccctgtacca gaccagcttg gatatgtgca acgatctgaa tcagtgctac 780

caaccgatta tctgcgccca gttcttcatt tcatctctgc aactctgcat gctgggatat 840

ctgttctcca ttacttttgc ccagacagag ggcgtgtact atgcctcttt catagccacc 900

atcattatac aagcctatat ctactgctac tgcggggaga acctgaagac ggagagtgcc 960

agcttcgagt gggccatcta cgacagtccg tggcacgaga gtttgggtgc tggtggagcc 1020

tctacctcga tctgccgatc cttgctgatc agcatgatgc gggctcatcg gggattccgc 1080

attacgggat acttcttcga ggcaaacatg gaggccttct catcgattgt tcgcacggct 1140

atgtcctaca tcacaatgct gagatcattc tcctaaatgt ggtttgacca caaggctttg 1200

gattgatttt tgtgcaattt ttgttttatt gctgagcatg cgttgccgta cgacatttaa 1260

caatcgatct tacgtaattt acatatgata atctcacata ttgttcgtta agcactaagt 1320

agaatgtaga atgtgaattg gctgtagaaa tgcacagatg aagcacgaaa aaaaaaaaaa 1380

aaaaaaaaaa a 1391

<210> SEQ ID NO 24
<211> LENGTH: 385
<212> TYPE: PRT
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR24

<400> SEQUENCE: 24

Met Asp Ser Phe Leu Gln Val Gln Lys Ser Thr Ile Ala Leu Leu Gly
1 5 10 15

Phe Asp Leu Phe Ser Glu Asn Arg Glu Met Trp Lys Arg Pro Tyr Arg
20 25 30

-continued

```
Ala Met Asn Val Phe Ser Ile Ala Ala Ile Phe Pro Phe Ile Leu Ala
        35                  40                  45

Ala Val Leu His Asn Trp Lys Asn Val Leu Leu Leu Ala Asp Ala Met
    50                  55                  60

Val Ala Leu Leu Ile Thr Ile Leu Gly Leu Phe Lys Phe Ser Met Ile
65                  70                  75                  80

Leu Tyr Leu Arg Arg Asp Phe Lys Arg Leu Ile Asp Lys Phe Arg Leu
                85                  90                  95

Leu Met Ser Asn Glu Ala Glu Gln Gly Glu Glu Tyr Ala Glu Ile Leu
            100                 105                 110

Asn Ala Ala Asn Lys Gln Asp Gln Arg Met Cys Thr Leu Phe Arg Thr
        115                 120                 125

Cys Phe Leu Leu Ala Trp Ala Leu Asn Ser Val Leu Pro Leu Val Arg
    130                 135                 140

Met Gly Leu Ser Tyr Trp Leu Ala Gly His Ala Glu Pro Glu Leu Pro
145                 150                 155                 160

Phe Pro Cys Leu Phe Pro Trp Asn Ile His Ile Ile Arg Asn Tyr Val
                165                 170                 175

Leu Ser Phe Ile Trp Ser Ala Phe Ala Ser Thr Gly Val Val Leu Pro
            180                 185                 190

Ala Val Ser Leu Asp Thr Ile Phe Cys Ser Phe Thr Ser Asn Leu Cys
        195                 200                 205

Ala Phe Phe Lys Ile Ala Gln Tyr Lys Val Val Arg Phe Lys Gly Gly
    210                 215                 220

Ser Leu Lys Glu Ser Gln Ala Thr Leu Asn Lys Val Phe Ala Leu Tyr
225                 230                 235                 240

Gln Thr Ser Leu Asp Met Cys Asn Asp Leu Asn Gln Cys Tyr Gln Pro
                245                 250                 255

Ile Ile Cys Ala Gln Phe Phe Ile Ser Ser Leu Gln Leu Cys Met Leu
            260                 265                 270

Gly Tyr Leu Phe Ser Ile Thr Phe Ala Gln Thr Glu Gly Val Tyr Tyr
        275                 280                 285

Ala Ser Phe Ile Ala Thr Ile Ile Ile Gln Ala Tyr Ile Tyr Cys Tyr
    290                 295                 300

Cys Gly Glu Asn Leu Lys Thr Glu Ser Ala Ser Phe Glu Trp Ala Ile
305                 310                 315                 320

Tyr Asp Ser Pro Trp His Glu Ser Leu Gly Ala Gly Gly Ala Ser Thr
                325                 330                 335

Ser Ile Cys Arg Ser Leu Leu Ile Ser Met Met Arg Ala His Arg Gly
            340                 345                 350

Phe Arg Ile Thr Gly Tyr Phe Phe Glu Ala Asn Met Glu Ala Phe Ser
        355                 360                 365

Ser Ile Val Arg Thr Ala Met Ser Tyr Ile Thr Met Leu Arg Ser Phe
    370                 375                 380

Ser
385
```

<210> SEQ ID NO 25
<211> LENGTH: 900
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR10

-continued

<400> SEQUENCE: 25

```
atggaaaaac tacgttccta tgaggatttc atcttcatgg ccaacatgat gttcaagacc     60
cttggctacg atctattcca tacacccaaa ccctggtggc gctatctgct tgtgcgagga    120
tacttcgttt tgtgcacgat cagcaacttt tacgaggctt ccatggtgac gacaaggata    180
attgagtggg aatccttggc cggaagtccc tccaaaataa tgcgacaggg tctgcacttc    240
ttttacatgt tgagtagcca attgaaattt atcacattca tgataaatcg caaacgccta    300
ctgcagctga gccatcgttt gaaagagttg tatcctcata aagagcaaaa tcaaaggaag    360
tacgaggtga ataaatacta cctatcctgt tccacgcgca atgttttgta cgtgtactac    420
tttgtaatgg tcgtcatggc actggaaccc ctcgttcagt cccagttcat agtgaatgtg    480
agcctgggca cagatctgtg gatgatgtgc gtctcaagcc aaatatcgat gcacttgggc    540
tatctggcca atatgttggc ctccattcga ccaagtccag aaacggaaca acaagactgt    600
gacttcttgg ccagcattat aaagagacat caactaatga tcaggcttca aaaggacgtg    660
aactatgttt ttggactctt attggcatct aatctgttta ccacatcctg tttactttgc    720
tgcatggcgt actataccgt cgtcgaaggt ttcaattggg agggcatttc ctatatgatg    780
ctctttgcta gtgtagctgc ccagttctac gttgtcagct cacacggaca aatgttaata    840
gatttgttga tgaccatcac atacagattt ttcgcggtta tacgacaaac tgtagaaaag    900
```

<210> SEQ ID NO 26
<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR10

<400> SEQUENCE: 26

```
Met Glu Lys Leu Arg Ser Tyr Glu Asp Phe Ile Phe Met Ala Asn Met
1               5                   10                  15

Met Phe Lys Thr Leu Gly Tyr Asp Leu Phe His Thr Pro Lys Pro Trp
            20                  25                  30

Trp Arg Tyr Leu Leu Val Arg Gly Tyr Phe Val Leu Cys Thr Ile Ser
        35                  40                  45

Asn Phe Tyr Glu Ala Ser Met Val Thr Thr Arg Ile Ile Glu Trp Glu
    50                  55                  60

Ser Leu Ala Gly Ser Pro Ser Lys Ile Met Arg Gln Gly Leu His Phe
65                  70                  75                  80

Phe Tyr Met Leu Ser Ser Gln Leu Lys Phe Ile Thr Phe Met Ile Asn
                85                  90                  95

Arg Lys Arg Leu Leu Gln Leu Ser His Arg Leu Lys Glu Leu Tyr Pro
            100                 105                 110

His Lys Glu Gln Asn Gln Arg Lys Tyr Glu Val Asn Lys Tyr Tyr Leu
        115                 120                 125

Ser Cys Ser Thr Arg Asn Val Leu Tyr Val Tyr Tyr Phe Val Met Val
    130                 135                 140

Val Met Ala Leu Glu Pro Leu Val Gln Ser Gln Phe Ile Val Asn Val
145                 150                 155                 160

Ser Leu Gly Thr Asp Leu Trp Met Met Cys Val Ser Ser Gln Ile Ser
                165                 170                 175

Met His Leu Gly Tyr Leu Ala Asn Met Leu Ala Ser Ile Arg Pro Ser
            180                 185                 190
```

-continued

```
Pro Glu Thr Glu Gln Gln Asp Cys Asp Phe Leu Ala Ser Ile Ile Lys
        195                 200                 205

Arg His Gln Leu Met Ile Arg Leu Gln Lys Asp Val Asn Tyr Val Phe
    210                 215                 220

Gly Leu Leu Leu Ala Ser Asn Leu Phe Thr Thr Ser Cys Leu Leu Cys
225                 230                 235                 240

Cys Met Ala Tyr Tyr Thr Val Val Glu Gly Phe Asn Trp Glu Gly Ile
                245                 250                 255

Ser Tyr Met Met Leu Phe Ala Ser Val Ala Ala Gln Phe Tyr Val Val
            260                 265                 270

Ser Ser His Gly Gln Met Leu Ile Asp Leu Leu Met Thr Ile Thr Tyr
        275                 280                 285

Arg Phe Phe Ala Val Ile Arg Gln Thr Val Glu Lys
    290                 295                 300


<210> SEQ ID NO 27
<211> LENGTH: 1125
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster  DOR105

<400> SEQUENCE: 27

atgtttgaag acattcagct aatctacatg aatatcaaga tattgcgatt ctgggccctg      60

ctctatgaca aaaacttgag gcgttatgtg tgcattggac tggcctcatt ccacatcttc     120

acccaaatcg tctacatgat gagtaccaat gaaggactaa ccgggataat tcgtaactca     180

tatatgctcg tcctttggat taatacggtg ctgcgagctt atctcttgct ggcggatcac     240

gacagatatt tggctttgat ccaaaaacta actgaggcct attacgattt actgaatctg     300

aacgattcgt atatatcgga aatattggac caggtgaaca aggtgggaaa gttgatggct     360

aggggcaatc tgttctttgg catgctcaca tccatgggat tcggtctgta cccattgtcc     420

tccagcgaaa gagtcctgcc atttggcagc aaaattcctg gtctaaatga gtacgagagt     480

ccgtactatg agatgtggta catctttcag atgctcatca ccccgatggg ctgttgcatg     540

tacattccgt acaccagtct gattgtgggc ttgataatgt tcggcattgt gaggtgcaag     600

gctttgcagc atcgcctccg ccaggtggcg cttaagcatc cgtacggaga tcgcgatccc     660

cgtgaactga gggaggagat catagcctgc atacgttacc agcagagcat tatcgagtac     720

atggatcaca taaacgagct gaccaccatg atgttcctat tcgaactgat ggccttttcg     780

gcgctgctct gtgcgctgct ctttatgctg attatcgtca gcggcaccag tcagctgata     840

attgtttgca tgtacattaa catgattctg gcccaaatac tggccctcta ttggtatgca     900

aatgagttaa gggaacagaa tctggcggtg gccaccgcag cctacgaaac ggagtggttc     960

accttcgacg ttccactgcg caaaaacatc ctgttcatga tgatgagggc acagcggcca    1020

gctgcaatac tactgggcaa tatacgcccc atcactttgg aactgttcca aaacctactg    1080

aacacaacct atacattttt tacggttctc aagcgagtct acgga                    1125


<210> SEQ ID NO 28
<211> LENGTH: 375
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster  DOR105

<400> SEQUENCE: 28

Met Phe Glu Asp Ile Gln Leu Ile Tyr Met Asn Ile Lys Ile Leu Arg
```

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```
1               5                   10                  15

Phe Trp Ala Leu Leu Tyr Asp Lys Asn Leu Arg Arg Tyr Val Cys Ile
            20                  25                  30

Gly Leu Ala Ser Phe His Ile Phe Thr Gln Ile Val Tyr Met Met Ser
        35                  40                  45

Thr Asn Glu Gly Leu Thr Gly Ile Ile Arg Asn Ser Tyr Met Leu Val
    50                  55                  60

Leu Trp Ile Asn Thr Val Leu Arg Ala Tyr Leu Leu Leu Ala Asp His
65                  70                  75                  80

Asp Arg Tyr Leu Ala Leu Ile Gln Lys Leu Thr Glu Ala Tyr Tyr Asp
                85                  90                  95

Leu Leu Asn Leu Asn Asp Ser Tyr Ile Ser Glu Ile Leu Asp Gln Val
            100                 105                 110

Asn Lys Val Gly Lys Leu Met Ala Arg Gly Asn Leu Phe Phe Gly Met
        115                 120                 125

Leu Thr Ser Met Gly Phe Gly Leu Tyr Pro Leu Ser Ser Ser Glu Arg
    130                 135                 140

Val Leu Pro Phe Gly Ser Lys Ile Pro Gly Leu Asn Glu Tyr Glu Ser
145                 150                 155                 160

Pro Tyr Tyr Glu Met Trp Tyr Ile Phe Gln Met Leu Ile Thr Pro Met
                165                 170                 175

Gly Cys Cys Met Tyr Ile Pro Tyr Thr Ser Leu Ile Val Gly Leu Ile
            180                 185                 190

Met Phe Gly Ile Val Arg Cys Lys Ala Leu Gln His Arg Leu Arg Gln
        195                 200                 205

Val Ala Leu Lys His Pro Tyr Gly Asp Arg Asp Pro Arg Glu Leu Arg
    210                 215                 220

Glu Glu Ile Ile Ala Cys Ile Arg Tyr Gln Gln Ser Ile Ile Glu Tyr
225                 230                 235                 240

Met Asp His Ile Asn Glu Leu Thr Thr Met Met Phe Leu Phe Glu Leu
                245                 250                 255

Met Ala Phe Ser Ala Leu Leu Cys Ala Leu Leu Phe Met Leu Ile Ile
            260                 265                 270

Val Ser Gly Thr Ser Gln Leu Ile Ile Val Cys Met Tyr Ile Asn Met
        275                 280                 285

Ile Leu Ala Gln Ile Leu Ala Leu Tyr Trp Tyr Ala Asn Glu Leu Arg
    290                 295                 300

Glu Gln Asn Leu Ala Val Ala Thr Ala Ala Tyr Glu Thr Glu Trp Phe
305                 310                 315                 320

Thr Phe Asp Val Pro Leu Arg Lys Asn Ile Leu Phe Met Met Met Arg
                325                 330                 335

Ala Gln Arg Pro Ala Ala Ile Leu Leu Gly Asn Ile Arg Pro Ile Thr
            340                 345                 350

Leu Glu Leu Phe Gln Asn Leu Leu Asn Thr Thr Tyr Thr Phe Phe Thr
        355                 360                 365

Val Leu Lys Arg Val Tyr Gly
    370                 375
```

<210> SEQ ID NO 29
<211> LENGTH: 1188
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR107

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<400> SEQUENCE: 29

```
atgtatccgc gattcctcag ccgtaactat ccgctggcca agcatttgtt cttcgtcacc      60
agatactcct ttggcctgct gggcctgaga tttggcaaag agcaatcgtg gcttcacctc     120
ttgtggctgg tgttcaattt cgttaacctg gcgcactgct gccaggcgga gttcgtcttc     180
ggctggagtc acttgcgcac cagtcccgtg gatgccatgg acgccttttg tcctctggcc     240
tgcagtttca ccacgctctt caagctggga tggatgtggt ggcgtcgcca ggaagtagct     300
gatctaatgg accgcatccg cttgctcatc ggggagcagg agaagaggga ggactcccgg     360
agaaaggtgg ctcaaaggag ctactatctc atggtcacca ggtgcggtat gctggtcttc     420
accctgggca gcattaccac tggagccttc gttctgcgtt ccctttggga aatgtgggtg     480
cgtcgtcatc aggagttcaa attcgatatg ccctttcgca tgctgttcca cgactttgcg     540
catcgcatgc cctggtttcc agttttctat ctctactcca catggagtgg ccaggtcact     600
gtgtacgcct ttgctggtac agatggtttc ttctttggct ttaccctcta catggccttc     660
ttgctgcagg ccttaagata cgatatccag gatgccctca agccaataag agatccctcg     720
cttagggaat ccaaaatctg ctgtcagcga ttggcggaca tcgtggatcg ccacaatgag     780
atagagaaga tagtcaagga attttctgga attatggctg ctccaacttt tgttcacttc     840
gtatcagcca gcttagtgat agccaccagc gtcattgata tactattgta ttccggctat     900
aacatcatcc gttacgtggt gtacaccttc acggtttcct cggccatctt cctctattgc     960
tacggaggca cagaaatgtc aactgagagc ctttccttgg gagaagcagc ctacagcagt    1020
gcctggtata cttgggatcg agagacccgc aggcgggtct ttctcattat cctgcgtgct    1080
caacgaccca ttacggtgag ggtgcccttt tttgcaccat cgttaccagt cttcacatcg    1140
gtcatcaagt ttacaggttc gattgtggca ctggctaaga cgatactg                 1188
```

<210> SEQ ID NO 30
<211> LENGTH: 396
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR107

<400> SEQUENCE: 30

```
Met Tyr Pro Arg Phe Leu Ser Arg Asn Tyr Pro Leu Ala Lys His Leu
1               5                   10                  15

Phe Phe Val Thr Arg Tyr Ser Phe Gly Leu Leu Gly Leu Arg Phe Gly
            20                  25                  30

Lys Glu Gln Ser Trp Leu His Leu Leu Trp Leu Val Phe Asn Phe Val
        35                  40                  45

Asn Leu Ala His Cys Cys Gln Ala Glu Phe Val Phe Gly Trp Ser His
    50                  55                  60

Leu Arg Thr Ser Pro Val Asp Ala Met Asp Ala Phe Cys Pro Leu Ala
65                  70                  75                  80

Cys Ser Phe Thr Thr Leu Phe Lys Leu Gly Trp Met Trp Trp Arg Arg
                85                  90                  95

Gln Glu Val Ala Asp Leu Met Asp Arg Ile Arg Leu Leu Ile Gly Glu
            100                 105                 110

Gln Glu Lys Arg Glu Asp Ser Arg Arg Lys Val Ala Gln Arg Ser Tyr
        115                 120                 125

Tyr Leu Met Val Thr Arg Cys Gly Met Leu Val Phe Thr Leu Gly Ser
```

-continued

```
    130                 135                 140

Ile Thr Thr Gly Ala Phe Val Leu Arg Ser Leu Trp Glu Met Trp Val
145                 150                 155                 160

Arg Arg His Gln Glu Phe Lys Phe Asp Met Pro Phe Arg Met Leu Phe
                165                 170                 175

His Asp Phe Ala His Arg Met Pro Trp Phe Pro Val Phe Tyr Leu Tyr
            180                 185                 190

Ser Thr Trp Ser Gly Gln Val Thr Val Tyr Ala Phe Ala Gly Thr Asp
        195                 200                 205

Gly Phe Phe Phe Gly Phe Thr Leu Tyr Met Ala Phe Leu Leu Gln Ala
    210                 215                 220

Leu Arg Tyr Asp Ile Gln Asp Ala Leu Lys Pro Ile Arg Asp Pro Ser
225                 230                 235                 240

Leu Arg Glu Ser Lys Ile Cys Cys Gln Arg Leu Ala Asp Ile Val Asp
                245                 250                 255

Arg His Asn Glu Ile Glu Lys Ile Val Lys Glu Phe Ser Gly Ile Met
            260                 265                 270

Ala Ala Pro Thr Phe Val His Phe Val Ser Ala Ser Leu Val Ile Ala
        275                 280                 285

Thr Ser Val Ile Asp Ile Leu Leu Tyr Ser Gly Tyr Asn Ile Ile Arg
    290                 295                 300

Tyr Val Val Tyr Thr Phe Thr Val Ser Ser Ala Ile Phe Leu Tyr Cys
305                 310                 315                 320

Tyr Gly Gly Thr Glu Met Ser Thr Glu Ser Leu Ser Leu Gly Glu Ala
                325                 330                 335

Ala Tyr Ser Ser Ala Trp Tyr Thr Trp Asp Arg Glu Thr Arg Arg Arg
            340                 345                 350

Val Phe Leu Ile Ile Leu Arg Ala Gln Arg Pro Ile Thr Val Arg Val
        355                 360                 365

Pro Phe Phe Ala Pro Ser Leu Pro Val Phe Thr Ser Val Ile Lys Phe
    370                 375                 380

Thr Gly Ser Ile Val Ala Leu Ala Lys Thr Ile Leu
385                 390                 395
```

<210> SEQ ID NO 31
<211> LENGTH: 1161
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR108

<400> SEQUENCE: 31

```
atggataaac acaaggatcg cattgaatcc atgcgcctaa ttcttcaggt catgcaacta     60

tttggcctct ggccgtggtc cttgaaatcg gaagaggagt ggactttcac cggttttgta    120

aagcgcaact atcgcttcct gctccatctg cccattacct tcacctttat tggactcatg    180

tggctggagg ccttcatctc gagcaatctg gagcaggctg gccaggttct gtacatgtcc    240

atcaccgaga tggctttggt ggtgaaaatc ctgagcattt ggcactatcg caccgaagct    300

tggcggctga tgtacgaact ccaacatgct ccggactacc aactccacaa ccaggaggag    360

gtagactttt ggcgccggga gcaacgattc ttcaagtggt tcttctacat ctacattctg    420

attagcttgg gcgtggtata tagtggctgc actggagtac tttttctgga gggctacgaa    480

ctgccctttg cctactacgt gcccttcgaa tggcagaacg agagaaggta ctggttcgcc    540
```

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tatggttacg atatggcggg catgacgctg acctgcatct caaacattac cctggacacc    600

ctgggttgct atttcctgtt ccatatctct cttttgtacc gactgcttgg tctgcgattg    660

agggaaacga agaatatgaa gaatgatacc atttttggcc agcagttgcg tgccatcttc    720

attatgcatc agaggattag aagcctaacc ctgacctgcc agagaatcgt atctccctat    780

atcctatctc agatcatttt gagtgccctg atcatctgct ttagtggata ccgcttgcag    840

catgtgggaa ttcgcgataa tcccggccag tttatatcca tgttgcagtt tgtcagtgtg    900

atgatcctgc agatttactt gccctgctac tatggaaacg agataaccgt gtatgccaat    960

cagctgacca acgaggttta ccataccaat tggctggaat gtcggccacc gattcgaaag   1020

ttactcaatg cctacatgga gcacctgaag aaaccggtga ccatccgggc tggcaactcc   1080

ttcgccgtgg gactaccaat ttttgttaag accatcaaca acgcctacag tttcttggct   1140

ttattactaa atgtatcgaa t                                             1161


&lt;210&gt; SEQ ID NO 32
&lt;211&gt; LENGTH: 387
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Drosophila Melanogaster  DOR108

&lt;400&gt; SEQUENCE: 32

Met Asp Lys His Lys Asp Arg Ile Glu Ser Met Arg Leu Ile Leu Gln
1               5                   10                  15

Val Met Gln Leu Phe Gly Leu Trp Pro Trp Ser Leu Lys Ser Glu Glu
            20                  25                  30

Glu Trp Thr Phe Thr Gly Phe Val Lys Arg Asn Tyr Arg Phe Leu Leu
        35                  40                  45

His Leu Pro Ile Thr Phe Thr Phe Ile Gly Leu Met Trp Leu Glu Ala
    50                  55                  60

Phe Ile Ser Ser Asn Leu Glu Gln Ala Gly Gln Val Leu Tyr Met Ser
65                  70                  75                  80

Ile Thr Glu Met Ala Leu Val Val Lys Ile Leu Ser Ile Trp His Tyr
                85                  90                  95

Arg Thr Glu Ala Trp Arg Leu Met Tyr Glu Leu Gln His Ala Pro Asp
            100                 105                 110

Tyr Gln Leu His Asn Gln Glu Glu Val Asp Phe Trp Arg Arg Glu Gln
        115                 120                 125

Arg Phe Phe Lys Trp Phe Phe Tyr Ile Tyr Ile Leu Ile Ser Leu Gly
    130                 135                 140

Val Val Tyr Ser Gly Cys Thr Gly Val Leu Phe Leu Glu Gly Tyr Glu
145                 150                 155                 160

Leu Pro Phe Ala Tyr Tyr Val Pro Phe Glu Trp Gln Asn Glu Arg Arg
                165                 170                 175

Tyr Trp Phe Ala Tyr Gly Tyr Asp Met Ala Gly Met Thr Leu Thr Cys
            180                 185                 190

Ile Ser Asn Ile Thr Leu Asp Thr Leu Gly Cys Tyr Phe Leu Phe His
        195                 200                 205

Ile Ser Leu Leu Tyr Arg Leu Leu Gly Leu Arg Leu Arg Glu Thr Lys
    210                 215                 220

Asn Met Lys Asn Asp Thr Ile Phe Gly Gln Gln Leu Arg Ala Ile Phe
225                 230                 235                 240

Ile Met His Gln Arg Ile Arg Ser Leu Thr Leu Thr Cys Gln Arg Ile
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            245                 250                 255

Val Ser Pro Tyr Ile Leu Ser Gln Ile Ile Leu Ser Ala Leu Ile Ile
        260                 265                 270

Cys Phe Ser Gly Tyr Arg Leu Gln His Val Gly Ile Arg Asp Asn Pro
    275                 280                 285

Gly Gln Phe Ile Ser Met Leu Gln Phe Val Ser Val Met Ile Leu Gln
    290                 295                 300

Ile Tyr Leu Pro Cys Tyr Tyr Gly Asn Glu Ile Thr Val Tyr Ala Asn
305                 310                 315                 320

Gln Leu Thr Asn Glu Val Tyr His Thr Asn Trp Leu Glu Cys Arg Pro
            325                 330                 335

Pro Ile Arg Lys Leu Leu Asn Ala Tyr Met Glu His Leu Lys Lys Pro
        340                 345                 350

Val Thr Ile Arg Ala Gly Asn Ser Phe Ala Val Gly Leu Pro Ile Phe
    355                 360                 365

Val Lys Thr Ile Asn Asn Ala Tyr Ser Phe Leu Ala Leu Leu Leu Asn
    370                 375                 380

Val Ser Asn
385


<210> SEQ ID NO 33
<211> LENGTH: 1149
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster  DOR109

<400> SEQUENCE: 33

atggagtcta caaatcgcct aagtgccatc caaacacttt tagtaatcca acgttggata     60

ggacttctta aatgggaaaa cgagggcgag gatggagtat taacctggct aaaacgaata    120

tatcctttttg tactgcacct tccactgacc ttcacgtata ttgccttaat gtggtatgaa    180

gctattacat cgtcagattt tgaggaagct ggtcaagttc tgtacatgtc catcaccgaa    240

ctggcattgg tcactaaact gctgaatatt tggtatcgtc gtcatgaagc tgctagtcta    300

atccacgaat tgcaacacga tcccgcattt aatctgcgca attcggagga aatcaaattc    360

tggcagcaaa atcagaggaa ctttaagaga atattttact ggtacatctg ggcagcctt    420

ttcgtggctg taatgggtta tataagcgtg tttttccagg aggattacga gctgcccttt    480

ggctactacg tgccattcga gtggcgcacc agggaacgat acttctacgc ttggggctat    540

aatgtggtgg ccatgaccct gtgctgtcta tccaacatcc tactggacac actaggctgt    600

tatttcatgt tccacatcgc ctcgcttttc aggcttttgg gaatgcgact ggaggccttg    660

aaaaatgcag ccgaagagaa agccagaccg gagttgcgcc gcattttcca actgcacact    720

aaagtccgcc gattgacgag ggaatgcgaa gtgttagttt caccctatgt tctatcccaa    780

gtggtcttca gtgccttcat catctgcttc agtgcctatc gactggtgca catgggcttc    840

aagcagcgac ctggactctt cgtgaccacc gtgcaattcg tggccgtcat gatcgtccag    900

attttcttgc cctgttacta cggcaatgag ttgacctttc atgccaatgc actcactaat    960

agtgtcttcg gtaccaattg gctggagtac tccgtgggca ctcgcaagct gcttaactgc   1020

tacatggagt tcctcaagcg accggttaaa gtgcgagctg ggtgttcttt tgaaatagga   1080

ctacccatct ttgtgaagac catcaacaat gcctacagtt tcttcgccct gctgctaaag   1140

atatccaag                                                           1149
```

-continued

<210> SEQ ID NO 34
<211> LENGTH: 383
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR109

<400> SEQUENCE: 34

Met Glu Ser Thr Asn Arg Leu Ser Ala Ile Gln Thr Leu Leu Val Ile
1   5   10   15

Gln Arg Trp Ile Gly Leu Leu Lys Trp Glu Asn Glu Gly Glu Asp Gly
            20   25   30

Val Leu Thr Trp Leu Lys Arg Ile Tyr Pro Phe Val Leu His Leu Pro
        35   40   45

Leu Thr Phe Thr Tyr Ile Ala Leu Met Trp Tyr Glu Ala Ile Thr Ser
    50   55   60

Ser Asp Phe Glu Glu Ala Gly Gln Val Leu Tyr Met Ser Ile Thr Glu
65   70   75   80

Leu Ala Leu Val Thr Lys Leu Leu Asn Ile Trp Tyr Arg Arg His Glu
                85   90   95

Ala Ala Ser Leu Ile His Glu Leu Gln His Asp Pro Ala Phe Asn Leu
            100   105   110

Arg Asn Ser Glu Glu Ile Lys Phe Trp Gln Gln Asn Gln Arg Asn Phe
        115   120   125

Lys Arg Ile Phe Tyr Trp Tyr Ile Trp Gly Ser Leu Phe Val Ala Val
    130   135   140

Met Gly Tyr Ile Ser Val Phe Phe Gln Glu Asp Tyr Glu Leu Pro Phe
145   150   155   160

Gly Tyr Tyr Val Pro Phe Glu Trp Arg Thr Arg Glu Arg Tyr Phe Tyr
                165   170   175

Ala Trp Gly Tyr Asn Val Val Ala Met Thr Leu Cys Cys Leu Ser Asn
            180   185   190

Ile Leu Leu Asp Thr Leu Gly Cys Tyr Phe Met Phe His Ile Ala Ser
        195   200   205

Leu Phe Arg Leu Leu Gly Met Arg Leu Glu Ala Leu Lys Asn Ala Ala
    210   215   220

Glu Glu Lys Ala Arg Pro Glu Leu Arg Arg Ile Phe Gln Leu His Thr
225   230   235   240

Lys Val Arg Arg Leu Thr Arg Glu Cys Glu Val Leu Val Ser Pro Tyr
                245   250   255

Val Leu Ser Gln Val Val Phe Ser Ala Phe Ile Ile Cys Phe Ser Ala
            260   265   270

Tyr Arg Leu Val His Met Gly Phe Lys Gln Arg Pro Gly Leu Phe Val
        275   280   285

Thr Thr Val Gln Phe Val Ala Val Met Ile Val Gln Ile Phe Leu Pro
    290   295   300

Cys Tyr Tyr Gly Asn Glu Leu Thr Phe His Ala Asn Ala Leu Thr Asn
305   310   315   320

Ser Val Phe Gly Thr Asn Trp Leu Glu Tyr Ser Val Gly Thr Arg Lys
                325   330   335

Leu Leu Asn Cys Tyr Met Glu Phe Leu Lys Arg Pro Val Lys Val Arg
            340   345   350

Ala Gly Val Phe Phe Glu Ile Gly Leu Pro Ile Phe Val Lys Thr Ile

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        355                 360                 365

Asn Asn Ala Tyr Ser Phe Phe Ala Leu Leu Leu Lys Ile Ser Lys
    370                 375                 380
```

<210> SEQ ID NO 35
<211> LENGTH: 1161
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR110

<400> SEQUENCE: 35

```
atgttgttca actatctgcg aaagccgaat cccacaaacc ttttgacttc tccggactca     60

tttagatact ttgagtatgg aatgttttgc atgggatggc acacaccagc aacgcataag    120

ataatctact atataacatc ctgtttgatt tttgcttggt gtgccgtata cttgccaatc    180

ggaatcatca ttagtttcaa aacggatatt aacacattca caccgaatga actgttgaca    240

gttatgcaat tatttttcaa ttcagtggga atgccattca aggttctgtt cttcaatttg    300

tatatttctg gattttacaa ggccaaaaag ctccttagcg aaatggacaa acgttgcacc    360

actttgaagg agcgagtgga agtgcaccaa ggtgtggtcc gttgcaacaa ggcctacctc    420

atttaccagt tcatttatac cgcgtacact atttcaacat ttctatcggc ggctcttagt    480

ggaaaattgc catggcgcat ctataatcct tttgtggatt ttcgagaaag tagatccagt    540

ttttggaaag ctgccctcaa cgagacagca cttatgctat ttgctgtgac tcaaacccta    600

atgagtgata tatatccact gctttatggt ttgatcctga gagttcacct caaacttttg    660

cgactaagag tggagagcct gtgcacagat tctggaaaaa gcgatgctga aaacgagcaa    720

gatttgatta actatgctgc agcaatacga ccagcggtta cccgcacaat tttcgttcaa    780

ttcctcttga tcggaatttg ccttggcctt tcaatgatca atctactctt ctttgccgac    840

atctggacag gattggccac agtggcttac atcaatggtc taatggtgca gacatttcca    900

ttttgcttcg tttgtgatct actcaaaaag gattgtgaac ttcttgtgtc ggccatattt    960

cattccaact ggattaattc aagccgcagt tacaagtcat ctttgagata ttttctgaag   1020

aacgcccaga aatcaattgc ttttacagcc ggctctattt ttcccatttc tactggctcg   1080

aatattaagg tggctaagct ggcattttcg gtggttactt ttgtcaatca acttaacata   1140

gctgacagat tgacaaagaa c                                              1161
```

<210> SEQ ID NO 36
<211> LENGTH: 387
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR110

<400> SEQUENCE: 36

```
Met Leu Phe Asn Tyr Leu Arg Lys Pro Asn Pro Thr Asn Leu Leu Thr
1               5                   10                  15

Ser Pro Asp Ser Phe Arg Tyr Phe Glu Tyr Gly Met Phe Cys Met Gly
            20                  25                  30

Trp His Thr Pro Ala Thr His Lys Ile Ile Tyr Tyr Ile Thr Ser Cys
        35                  40                  45

Leu Ile Phe Ala Trp Cys Ala Val Tyr Leu Pro Ile Gly Ile Ile Ile
    50                  55                  60

Ser Phe Lys Thr Asp Ile Asn Thr Phe Thr Pro Asn Glu Leu Leu Thr
65                  70                  75                  80
```

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```
Val Met Gln Leu Phe Phe Asn Ser Val Gly Met Pro Phe Lys Val Leu
                85                  90                  95

Phe Phe Asn Leu Tyr Ile Ser Gly Phe Tyr Lys Ala Lys Lys Leu Leu
            100                 105                 110

Ser Glu Met Asp Lys Arg Cys Thr Thr Leu Lys Glu Arg Val Glu Val
        115                 120                 125

His Gln Gly Val Val Arg Cys Asn Lys Ala Tyr Leu Ile Tyr Gln Phe
    130                 135                 140

Ile Tyr Thr Ala Tyr Thr Ile Ser Thr Phe Leu Ser Ala Ala Leu Ser
145                 150                 155                 160

Gly Lys Leu Pro Trp Arg Ile Tyr Asn Pro Phe Val Asp Phe Arg Glu
                165                 170                 175

Ser Arg Ser Ser Phe Trp Lys Ala Ala Leu Asn Glu Thr Ala Leu Met
            180                 185                 190

Leu Phe Ala Val Thr Gln Thr Leu Met Ser Asp Ile Tyr Pro Leu Leu
        195                 200                 205

Tyr Gly Leu Ile Leu Arg Val His Leu Lys Leu Leu Arg Leu Arg Val
    210                 215                 220

Glu Ser Leu Cys Thr Asp Ser Gly Lys Ser Asp Ala Glu Asn Glu Gln
225                 230                 235                 240

Asp Leu Ile Asn Tyr Ala Ala Ala Ile Arg Pro Ala Val Thr Arg Thr
                245                 250                 255

Ile Phe Val Gln Phe Leu Leu Ile Gly Ile Cys Leu Gly Leu Ser Met
            260                 265                 270

Ile Asn Leu Leu Phe Phe Ala Asp Ile Trp Thr Gly Leu Ala Thr Val
        275                 280                 285

Ala Tyr Ile Asn Gly Leu Met Val Gln Thr Phe Pro Phe Cys Phe Val
    290                 295                 300

Cys Asp Leu Leu Lys Lys Asp Cys Glu Leu Leu Val Ser Ala Ile Phe
305                 310                 315                 320

His Ser Asn Trp Ile Asn Ser Ser Arg Ser Tyr Lys Ser Ser Leu Arg
                325                 330                 335

Tyr Phe Leu Lys Asn Ala Gln Lys Ser Ile Ala Phe Thr Ala Gly Ser
            340                 345                 350

Ile Phe Pro Ile Ser Thr Gly Ser Asn Ile Lys Val Ala Lys Leu Ala
        355                 360                 365

Phe Ser Val Val Thr Phe Val Asn Gln Leu Asn Ile Ala Asp Arg Leu
    370                 375                 380

Thr Lys Asn
385


<210> SEQ ID NO 37
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster  DOR111

<400> SEQUENCE: 37

atgctgttcc gcaaacgtaa gccaaaaagt gacgatgaag tcatcacctt cgacgaactt      60

acccggtttc cgatgacttt ctacaagacc atcggcgagg atctgtactc cgataggat     120

ccgaatgtga taaggcgtta cctgctacgt ttttatctgg tactcggttt tctcaacttc    180

aatgcctatg tggtgggcga aatcgcgtac tttatagtcc atataatgtc gacgactact    240
```

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```
cttttggagg ccactgcagt ggcaccgtgc attggcttca gcttcatggc cgactttaag    300

cagttcggtc tcacagtgaa tagaaagcga ttggtcagat tgctggatga tctcaaggag    360

atatttcctt tagatttaga agcgcagcgg aagtataacg tatcgtttta ccggaaacac    420

atgaacaggg tcatgaccct attcaccatc ctctgcatga cctacacctc gtcatttagc    480

ttttatccag ccatcaagtc gaccataaag tattacctta tgggatcgga aatctttgag    540

cgcaactacg gatttcacat tttgtttccc tacgacgcag aaacggatct gacggtctac    600

tggttttcct actggggatt ggctcattgt gcctatgtgg ccggagtttc ctacgtctgc    660

gtggatctcc tgctgatcgc gaccataacc cagctgacca tgcacttcaa ctttatagcg    720

aatgatttgg aggcctacga aggaggtgat catacggatg aagaaaatat caaatacctg    780

cacaacttgg tcgtctatca tgccagggcg ctggatatta acaagaaatg tacatttcag    840

agctctcgga ttggccattc ggcatttaat cagaactggt tgccatgcag caccaaatac    900

aaacgcatcc tgcaatttat tatcgcgcgc agccagaagc ccgcctctat aagaccgcct    960

acctttccac ccatatcttt taatacccttt atgaaggtaa tcagcatgtc gtatcagttt   1020

tttgcactgc tccgcaccac atattatggt                                     1050
```

```
<210> SEQ ID NO 38
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster  DOR111

<400> SEQUENCE: 38

Met Leu Phe Arg Lys Arg Lys Pro Lys Ser Asp Asp Glu Val Ile Thr
1               5                   10                  15

Phe Asp Glu Leu Thr Arg Phe Pro Met Thr Phe Tyr Lys Thr Ile Gly
            20                  25                  30

Glu Asp Leu Tyr Ser Asp Arg Asp Pro Asn Val Ile Arg Arg Tyr Leu
        35                  40                  45

Leu Arg Phe Tyr Leu Val Leu Gly Phe Leu Asn Phe Asn Ala Tyr Val
    50                  55                  60

Val Gly Glu Ile Ala Tyr Phe Ile Val His Ile Met Ser Thr Thr Thr
65                  70                  75                  80

Leu Leu Glu Ala Thr Ala Val Ala Pro Cys Ile Gly Phe Ser Phe Met
                85                  90                  95

Ala Asp Phe Lys Gln Phe Gly Leu Thr Val Asn Arg Lys Arg Leu Val
            100                 105                 110

Arg Leu Leu Asp Asp Leu Lys Glu Ile Phe Pro Leu Asp Leu Glu Ala
        115                 120                 125

Gln Arg Lys Tyr Asn Val Ser Phe Tyr Arg Lys His Met Asn Arg Val
    130                 135                 140

Met Thr Leu Phe Thr Ile Leu Cys Met Thr Tyr Thr Ser Ser Phe Ser
145                 150                 155                 160

Phe Tyr Pro Ala Ile Lys Ser Thr Ile Lys Tyr Tyr Leu Met Gly Ser
                165                 170                 175

Glu Ile Phe Glu Arg Asn Tyr Gly Phe His Ile Leu Phe Pro Tyr Asp
            180                 185                 190

Ala Glu Thr Asp Leu Thr Val Tyr Trp Phe Ser Tyr Trp Gly Leu Ala
        195                 200                 205

His Cys Ala Tyr Val Ala Gly Val Ser Tyr Val Cys Val Asp Leu Leu
```

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```
    210                 215                 220

Leu Ile Ala Thr Ile Thr Gln Leu Thr Met His Phe Asn Phe Ile Ala
225                 230                 235                 240

Asn Asp Leu Glu Ala Tyr Glu Gly Gly Asp His Thr Asp Glu Glu Asn
                245                 250                 255

Ile Lys Tyr Leu His Asn Leu Val Val Tyr His Ala Arg Ala Leu Asp
            260                 265                 270

Ile Asn Lys Lys Cys Thr Phe Gln Ser Ser Arg Ile Gly His Ser Ala
        275                 280                 285

Phe Asn Gln Asn Trp Leu Pro Cys Ser Thr Lys Tyr Lys Arg Ile Leu
    290                 295                 300

Gln Phe Ile Ile Ala Arg Ser Gln Lys Pro Ala Ser Ile Arg Pro Pro
305                 310                 315                 320

Thr Phe Pro Pro Ile Ser Phe Asn Thr Phe Met Lys Val Ile Ser Met
                325                 330                 335

Ser Tyr Gln Phe Phe Ala Leu Leu Arg Thr Thr Tyr Tyr Gly
            340                 345                 350


<210> SEQ ID NO 39
<211> LENGTH: 1236
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster  DOR114

<400> SEQUENCE: 39

atgttgacta agaaggatac tcaaagtgcc aaggagcagg aaaagttgaa ggccattcca      60

ttgcacagct ttctgaaata tgccaacgtg ttctatttat cgattggaat gatggcctac     120

gatcacaagt acagtcaaaa gtggaaggag gtcctgctgc actggacatt cattgcccag     180

atggtcaatc tgaatacagt gctcatctcg gaactgattt acgtattcct ggcgatcggc     240

aaaggtagca attttctgga ggccaccatg aatctgtctt tcattggatt tgtcatcgtt     300

ggtgacttca aaatctggaa catttcgcgg cagagaaaga gactcaccca agtggtcagc     360

cgattggaag aactgcatcc gcaaggcttg gctcaacaag aaccctataa tatagggcat     420

catctgagcg gctatagccg atatagcaaa ttttacttcg gcatgcacat ggtgctgata     480

tggacgtaca acctgtattg ggccgtttac tatctggtct gtgatttctg gctgggaatg     540

cgtcaatttg agaggatgct gccctactac tgctgggttc cctgggattg gagtaccgga     600

tatagctact atttcatgta tatctcacag aatatcggcg gtcaggcttg tctgtccggt     660

cagctagcag ctgacatgtt aatgtgcgcc ctggtcactt tggtggtgat gcacttcatc     720

cggctttccg ctcacatcga gagtcatgtt gcgggcattg gctcattcca gcacgatttg     780

gagttcctcc aagcgacggt ggcgtatcac cagagcttga tccacctctg ccaggatatc     840

aatgagatat tcggtgtttc actgttgtcc aactttgtat cctcgtcgtt tatcatctgc     900

ttcgtgggtt tccagatgac catcggcagc aagatcgaca acctggtaat gcttgtgctt     960

ttcctgtttt gtgccatggt tcaggtcttc atgattgcca cccatgctca gaggctcgtt    1020

gatgcgagtg aacagattgg tcaagcggtc tataatcacg actggttccg tgctgatctg    1080

cggtatcgta aaatgctgat cctgattatt aagagggccc aacagccgag tcgactcaag    1140

gccacaatgt tcctgaacat ctcactggtc accgtgtcgg atctcttgca actctcgtac    1200

aaattctttg cccttctgcg cacaatgtac gtgaat                              1236
```

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<210> SEQ ID NO 40
<211> LENGTH: 412
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR114

<400> SEQUENCE: 40

```
Met Leu Thr Lys Lys Asp Thr Gln Ser Ala Lys Glu Gln Glu Lys Leu
1               5                   10                  15

Lys Ala Ile Pro Leu His Ser Phe Leu Lys Tyr Ala Asn Val Phe Tyr
            20                  25                  30

Leu Ser Ile Gly Met Met Ala Tyr Asp His Lys Tyr Ser Gln Lys Trp
        35                  40                  45

Lys Glu Val Leu Leu His Trp Thr Phe Ile Ala Gln Met Val Asn Leu
    50                  55                  60

Asn Thr Val Leu Ile Ser Glu Leu Ile Tyr Val Phe Leu Ala Ile Gly
65                  70                  75                  80

Lys Gly Ser Asn Phe Leu Glu Ala Thr Met Asn Leu Ser Phe Ile Gly
                85                  90                  95

Phe Val Ile Val Gly Asp Phe Lys Ile Trp Asn Ile Ser Arg Gln Arg
            100                 105                 110

Lys Arg Leu Thr Gln Val Val Ser Arg Leu Glu Glu Leu His Pro Gln
        115                 120                 125

Gly Leu Ala Gln Gln Glu Pro Tyr Asn Ile Gly His His Leu Ser Gly
    130                 135                 140

Tyr Ser Arg Tyr Ser Lys Phe Tyr Phe Gly Met His Met Val Leu Ile
145                 150                 155                 160

Trp Thr Tyr Asn Leu Tyr Trp Ala Val Tyr Tyr Leu Val Cys Asp Phe
                165                 170                 175

Trp Leu Gly Met Arg Gln Phe Glu Arg Met Leu Pro Tyr Tyr Cys Trp
            180                 185                 190

Val Pro Trp Asp Trp Ser Thr Gly Tyr Ser Tyr Tyr Phe Met Tyr Ile
        195                 200                 205

Ser Gln Asn Ile Gly Gly Gln Ala Cys Leu Ser Gly Gln Leu Ala Ala
    210                 215                 220

Asp Met Leu Met Cys Ala Leu Val Thr Leu Val Val Met His Phe Ile
225                 230                 235                 240

Arg Leu Ser Ala His Ile Glu Ser His Val Ala Gly Ile Gly Ser Phe
                245                 250                 255

Gln His Asp Leu Glu Phe Leu Gln Ala Thr Val Ala Tyr His Gln Ser
            260                 265                 270

Leu Ile His Leu Cys Gln Asp Ile Asn Glu Ile Phe Gly Val Ser Leu
        275                 280                 285

Leu Ser Asn Phe Val Ser Ser Ser Phe Ile Ile Cys Phe Val Gly Phe
    290                 295                 300

Gln Met Thr Ile Gly Ser Lys Ile Asp Asn Leu Val Met Leu Val Leu
305                 310                 315                 320

Phe Leu Phe Cys Ala Met Val Gln Val Phe Met Ile Ala Thr His Ala
                325                 330                 335

Gln Arg Leu Val Asp Ala Ser Glu Gln Ile Gly Gln Ala Val Tyr Asn
            340                 345                 350

His Asp Trp Phe Arg Ala Asp Leu Arg Tyr Arg Lys Met Leu Ile Leu
        355                 360                 365
```

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```
Ile Ile Lys Arg Ala Gln Gln Pro Ser Arg Leu Lys Ala Thr Met Phe
    370                 375                 380

Leu Asn Ile Ser Leu Val Thr Val Ser Asp Leu Leu Gln Leu Ser Tyr
385                 390                 395                 400

Lys Phe Phe Ala Leu Leu Arg Thr Met Tyr Val Asn
                405                 410


<210> SEQ ID NO 41
<211> LENGTH: 1140
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster  DOR115

<400> SEQUENCE: 41

atggagaagc taatgaagta cgctagcttc ttctacacag cagtgggcat acggccatat     60

accaatggtg aagaatccaa aatgaacaaa cttatatttc acatagtttt ttggtccaat    120

gtgattaacc tcagcttcgt tggattattt gagagcattt acgtttacag tgccttcatg    180

gataataagt tcctggaagc agtcactgcg ttgtcctaca ttggcttcgt aaccgtaggc    240

atgagcaaga tgttcttcat ccggtggaag aaaacggcta taactgaact gattaatgaa    300

ttgaaggaga tctatccgaa tggtttgatc cgagaggaaa gatacaatct gccgatgtat    360

ctgggcacct gctccagaat cagccttata tattccttgc tctactctgt tctcatctgg    420

acattcaact tgttttgtgt aatggagtat tgggtctatg acaagtggct caacattcga    480

gtggtgggca aacagttgcc gtacctcatg tacattcctt ggaaatggca ggataactgg    540

tcgtactatc cactgttatt ctcccagaat tttgcaggat acacatctgc agctggtcaa    600

atttcaaccg atgtcttgct ctgcgcggtg gccactcagt tggtaatgca cttcgacttt    660

ctctcaaata gtatggaacg ccacgaattg agtggagatt ggaagaagga ctcccgattt    720

ctggtggaca ttgttaggta tcacgaacgt atactccgcc tttcagatgc agtgaacgat    780

atatttggaa ttccactact actcaacttc atggtatcct cgttcgtcat ctgcttcgtg    840

ggattccaga tgactgttgg agttccgccg gatatagttg tgaagctctt cctcttcctt    900

gtctcttcga tgagtcaggt ctatttgatt tgtcactatg gtcaactggt ggccgatgct    960

agctacggat tttcggttgc cacctacaat cagaagtggt ataaagccga tgtgcgctat   1020

aaacgagcct tggttattat tatagctaga tcgcagaagg taacttttct aaaggccact   1080

atattcttgg atattaccag gtccactatg acagatgtac gcaactgtgt attgtcagtg   1140


<210> SEQ ID NO 42
<211> LENGTH: 380
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster  DOR115

<400> SEQUENCE: 42

Met Glu Lys Leu Met Lys Tyr Ala Ser Phe Phe Tyr Thr Ala Val Gly
1               5                   10                  15

Ile Arg Pro Tyr Thr Asn Gly Glu Glu Ser Lys Met Asn Lys Leu Ile
            20                  25                  30

Phe His Ile Val Phe Trp Ser Asn Val Ile Asn Leu Ser Phe Val Gly
        35                  40                  45

Leu Phe Glu Ser Ile Tyr Val Tyr Ser Ala Phe Met Asp Asn Lys Phe
    50                  55                  60
```

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```
Leu Glu Ala Val Thr Ala Leu Ser Tyr Ile Gly Phe Val Thr Val Gly
65                  70                  75                  80

Met Ser Lys Met Phe Phe Ile Arg Trp Lys Lys Thr Ala Ile Thr Glu
                85                  90                  95

Leu Ile Asn Glu Leu Lys Glu Ile Tyr Pro Asn Gly Leu Ile Arg Glu
            100                 105                 110

Glu Arg Tyr Asn Leu Pro Met Tyr Leu Gly Thr Cys Ser Arg Ile Ser
        115                 120                 125

Leu Ile Tyr Ser Leu Leu Tyr Ser Val Leu Ile Trp Thr Phe Asn Leu
    130                 135                 140

Phe Cys Val Met Glu Tyr Trp Val Tyr Asp Lys Trp Leu Asn Ile Arg
145                 150                 155                 160

Val Val Gly Lys Gln Leu Pro Tyr Leu Met Tyr Ile Pro Trp Lys Trp
                165                 170                 175

Gln Asp Asn Trp Ser Tyr Tyr Pro Leu Leu Phe Ser Gln Asn Phe Ala
            180                 185                 190

Gly Tyr Thr Ser Ala Ala Gly Gln Ile Ser Thr Asp Val Leu Leu Cys
        195                 200                 205

Ala Val Ala Thr Gln Leu Val Met His Phe Asp Phe Leu Ser Asn Ser
    210                 215                 220

Met Glu Arg His Glu Leu Ser Gly Asp Trp Lys Lys Asp Ser Arg Phe
225                 230                 235                 240

Leu Val Asp Ile Val Arg Tyr His Glu Arg Ile Leu Arg Leu Ser Asp
                245                 250                 255

Ala Val Asn Asp Ile Phe Gly Ile Pro Leu Leu Leu Asn Phe Met Val
            260                 265                 270

Ser Ser Phe Val Ile Cys Phe Val Gly Phe Gln Met Thr Val Gly Val
        275                 280                 285

Pro Pro Asp Ile Val Val Lys Leu Phe Leu Phe Leu Val Ser Ser Met
    290                 295                 300

Ser Gln Val Tyr Leu Ile Cys His Tyr Gly Gln Leu Val Ala Asp Ala
305                 310                 315                 320

Ser Tyr Gly Phe Ser Val Ala Thr Tyr Asn Gln Lys Trp Tyr Lys Ala
                325                 330                 335

Asp Val Arg Tyr Lys Arg Ala Leu Val Ile Ile Ile Ala Arg Ser Gln
            340                 345                 350

Lys Val Thr Phe Leu Lys Ala Thr Ile Phe Leu Asp Ile Thr Arg Ser
        355                 360                 365

Thr Met Thr Asp Val Arg Asn Cys Val Leu Ser Val
    370                 375                 380
```

<210> SEQ ID NO 43
<211> LENGTH: 759
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR116

<400> SEQUENCE: 43

```
atggaactcc tgccattggc catgctaatg tacgatggaa cccgggttac tgcgatgcag      60

tatttaattc cgggtctacc gcttgagaac aattattgct acgtagtcac gtacatgatt     120

cagacggtga caatgctcgt gcaaggagtc ggattctact ccggtgattt gttcgtattt     180

ctcggcttaa cgcagatcct aactttcgcc gatatgctgc aggtgaaggt gaaagagcta     240
```

-continued

```
aacgatgccc tggaacaaaa agcggaatac agagctctag tccgagttgg agcttctatt    300

gatggagcgg aaaatcgtca acgccttctc ttggatgtta taagatggca tcaattattc    360

acggactact gtcgcgccat aaatgccctc tactacgaat tgatcgccac tcaggttctt    420

tcgatggctt tggccatgat gctcagcttc tgcattaatt tgagcagctt tcacatgcct    480

tcggctatct ttttcgtggt ttctgcctac agcatgtcca tctattgcat tctgggcacc    540

attcttgagt ttgcatatga ccaggtgtac gagagcatct gtaatgtgac ctggtatgag    600

ttgagtggcg aacagcgaaa gctttttggt tttttgttgc gggaatccca gtatccgcac    660

aatattcaga tacttggagt tatgtcgctt tccgtgagaa cggctctgca gattgttaaa    720

ctaatttata gcgtatccat gatgatgatg aatcgggcg                           759
```

```
<210> SEQ ID NO 44
<211> LENGTH: 253
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR116

<400> SEQUENCE: 44

Met Glu Leu Leu Pro Leu Ala Met Leu Met Tyr Asp Gly Thr Arg Val
1               5                   10                  15

Thr Ala Met Gln Tyr Leu Ile Pro Gly Leu Pro Leu Glu Asn Asn Tyr
            20                  25                  30

Cys Tyr Val Val Thr Tyr Met Ile Gln Thr Val Thr Met Leu Val Gln
        35                  40                  45

Gly Val Gly Phe Tyr Ser Gly Asp Leu Phe Val Phe Leu Gly Leu Thr
    50                  55                  60

Gln Ile Leu Thr Phe Ala Asp Met Leu Gln Val Lys Val Lys Glu Leu
65                  70                  75                  80

Asn Asp Ala Leu Glu Gln Lys Ala Glu Tyr Arg Ala Leu Val Arg Val
                85                  90                  95

Gly Ala Ser Ile Asp Gly Ala Glu Asn Arg Gln Arg Leu Leu Leu Asp
            100                 105                 110

Val Ile Arg Trp His Gln Leu Phe Thr Asp Tyr Cys Arg Ala Ile Asn
        115                 120                 125

Ala Leu Tyr Tyr Glu Leu Ile Ala Thr Gln Val Leu Ser Met Ala Leu
    130                 135                 140

Ala Met Met Leu Ser Phe Cys Ile Asn Leu Ser Ser Phe His Met Pro
145                 150                 155                 160

Ser Ala Ile Phe Phe Val Val Ser Ala Tyr Ser Met Ser Ile Tyr Cys
                165                 170                 175

Ile Leu Gly Thr Ile Leu Glu Phe Ala Tyr Asp Gln Val Tyr Glu Ser
            180                 185                 190

Ile Cys Asn Val Thr Trp Tyr Glu Leu Ser Gly Glu Gln Arg Lys Leu
        195                 200                 205

Phe Gly Phe Leu Leu Arg Glu Ser Gln Tyr Pro His Asn Ile Gln Ile
    210                 215                 220

Leu Gly Val Met Ser Leu Ser Val Arg Thr Ala Leu Gln Ile Val Lys
225                 230                 235                 240

Leu Ile Tyr Ser Val Ser Met Met Met Met Asn Arg Ala
                245                 250

<210> SEQ ID NO 45
```

-continued

<211> LENGTH: 1152
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR117

<400> SEQUENCE: 45

```
atggatctgc gaaggtggtt tccgaccttg tacacccagt cgaaggattc gccagttcgc     60
tcccgagacg cgaccctgta cctcctacgc tgcgtcttct taatgggcgt ccgcaagcca    120
cctgccaagt tttcgtggc ctacgtgctc tggtccttcg cactgaattt ctgctcaaca    180
ttttatcagc caattggctt tctcacaggc tatataagcc atttatcaga gttctccccg    240
ggagagtttc taacttcgct gcaggtggcc tttaatgctt ggtcctgctc tacaaaagtc    300
ctgatagtgt gggcactagt taagcgcttt gacgaggcta ataaccttct cgacgagatg    360
gataggcgta tcacagaccc cggagagcgt cttcagattc atcgcgctgt ctccctcagt    420
aaccgtatat tcttcttttt catggcagtc tacatggttt atgccactaa tacgtttctg    480
tcggcgatct tcattggaag gccaccgtac caaaattact accctttttct ggactggcga    540
tctagcactc tgcatctagc tctgcaggcc ggtctggaat acttcgccat ggctggcgcc    600
tgcttccagg acgtttgcgt tgattgctac ccagtcaatt tcgttttggt cctgcgtgcc    660
cacatgtcga tcttcgcgga gcgccttcga cgtttgggaa cttatcctta tgaaagccag    720
gagcagaaat atgaacgatt ggttcagtgc atacaagatc acaaagtaat tttgcgattt    780
gttgactgcc tgcgtcctgt tatttctggt accatcttcg tgcaattctt ggttgtgggg    840
ttggtgctgg gctttaccct aattaacatt gtcctgttcg ccaacttggg atcggccatc    900
gcagcgctct cgtttatggc cgcagtgctt ctagagacga ctcccttctg catattgtgc    960
aattatctca cagaagactg ctacaagctg gccgatgccc tgtttcagtc aaactggatt   1020
gatgaggaga aacgatacca aaagacactc atgtacttcc tacagaaact gcagcagcct   1080
ataaccttca tggctatgaa cgtgtttcca atatctgtgg gaactaacat cagtgtaagc   1140
agatgtgccc tt                                                       1152
```

<210> SEQ ID NO 46
<211> LENGTH: 384
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR117

<400> SEQUENCE: 46

```
Met Asp Leu Arg Arg Trp Phe Pro Thr Leu Tyr Thr Gln Ser Lys Asp
1               5                   10                  15

Ser Pro Val Arg Ser Arg Asp Ala Thr Leu Tyr Leu Leu Arg Cys Val
            20                  25                  30

Phe Leu Met Gly Val Arg Lys Pro Pro Ala Lys Phe Phe Val Ala Tyr
        35                  40                  45

Val Leu Trp Ser Phe Ala Leu Asn Phe Cys Ser Thr Phe Tyr Gln Pro
    50                  55                  60

Ile Gly Phe Leu Thr Gly Tyr Ile Ser His Leu Ser Glu Phe Ser Pro
65                  70                  75                  80

Gly Glu Phe Leu Thr Ser Leu Gln Val Ala Phe Asn Ala Trp Ser Cys
                85                  90                  95

Ser Thr Lys Val Leu Ile Val Trp Ala Leu Val Lys Arg Phe Asp Glu
            100                 105                 110

Ala Asn Asn Leu Leu Asp Glu Met Asp Arg Arg Ile Thr Asp Pro Gly
```

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```
        115                 120                 125

Glu Arg Leu Gln Ile His Arg Ala Val Ser Leu Ser Asn Arg Ile Phe
    130                 135                 140

Phe Phe Phe Met Ala Val Tyr Met Val Tyr Ala Thr Asn Thr Phe Leu
145                 150                 155                 160

Ser Ala Ile Phe Ile Gly Arg Pro Pro Tyr Gln Asn Tyr Tyr Pro Phe
                165                 170                 175

Leu Asp Trp Arg Ser Ser Thr Leu His Leu Ala Leu Gln Ala Gly Leu
            180                 185                 190

Glu Tyr Phe Ala Met Ala Gly Ala Cys Phe Gln Asp Val Cys Val Asp
        195                 200                 205

Cys Tyr Pro Val Asn Phe Val Leu Val Leu Arg Ala His Met Ser Ile
    210                 215                 220

Phe Ala Glu Arg Leu Arg Arg Leu Gly Thr Tyr Pro Tyr Glu Ser Gln
225                 230                 235                 240

Glu Gln Lys Tyr Glu Arg Leu Val Gln Cys Ile Gln Asp His Lys Val
                245                 250                 255

Ile Leu Arg Phe Val Asp Cys Leu Arg Pro Val Ile Ser Gly Thr Ile
            260                 265                 270

Phe Val Gln Phe Leu Val Val Gly Leu Val Leu Gly Phe Thr Leu Ile
        275                 280                 285

Asn Ile Val Leu Phe Ala Asn Leu Gly Ser Ala Ile Ala Ala Leu Ser
    290                 295                 300

Phe Met Ala Ala Val Leu Leu Glu Thr Thr Pro Phe Cys Ile Leu Cys
305                 310                 315                 320

Asn Tyr Leu Thr Glu Asp Cys Tyr Lys Leu Ala Asp Ala Leu Phe Gln
                325                 330                 335

Ser Asn Trp Ile Asp Glu Glu Lys Arg Tyr Gln Lys Thr Leu Met Tyr
            340                 345                 350

Phe Leu Gln Lys Leu Gln Gln Pro Ile Thr Phe Met Ala Met Asn Val
        355                 360                 365

Phe Pro Ile Ser Val Gly Thr Asn Ile Ser Val Ser Arg Cys Ala Leu
    370                 375                 380
```

<210> SEQ ID NO 47
<211> LENGTH: 1116
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DOR118

<400> SEQUENCE: 47

```
atgaagttta ttggatggct gccccccaag cagggtgtgc tccggtatgt gtacctcacc     60

tggacgctaa tgacgttcgt gtggtgtaca acgtacctgc cgcttggctt ccttggtagc    120

tacatgacgc agatcaagtc cttctcccct ggagagtttc tcacttcact ccaggtgtgc    180

attaatgcct acggctcatc ggtaaaagtt gcaatcacat actccatgct ctggcgcctt    240

atcaaggcca agaacatttt ggaccagctg gacctgcgct gcaccgccat ggaggagcgc    300

gaaaagatcc acctagtggt ggcccgcagc aaccatgcct ttctcatctt cacctttgtc    360

tactgcggat atgccggctc cacctacctg agctcggttc tcagcgggcg tccgccctgg    420

cagctgtaca atccctttat tgattggcat gacggcacac tcaagctctg ggtggcctcc    480

acgttggagt acatggtgat gtcaggcgcc gttctgcagg atcaactctc ggactcttac    540
```

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```
ccattgatct ataccctcat ccttcgtgct cacttggaca tgctaaggga gcgcatccga    600

cgcctccgtt ccgatgagaa cctgagcgag gccgagagct atgaagagct ggtcaaatgt    660

gtgatggacc acaagctcat tctaagatac tgcgcgatta ttaaaccagt aatccagggg    720

accatcttca cacagtttct gctgatcggc ctggttctgg gcttcacgct gatcaacgtg    780

tttttcttct cagacatctg gacgggcatc gcatcattta tgtttgttat aaccattttg    840

ctgcagacct tccccttctg ctacacatgc aacctcatca tggaggactg cgagtccttg    900

acccatgcta ttttccagtc caactgggtg gatgccagtc gtcgctacaa aacaacacta    960

ctgtattttc tccaaaacgt gcagcagcct atcgttttca ttgcaggcgg tatctttcag   1020

atatccatga gcagcaacat aagtgtggca aagtttgctt tctccgtgat aaccattacc   1080

aagcaaatga atatagctga caaatttaag acggac                             1116
```

<210> SEQ ID NO 48
<211> LENGTH: 372
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR118

<400> SEQUENCE: 48

```
Met Lys Phe Ile Gly Trp Leu Pro Pro Lys Gln Gly Val Leu Arg Tyr
1               5                   10                  15

Val Tyr Leu Thr Trp Thr Leu Met Thr Phe Val Trp Cys Thr Thr Tyr
            20                  25                  30

Leu Pro Leu Gly Phe Leu Gly Ser Tyr Met Thr Gln Ile Lys Ser Phe
        35                  40                  45

Ser Pro Gly Glu Phe Leu Thr Ser Leu Gln Val Cys Ile Asn Ala Tyr
    50                  55                  60

Gly Ser Ser Val Lys Val Ala Ile Thr Tyr Ser Met Leu Trp Arg Leu
65                  70                  75                  80

Ile Lys Ala Lys Asn Ile Leu Asp Gln Leu Asp Leu Arg Cys Thr Ala
                85                  90                  95

Met Glu Glu Arg Glu Lys Ile His Leu Val Val Ala Arg Ser Asn His
            100                 105                 110

Ala Phe Leu Ile Phe Thr Phe Val Tyr Cys Gly Tyr Ala Gly Ser Thr
        115                 120                 125

Tyr Leu Ser Ser Val Leu Ser Gly Arg Pro Pro Trp Gln Leu Tyr Asn
    130                 135                 140

Pro Phe Ile Asp Trp His Asp Gly Thr Leu Lys Leu Trp Val Ala Ser
145                 150                 155                 160

Thr Leu Glu Tyr Met Val Met Ser Gly Ala Val Leu Gln Asp Gln Leu
                165                 170                 175

Ser Asp Ser Tyr Pro Leu Ile Tyr Thr Leu Ile Leu Arg Ala His Leu
            180                 185                 190

Asp Met Leu Arg Glu Arg Ile Arg Arg Leu Arg Ser Asp Glu Asn Leu
        195                 200                 205

Ser Glu Ala Glu Ser Tyr Glu Glu Leu Val Lys Cys Val Met Asp His
    210                 215                 220

Lys Leu Ile Leu Arg Tyr Cys Ala Ile Ile Lys Pro Val Ile Gln Gly
225                 230                 235                 240

Thr Ile Phe Thr Gln Phe Leu Leu Ile Gly Leu Val Leu Gly Phe Thr
                245                 250                 255
```

-continued

```
Leu Ile Asn Val Phe Phe Phe Ser Asp Ile Trp Thr Gly Ile Ala Ser
            260                 265                 270

Phe Met Phe Val Ile Thr Ile Leu Leu Gln Thr Phe Pro Phe Cys Tyr
        275                 280                 285

Thr Cys Asn Leu Ile Met Glu Asp Cys Glu Ser Leu Thr His Ala Ile
    290                 295                 300

Phe Gln Ser Asn Trp Val Asp Ala Ser Arg Arg Tyr Lys Thr Thr Leu
305                 310                 315                 320

Leu Tyr Phe Leu Gln Asn Val Gln Gln Pro Ile Val Phe Ile Ala Gly
                325                 330                 335

Gly Ile Phe Gln Ile Ser Met Ser Ser Asn Ile Ser Val Ala Lys Phe
            340                 345                 350

Ala Phe Ser Val Ile Thr Ile Thr Lys Gln Met Asn Ile Ala Asp Lys
        355                 360                 365

Phe Lys Thr Asp
    370


<210> SEQ ID NO 49
<211> LENGTH: 1194
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DOR119

<400> SEQUENCE: 49

atggcggtgt tcaagctaat caaaccggct ccgttgaccg agaaggtgca gtcccgccag     60

gggaatatat atctgtaccg tgccatgtgg ctcatcggat ggattccgcc gaaggaggga    120

gtcctgcgct acgtgtatct cttctggacc tgcgtgccct tcgccttcgg ggtgttttac    180

ctgcccgtgg gcttcatcat cagctacgtg caggagttca agaacttcac gccgggcgag    240

ttccttacct cgctgcaggt gtgcatcaat gtgtatggcg cctcggtgaa gtccaccatc    300

acctacctct tcctctggcg actgcgcaag acggagatcc ttctggactc cctggacaag    360

aggctggcga acgacagcga tcgcgagagg atccacaata tggtggcgcg ctgcaactac    420

gcctttctca tctacagctt catctactgc ggatacgcgg gttccacttt cctgtcctac    480

gccctcagtg gtcgtcctcc gtggtccgtc tacaatccct tcatcgattg gcgcgatggc    540

atgggcagcc tgtggatcca ggccatattc gagtacatca ccatgtcctt cgccgtgctg    600

caggaccagc tatccgacac gtatcccctg atgttcacca ttatgttccg ggcccacatg    660

gaggtcctca aggatcacgt gcggagcctg cgcatggatc ccgagcgcag tgaggcagac    720

aactatcagg atctggtgaa ctgcgtgctg gaccacaaga ctatactgaa atgctgtgac    780

atgattcgcc ccatgatatc ccgcaccatc ttcgtgcaat tcgcgctgat tggttccgtt    840

ttgggcctga ccctggtgaa cgtgttcttc ttctcgaact tctggaaggg cgtggcctcg    900

ctcctgttcg tcatcaccat cctgctgcag accttcccgt tctgctacac ctgcaacatg    960

ctgatcgacg atgcccagga tctgtccaac gagattttcc agtccaactg ggtggacgcg   1020

gagccgcgct acaaggcgac gctggtgctc ttcatgcacc atgttcagca gcccataatc   1080

ttcattgccg gaggcatctt tcccatctct atgaacagca acataaccgt ggccaagttc   1140

gccttcagca tcattacaat agtgcgacaa atgaatctgg ccgagcagtt ccag         1194


<210> SEQ ID NO 50
<211> LENGTH: 398
<212> TYPE: PRT
```

-continued

<213> ORGANISM: Drosophila Melanogaster DOR119

<400> SEQUENCE: 50

```
Met Ala Val Phe Lys Leu Ile Lys Pro Ala Pro Leu Thr Glu Lys Val
1               5                   10                  15

Gln Ser Arg Gln Gly Asn Ile Tyr Leu Tyr Arg Ala Met Trp Leu Ile
            20                  25                  30

Gly Trp Ile Pro Pro Lys Glu Gly Val Leu Arg Tyr Val Tyr Leu Phe
        35                  40                  45

Trp Thr Cys Val Pro Phe Ala Phe Gly Val Phe Tyr Leu Pro Val Gly
    50                  55                  60

Phe Ile Ile Ser Tyr Val Gln Glu Phe Lys Asn Phe Thr Pro Gly Glu
65                  70                  75                  80

Phe Leu Thr Ser Leu Gln Val Cys Ile Asn Val Tyr Gly Ala Ser Val
                85                  90                  95

Lys Ser Thr Ile Thr Tyr Leu Phe Leu Trp Arg Leu Arg Lys Thr Glu
            100                 105                 110

Ile Leu Leu Asp Ser Leu Asp Lys Arg Leu Ala Asn Asp Ser Asp Arg
        115                 120                 125

Glu Arg Ile His Asn Met Val Ala Arg Cys Asn Tyr Ala Phe Leu Ile
    130                 135                 140

Tyr Ser Phe Ile Tyr Cys Gly Tyr Ala Gly Ser Thr Phe Leu Ser Tyr
145                 150                 155                 160

Ala Leu Ser Gly Arg Pro Pro Trp Ser Val Tyr Asn Pro Phe Ile Asp
                165                 170                 175

Trp Arg Asp Gly Met Gly Ser Leu Trp Ile Gln Ala Ile Phe Glu Tyr
            180                 185                 190

Ile Thr Met Ser Phe Ala Val Leu Gln Asp Gln Leu Ser Asp Thr Tyr
        195                 200                 205

Pro Leu Met Phe Thr Ile Met Phe Arg Ala His Met Glu Val Leu Lys
    210                 215                 220

Asp His Val Arg Ser Leu Arg Met Asp Pro Glu Arg Ser Glu Ala Asp
225                 230                 235                 240

Asn Tyr Gln Asp Leu Val Asn Cys Val Leu Asp His Lys Thr Ile Leu
                245                 250                 255

Lys Cys Cys Asp Met Ile Arg Pro Met Ile Ser Arg Thr Ile Phe Val
            260                 265                 270

Gln Phe Ala Leu Ile Gly Ser Val Leu Gly Leu Thr Leu Val Asn Val
        275                 280                 285

Phe Phe Phe Ser Asn Phe Trp Lys Gly Val Ala Ser Leu Leu Phe Val
    290                 295                 300

Ile Thr Ile Leu Leu Gln Thr Phe Pro Phe Cys Tyr Thr Cys Asn Met
305                 310                 315                 320

Leu Ile Asp Asp Ala Gln Asp Leu Ser Asn Glu Ile Phe Gln Ser Asn
                325                 330                 335

Trp Val Asp Ala Glu Pro Arg Tyr Lys Ala Thr Leu Val Leu Phe Met
            340                 345                 350

His His Val Gln Gln Pro Ile Ile Phe Ile Ala Gly Gly Ile Phe Pro
        355                 360                 365

Ile Ser Met Asn Ser Asn Ile Thr Val Ala Lys Phe Ala Phe Ser Ile
    370                 375                 380
```

-continued

```
Ile Thr Ile Val Arg Gln Met Asn Leu Ala Glu Gln Phe Gln
385                 390                 395


<210> SEQ ID NO 51
<211> LENGTH: 1233
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster  DOR120

<400> SEQUENCE: 51

atgaccaagt tcttcttcaa gcgcctgcaa actgctccac ttgatcagga ggtgagttcc     60

cttgatgcca gcgactacta ctaccgcatc gcatttttcc tgggctggac cccgcccaag    120

ggggctctgc tccgatggat ctactccctg tggactctga ccacgatgtg gctgggtatc    180

gtgtacctgc cgctcggact gagcctcacc tatgtgaagc acttcgatag attcacgccg    240

acggagttcc tgacctccct gcaggtggat atcaactgca tcgggaacgt gatcaagtca    300

tgcgtaactt attcccagat gtggcgtttt cgccggatga atgagcttat ctcgtccctg    360

gacaagagat gtgtgactac gacacagcgt cgaattttcc ataagatggt ggcacgggtt    420

aatctcatcg tgattctgtt cttgtccacg tacttgggct tctgctttct aactctgttc    480

acttcggttt tcgctggcaa agctccttgg cagctgtaca acccactggt ggactggcgg    540

aaaggccatt ggcagctatg gattgcctcc atcctggagt actgtgtggt ctccattggc    600

accatgcagg agttgatgtc cgacacctac gccatagtgt tcatctcctt gttccgctgc    660

cacctggcta ttctcagaga tcgcatagct aatctgcggc aggatccgaa actcagtgag    720

atggaacact atgagcagat ggtggcctgc attcaggatc atcgaaccat catacagtgc    780

tcccagatta ttcgacccat cctgtcgatc actatctttg cccagttcat gctggttggc    840

attgacttgg gtctggcggc catcagcatc ctcttctttc cgaacaccat ttggacgatc    900

atggcaaacg tgtcgttcat cgtggccatc tgtacagagt cctttccatg ctgcatgctc    960

tgcgagcatc tgatcgagga ctccgtccat gtgagcaacg ccctgttcca ctcaaactgg   1020

ataaccgcgg acaggagcta caagtcggcg gttctgtatt tcctgcaccg ggctcagcaa   1080

cccattcaat tcacggccgg ctccatattt cccatttcgg tgcagagcaa catagccgtg   1140

gccaagttcg cgttcacaat catcacaatc gtgaaccaaa tgaatctggg cgagaagttc   1200

ttcagtgaca ggagcaatgg cgatataaat cct                                1233


<210> SEQ ID NO 52
<211> LENGTH: 411
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR120

<400> SEQUENCE: 52

Met Thr Lys Phe Phe Phe Lys Arg Leu Gln Thr Ala Pro Leu Asp Gln
1               5                   10                  15

Glu Val Ser Ser Leu Asp Ala Ser Asp Tyr Tyr Tyr Arg Ile Ala Phe
            20                  25                  30

Phe Leu Gly Trp Thr Pro Pro Lys Gly Ala Leu Leu Arg Trp Ile Tyr
        35                  40                  45

Ser Leu Trp Thr Leu Thr Thr Met Trp Leu Gly Ile Val Tyr Leu Pro
    50                  55                  60

Leu Gly Leu Ser Leu Thr Tyr Val Lys His Phe Asp Arg Phe Thr Pro
65                  70                  75                  80
```

-continued

```
Thr Glu Phe Leu Thr Ser Leu Gln Val Asp Ile Asn Cys Ile Gly Asn
                85                  90                  95

Val Ile Lys Ser Cys Val Thr Tyr Ser Gln Met Trp Arg Phe Arg Arg
            100                 105                 110

Met Asn Glu Leu Ile Ser Ser Leu Asp Lys Arg Cys Val Thr Thr Thr
        115                 120                 125

Gln Arg Arg Ile Phe His Lys Met Val Ala Arg Val Asn Leu Ile Val
    130                 135                 140

Ile Leu Phe Leu Ser Thr Tyr Leu Gly Phe Cys Phe Leu Thr Leu Phe
145                 150                 155                 160

Thr Ser Val Phe Ala Gly Lys Ala Pro Trp Gln Leu Tyr Asn Pro Leu
                165                 170                 175

Val Asp Trp Arg Lys Gly His Trp Gln Leu Trp Ile Ala Ser Ile Leu
            180                 185                 190

Glu Tyr Cys Val Val Ser Ile Gly Thr Met Gln Glu Leu Met Ser Asp
        195                 200                 205

Thr Tyr Ala Ile Val Phe Ile Ser Leu Phe Arg Cys His Leu Ala Ile
    210                 215                 220

Leu Arg Asp Arg Ile Ala Asn Leu Arg Gln Asp Pro Lys Leu Ser Glu
225                 230                 235                 240

Met Glu His Tyr Glu Gln Met Val Ala Cys Ile Gln Asp His Arg Thr
                245                 250                 255

Ile Ile Gln Cys Ser Gln Ile Ile Arg Pro Ile Leu Ser Ile Thr Ile
            260                 265                 270

Phe Ala Gln Phe Met Leu Val Gly Ile Asp Leu Gly Leu Ala Ala Ile
        275                 280                 285

Ser Ile Leu Phe Phe Pro Asn Thr Ile Trp Thr Ile Met Ala Asn Val
    290                 295                 300

Ser Phe Ile Val Ala Ile Cys Thr Glu Ser Phe Pro Cys Cys Met Leu
305                 310                 315                 320

Cys Glu His Leu Ile Glu Asp Ser Val His Val Ser Asn Ala Leu Phe
                325                 330                 335

His Ser Asn Trp Ile Thr Ala Asp Arg Ser Tyr Lys Ser Ala Val Leu
            340                 345                 350

Tyr Phe Leu His Arg Ala Gln Gln Pro Ile Gln Phe Thr Ala Gly Ser
        355                 360                 365

Thr Phe Pro Ile Ser Val Gln Ser Asn Ile Ala Val Ala Lys Phe Ala
    370                 375                 380

Phe Thr Ile Ile Thr Ile Val Asn Gln Met Asn Leu Gly Glu Lys Phe
385                 390                 395                 400

Phe Ser Asp Arg Ser Asn Gly Asp Ile Asn Pro
                405                 410
```

<210> SEQ ID NO 53
<211> LENGTH: 1203
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR121

<400> SEQUENCE: 53

```
atgctgacgg acaagttcct ccgactgcag tccgctttat ttcgccttct cggactcgaa      60

ttgttgcacg agcaggatgt tggccatcga tatccttggc gcagcatctg ctgcattctc     120

tcggtggcca gtttcatgcc cctgaccatt gcgtttggcc tgcaaaacgt ccaaaatgtg     180
```

-continued

```
gagcaattaa ccgactcact ctgctcggtt ctcgtggatt tgctggccct gtgcaaaatc    240

gggcttttcc tttggcttta caaggacttc aagttcctaa tagggcagtt ctattgtgtt    300

ttgcaaacgg aaacccacac cgctgtcgct gaaatgatag tgaccaggga aagtcgtcgg    360

gatcagttca tcagtgctat gtatgcctac tgtttcatta cggctggcct ttcggcctgc    420

ctgatgtccc ctctatccat gctgattagc taccacgaac aggtgaattg cagccgaaat    480

ttccatttcc cagtgtgtaa gaaaaagtac tgcttaatat ccagaatatt aagatacagt    540

ttctgcagat atccctggga caatatgaag ctgtccaact acatcatttc ctatttctgg    600

aatgtgtgtg ctgcattggg cgtggcactg cccaccgttt gtgtggacac actgttctgt    660

tctctgagcc ataatctctg tgccctattc cagattgcca ggcacaaaat gatgcacttt    720

gagggcagaa ataccaaaga gactcatgag aacttaaagc acgtgtttca actatatgcg    780

ttgtgtttga acctgggcca tttcttaaac gaatatttca gaccgctcat ctgccagttt    840

gtggcagcct cactgcactt gtgtgtcctg tgctaccaac tgtctgccaa tatcctgcag    900

ccagcgttac tcttctatgc cgcatttacg gcagcagttg ttggccaggt gtctatatac    960

tgcttctgcg gatcgagcat ccattcggag tgtcagctat ttggccaggc catctacgag   1020

tccagctggc ccatctgct gcaggaaaac ctgcagcttg taagctcctt aaaaattgcc   1080

atgatgcgat cgagtttggg atgtcccatc gatggttact tcttcgaggc caatcgggag   1140

acgctcatca cggtgagtaa agcgtttata aaagtgtcca aaaagacacc tcaagtgaat   1200

gat                                                                1203
```

```
<210> SEQ ID NO 54
<211> LENGTH: 401
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster  DOR121

<400> SEQUENCE: 54

Met Leu Thr Asp Lys Phe Leu Arg Leu Gln Ser Ala Leu Phe Arg Leu
1               5                   10                  15

Leu Gly Leu Glu Leu Leu His Glu Gln Asp Val Gly His Arg Tyr Pro
            20                  25                  30

Trp Arg Ser Ile Cys Cys Ile Leu Ser Val Ala Ser Phe Met Pro Leu
        35                  40                  45

Thr Ile Ala Phe Gly Leu Gln Asn Val Gln Asn Val Glu Gln Leu Thr
    50                  55                  60

Asp Ser Leu Cys Ser Val Leu Val Asp Leu Leu Ala Leu Cys Lys Ile
65                  70                  75                  80

Gly Leu Phe Leu Trp Leu Tyr Lys Asp Phe Lys Phe Leu Ile Gly Gln
                85                  90                  95

Phe Tyr Cys Val Leu Gln Thr Glu Thr His Thr Ala Val Ala Glu Met
            100                 105                 110

Ile Val Thr Arg Glu Ser Arg Arg Asp Gln Phe Ile Ser Ala Met Tyr
        115                 120                 125

Ala Tyr Cys Phe Ile Thr Ala Gly Leu Ser Ala Cys Leu Met Ser Pro
    130                 135                 140

Leu Ser Met Leu Ile Ser Tyr His Glu Gln Val Asn Cys Ser Arg Asn
145                 150                 155                 160

Phe His Phe Pro Val Cys Lys Lys Lys Tyr Cys Leu Ile Ser Arg Ile
```

-continued

```
                165                 170                 175

Leu Arg Tyr Ser Phe Cys Arg Tyr Pro Trp Asp Asn Met Lys Leu Ser
            180                 185                 190

Asn Tyr Ile Ile Ser Tyr Phe Trp Asn Val Cys Ala Ala Leu Gly Val
        195                 200                 205

Ala Leu Pro Thr Val Cys Val Asp Thr Leu Phe Cys Ser Leu Ser His
    210                 215                 220

Asn Leu Cys Ala Leu Phe Gln Ile Ala Arg His Lys Met Met His Phe
225                 230                 235                 240

Glu Gly Arg Asn Thr Lys Glu Thr His Glu Asn Leu Lys His Val Phe
                245                 250                 255

Gln Leu Tyr Ala Leu Cys Leu Asn Leu Gly His Phe Leu Asn Glu Tyr
            260                 265                 270

Phe Arg Pro Leu Ile Cys Gln Phe Val Ala Ala Ser Leu His Leu Cys
        275                 280                 285

Val Leu Cys Tyr Gln Leu Ser Ala Asn Ile Leu Gln Pro Ala Leu Leu
    290                 295                 300

Phe Tyr Ala Ala Phe Thr Ala Ala Val Val Gly Gln Val Ser Ile Tyr
305                 310                 315                 320

Cys Phe Cys Gly Ser Ser Ile His Ser Glu Cys Gln Leu Phe Gly Gln
                325                 330                 335

Ala Ile Tyr Glu Ser Ser Trp Pro His Leu Leu Gln Glu Asn Leu Gln
            340                 345                 350

Leu Val Ser Ser Leu Lys Ile Ala Met Met Arg Ser Ser Leu Gly Cys
        355                 360                 365

Pro Ile Asp Gly Tyr Phe Phe Glu Ala Asn Arg Glu Thr Leu Ile Thr
    370                 375                 380

Val Ser Lys Ala Phe Ile Lys Val Ser Lys Lys Thr Pro Gln Val Asn
385                 390                 395                 400

Asp
```

<210> SEQ ID NO 55
<211> LENGTH: 1122
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR14

<400> SEQUENCE: 55

```
atggactacg atcgaattcg accggtgcga tttttgacgg gagtgctgaa atggtggcgt     60

ctctggccga ggaaggaatc ggtgtccaca ccggactgga ctaactggca ggcatatgcc    120

ttgcacgttc catttacatt cttgtttgtg ttgcttttgt ggttggaggc aatcaagagc    180

agggatatac agcataccgc cgatgtcctt ttgatttgcc taaccaccac tgccttggga    240

ggtaaagtta tcaatatctg gaagtatgcc catgtggccc aaggcatttt gtccgagtgg    300

agcacgtggg atcttttcga gctgaggagc aaacaggaag tggatatgtg gcgattcgag    360

catcgacgtt tcaatcgtgt ttttatgttt tactgtttgt gcagtgctgg tgtaatccca    420

tttattgtga ttcaaccgtt gtttgatatc ccaaatcgat tgcccttctg gatgtggaca    480

ccattcgatt ggcagcagcc tgttctcttc tggtatgcat tcatctatca ggccacaacc    540

attcctattg cctgtgcttg caacgtaacc atggacgctg ttaattggta cttgatgctg    600

catctgtcct tgtgtttgcg tatgttgggc cagcgattga gtaagcttca gcatgatgac    660
```

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```
aaggatctga gggagaagtt cctggaactg atccatctgc accagcgact caagcaacag    720

gccttgagca ttgaaatctt tatttcgaag agcacgttca cccaaattct ggtcagttcc    780

cttatcattt gcttcaccat ttacagcatg cagatggact tgccaggatt tgccgccatg    840

atgcagtacc tagtggccat gatcatgcag gtcatgctgc ccaccatata tggtaacgcc    900

gtcatcgatt ctgcaaatat gttgaccgat tccatgtaca attcggattg gccggatatg    960

aattgccgaa tgcgtcgcct agttttaatg tttatggtgt acttaaatcg accggtgacc   1020

ttaaaagccg gtggcttttt tcatattggt ttacctctgt ttaccaaggt tgtattttct   1080

actctggaaa atccttgtat aagttatctt tatttcagac ca                      1122
```

```
<210> SEQ ID NO 56
<211> LENGTH: 374
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR14

<400> SEQUENCE: 56

Met Asp Tyr Asp Arg Ile Arg Pro Val Arg Phe Leu Thr Gly Val Leu
1               5                   10                  15

Lys Trp Trp Arg Leu Trp Pro Arg Lys Glu Ser Val Ser Thr Pro Asp
            20                  25                  30

Trp Thr Asn Trp Gln Ala Tyr Ala Leu His Val Pro Phe Thr Phe Leu
        35                  40                  45

Phe Val Leu Leu Leu Trp Leu Glu Ala Ile Lys Ser Arg Asp Ile Gln
    50                  55                  60

His Thr Ala Asp Val Leu Leu Ile Cys Leu Thr Thr Thr Ala Leu Gly
65                  70                  75                  80

Gly Lys Val Ile Asn Ile Trp Lys Tyr Ala His Val Ala Gln Gly Ile
                85                  90                  95

Leu Ser Glu Trp Ser Thr Trp Asp Leu Phe Glu Leu Arg Ser Lys Gln
            100                 105                 110

Glu Val Asp Met Trp Arg Phe Glu His Arg Arg Phe Asn Arg Val Phe
        115                 120                 125

Met Phe Tyr Cys Leu Cys Ser Ala Gly Val Ile Pro Phe Ile Val Ile
    130                 135                 140

Gln Pro Leu Phe Asp Ile Pro Asn Arg Leu Pro Phe Trp Met Trp Thr
145                 150                 155                 160

Pro Phe Asp Trp Gln Gln Pro Val Leu Phe Trp Tyr Ala Phe Ile Tyr
                165                 170                 175

Gln Ala Thr Thr Ile Pro Ile Ala Cys Ala Cys Asn Val Thr Met Asp
            180                 185                 190

Ala Val Asn Trp Tyr Leu Met Leu His Leu Ser Leu Cys Leu Arg Met
        195                 200                 205

Leu Gly Gln Arg Leu Ser Lys Leu Gln His Asp Asp Lys Asp Leu Arg
    210                 215                 220

Glu Lys Phe Leu Glu Leu Ile His Leu His Gln Arg Leu Lys Gln Gln
225                 230                 235                 240

Ala Leu Ser Ile Glu Ile Phe Ile Ser Lys Ser Thr Phe Thr Gln Ile
                245                 250                 255

Leu Val Ser Ser Leu Ile Ile Cys Phe Thr Ile Tyr Ser Met Gln Met
            260                 265                 270

Asp Leu Pro Gly Phe Ala Ala Met Met Gln Tyr Leu Val Ala Met Ile
```

-continued

```
        275                 280                 285

Met Gln Val Met Leu Pro Thr Ile Tyr Gly Asn Ala Val Ile Asp Ser
    290                 295                 300

Ala Asn Met Leu Thr Asp Ser Met Tyr Asn Ser Asp Trp Pro Asp Met
305                 310                 315                 320

Asn Cys Arg Met Arg Arg Leu Val Leu Met Phe Met Val Tyr Leu Asn
                325                 330                 335

Arg Pro Val Thr Leu Lys Ala Gly Gly Phe Phe His Ile Gly Leu Pro
            340                 345                 350

Leu Phe Thr Lys Val Val Phe Ser Thr Leu Glu Asn Pro Cys Ile Ser
        355                 360                 365

Tyr Leu Tyr Phe Arg Pro
    370


<210> SEQ ID NO 57
<211> LENGTH: 1140
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DOR16

<400> SEQUENCE: 57

atgactgaca gcgggcagcc tgccattgcc gaccactttt atcggattcc ccgcatctcc     60

ggcctcattg tcggcctctg gccgcaaagg ataaggggcg ggggcggtcg tccttggcac    120

gcccatctgc tcttcgtgtt cgccttcgcc atggtggtgg tgggtgcggt gggcgaggtg    180

tcgtacggct gtgtccacct ggacaacctg gtggtggcgc tggaggcctt ctgccccgga    240

accaccaagg cggtctgcgt tttgaagctg tgggtcttct tccgctccaa tcgccggtgg    300

gcggagttgg tccagcgcct gcgggctatt ttgtgggaat cgcggcggca ggaggcccag    360

aggatgctgg tcggactggc caccacggcc aacaggctca gcctgttgtt gctcagctct    420

ggcacggcga caaatgccgc cttcaccttg caaccgctga ttatgggtct ctaccgctgg    480

attgtgcagc tgccaggtca aaccgagctg ccctttaata tcatactgcc ctcgtttgcc    540

gtgcagccag gagtctttcc gctcacctac gtgctgctga ccgcttccgg tgcctgcacc    600

gttttcgcct tcagcttcgt ggacggattc ttcatttgct cgtgcctcta catctgcggc    660

gctttccggc tggtgcagca ggacattcgc aggatatttg ccgatttgca tggcgactca    720

gtggatgtgt tcaccgagga gatgaacgcg gaggtgcggc acagactggc ccaagttgtc    780

gagcggcaca atgcgattat cgatttctgc acggacctaa cacgccagtt caccgttatc    840

gttttaatgc atttcctgtc cgccgccttc gtcctctgct cgaccatcct ggacatcatg    900

ttggtgagcc ccttttcaga ggccttcctt tggggcgggt atccttgggt ttgtcgcgcc    960

actggctttt cgcatcgcct gcattcggcg gctgttttaa aagtttttcc ctgttttcac   1020

tgtttgctgt ttttccctgg cttttccagc cgctccgttc tgattcggtt ttcccgattt   1080

gtttgtttgc tttgtggctg cggctgcggc tctctccggt ggcaatttat aagcgcatga   1140


<210> SEQ ID NO 58
<211> LENGTH: 379
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster  DOR16

<400> SEQUENCE: 58

Met Thr Asp Ser Gly Gln Pro Ala Ile Ala Asp His Phe Tyr Arg Ile
1               5                   10                  15
```

-continued

```
Pro Arg Ile Ser Gly Leu Ile Val Gly Leu Trp Pro Gln Arg Ile Arg
            20                  25                  30

Gly Gly Gly Gly Arg Pro Trp His Ala His Leu Leu Phe Val Phe Ala
        35                  40                  45

Phe Ala Met Val Val Val Gly Ala Val Gly Glu Val Ser Tyr Gly Cys
    50                  55                  60

Val His Leu Asp Asn Leu Val Val Ala Leu Glu Ala Phe Cys Pro Gly
65                  70                  75                  80

Thr Thr Lys Ala Val Cys Val Leu Lys Leu Trp Val Phe Phe Arg Ser
                85                  90                  95

Asn Arg Arg Trp Ala Glu Leu Val Gln Arg Leu Arg Ala Ile Leu Trp
            100                 105                 110

Glu Ser Arg Arg Gln Glu Ala Gln Arg Met Leu Val Gly Leu Ala Thr
        115                 120                 125

Thr Ala Asn Arg Leu Ser Leu Leu Leu Leu Ser Ser Gly Thr Ala Thr
    130                 135                 140

Asn Ala Ala Phe Thr Leu Gln Pro Leu Ile Met Gly Leu Tyr Arg Trp
145                 150                 155                 160

Ile Val Gln Leu Pro Gly Gln Thr Glu Leu Pro Phe Asn Ile Ile Leu
                165                 170                 175

Pro Ser Phe Ala Val Gln Pro Gly Val Phe Pro Leu Thr Tyr Val Leu
            180                 185                 190

Leu Thr Ala Ser Gly Ala Cys Thr Val Phe Ala Phe Ser Phe Val Asp
        195                 200                 205

Gly Phe Phe Ile Cys Ser Cys Leu Tyr Ile Cys Gly Ala Phe Arg Leu
    210                 215                 220

Val Gln Gln Asp Ile Arg Arg Ile Phe Ala Asp Leu His Gly Asp Ser
225                 230                 235                 240

Val Asp Val Phe Thr Glu Glu Met Asn Ala Glu Val Arg His Arg Leu
                245                 250                 255

Ala Gln Val Val Glu Arg His Asn Ala Ile Ile Asp Phe Cys Thr Asp
            260                 265                 270

Leu Thr Arg Gln Phe Thr Val Ile Val Leu Met His Phe Leu Ser Ala
        275                 280                 285

Ala Phe Val Leu Cys Ser Thr Ile Leu Asp Ile Met Leu Val Ser Pro
    290                 295                 300

Phe Ser Glu Ala Phe Leu Trp Gly Gly Tyr Pro Trp Val Cys Arg Ala
305                 310                 315                 320

Thr Gly Phe Ser His Arg Leu His Ser Ala Ala Val Leu Lys Val Phe
                325                 330                 335

Pro Cys Phe His Cys Leu Leu Phe Phe Pro Gly Phe Ser Ser Arg Ser
            340                 345                 350

Val Leu Ile Arg Phe Ser Arg Phe Val Cys Leu Leu Cys Gly Cys Gly
        355                 360                 365

Cys Gly Ser Leu Arg Trp Gln Phe Ile Ser Ala
    370                 375
```

<210> SEQ ID NO 59
<211> LENGTH: 1215
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR20

-continued

<400> SEQUENCE: 59

```
atgagcaaag gagtagaaat cttttacaag ggccagaagg cattcttgaa catcctctcg     60
ttgtggcctc agatagaacg ccggtggaga atcatccacc aggtgaacta tgtccacgta    120
attgtgtttt gggtgctgct ctttgatctc ctcttggtgc tccatgtgat ggctaatttg    180
agctacatgt ccgaggttgt gaaagccatc tttatcctgg ccaccagtgc agggcacacc    240
accaagctgc tgtccataaa ggcgaacaat gtgcagatgg aggagctctt taggagattg    300
gataacgaag agttccgtcc tagaggcgcc aacgaagagt tgatctttgc agcagcctgt    360
gaaagaagta ggaagcttcg ggacttctat ggagcgcttt cgtttgccgc cttgagcatg    420
attctcatac cccagttcgc cttggactgg tcccaccttc cgctcaaaac atacaatccg    480
cttggcgaga ataccggctc acctgcttat tggctcctct actgctatca gtgtctggcc    540
ttgtccgtat cctgcatcac caacatagga ttcgactcac tctgctcctc actgttcatc    600
ttcctcaagt gccagctgga cattctggcc gtgcgactgg acaagatcgg tcggttaatc    660
actacttctg gtggcactgt ggaacagcaa cttaaggaaa atatccgcta tcacatgacc    720
atcgttgaac tgtcgaaaac cgtggagcgt ctactttgca agccgatttc ggtgcagatc    780
ttctgctcgg ttttggtgct gactgccaat ttctatgcca ttgctgtggt gagctgtgaa    840
ttcgcaacaa gaagactatc agtatgtgac ctatcaggcg tgcatgttga ttcagatttt    900
tatattgtgc tactatgccg ggtgggtatt ccatatccga aatgcctccc caggccagta    960
atgaatttca tcgtcagtga ggtaacccag cgcagcctgg accttccgca cgagctgtac   1020
aagacctcct gggtggactg ggactacagg agccgaagga ttgcgctcct ctttatgcaa   1080
cgccttcact cgaccttgag gattaggaca cttaatccaa gtcttggttt tgacttaatg   1140
ctcttcagct cggtgagttc tttccgtgtt ttgacttttt tgtgcactgt agccaatttc   1200
cataatgagg ctcat                                                     1215
```

<210> SEQ ID NO 60
<211> LENGTH: 405
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR20

<400> SEQUENCE: 60

```
Met Ser Lys Gly Val Glu Ile Phe Tyr Lys Gly Gln Lys Ala Phe Leu
1               5                   10                  15

Asn Ile Leu Ser Leu Trp Pro Gln Ile Glu Arg Arg Trp Arg Ile Ile
            20                  25                  30

His Gln Val Asn Tyr Val His Val Ile Val Phe Trp Val Leu Leu Phe
        35                  40                  45

Asp Leu Leu Leu Val Leu His Val Met Ala Asn Leu Ser Tyr Met Ser
    50                  55                  60

Glu Val Val Lys Ala Ile Phe Ile Leu Ala Thr Ser Ala Gly His Thr
65                  70                  75                  80

Thr Lys Leu Leu Ser Ile Lys Ala Asn Asn Val Gln Met Glu Glu Leu
                85                  90                  95

Phe Arg Arg Leu Asp Asn Glu Glu Phe Arg Pro Arg Gly Ala Asn Glu
            100                 105                 110

Glu Leu Ile Phe Ala Ala Ala Cys Glu Arg Ser Arg Lys Leu Arg Asp
        115                 120                 125
```

-continued

```
Phe Tyr Gly Ala Leu Ser Phe Ala Ala Leu Ser Met Ile Leu Ile Pro
    130                 135                 140

Gln Phe Ala Leu Asp Trp Ser His Leu Pro Leu Lys Thr Tyr Asn Pro
145                 150                 155                 160

Leu Gly Glu Asn Thr Gly Ser Pro Ala Tyr Trp Leu Leu Tyr Cys Tyr
                165                 170                 175

Gln Cys Leu Ala Leu Ser Val Ser Cys Ile Thr Asn Ile Gly Phe Asp
            180                 185                 190

Ser Leu Cys Ser Ser Leu Phe Ile Phe Leu Lys Cys Gln Leu Asp Ile
        195                 200                 205

Leu Ala Val Arg Leu Asp Lys Ile Gly Arg Leu Ile Thr Thr Ser Gly
    210                 215                 220

Gly Thr Val Glu Gln Gln Leu Lys Glu Asn Ile Arg Tyr His Met Thr
225                 230                 235                 240

Ile Val Glu Leu Ser Lys Thr Val Glu Arg Leu Leu Cys Lys Pro Ile
                245                 250                 255

Ser Val Gln Ile Phe Cys Ser Val Leu Val Leu Thr Ala Asn Phe Tyr
            260                 265                 270

Ala Ile Ala Val Val Ser Cys Glu Phe Ala Thr Arg Arg Leu Ser Val
        275                 280                 285

Cys Asp Leu Ser Gly Val His Val Asp Ser Asp Phe Tyr Ile Val Leu
    290                 295                 300

Leu Cys Arg Val Gly Ile Pro Tyr Pro Lys Cys Leu Pro Arg Pro Val
305                 310                 315                 320

Met Asn Phe Ile Val Ser Glu Val Thr Gln Arg Ser Leu Asp Leu Pro
                325                 330                 335

His Glu Leu Tyr Lys Thr Ser Trp Val Asp Trp Asp Tyr Arg Ser Arg
            340                 345                 350

Arg Ile Ala Leu Leu Phe Met Gln Arg Leu His Ser Thr Leu Arg Ile
        355                 360                 365

Arg Thr Leu Asn Pro Ser Leu Gly Phe Asp Leu Met Leu Phe Ser Ser
    370                 375                 380

Val Ser Ser Phe Arg Val Leu Thr Phe Leu Cys Thr Val Ala Asn Phe
385                 390                 395                 400

His Asn Glu Ala His
                405
```

```
<210> SEQ ID NO 61
<211> LENGTH: 1203
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster  DOR25

<400> SEQUENCE: 61

atgaacgact cgggttatca atcaaatctc agccttctgc gggtttttct cgacgagttc     60

cgatcggttc tgcggcagga aagtcccggt ctcatcccac gcctggcttt ttactatgtt    120

cgcgcctttc tgagcttgcc cctgtaccga tggatcaact tgttcatcat gtgcaatgtg    180

atgaccattt tctggaccat gttcgtggcc ctgcccgagt cgaagaacgt gatcgaaatg    240

ggcgacgact tggtttggat ttcggggatg gcactggtgt tcaccaagat cttttacatg    300

catttgcgtt gcgacgagat cgatgaactt atttcggatt ttgaatacta caaccgggag    360

ctgagacccc ataatatcga tgaggaggtg ttgggttggc agagactgtg ctacgtgata    420
```

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```
gaatcgggtc tatatatcaa ctgcttttgc ctggtcaact tcttcagtgc cgctattttc    480

ctgcaacctc tgttgggcga gggaaagctg cccttccaca gcgtctatcc gtttcaatgg    540

catcgcttgg atctgcatcc ctacacgttc tggttcctct acatctggca gagtctgacc    600

tcgcagcaca acctaatgag cattctaatg gtggatatgg taggcatttc cacgttcctc    660

cagacggcgc tcaatctcaa gttgctttgc atcgagataa ggaaactggg ggacatggag    720

gtcagtgata agaggttcca cgaggagttt tgtcgtgtgg ttcgcttcca ccagcacatt    780

atcaagttgg tggggaaagc caatagagct ttcaatggcg ccttcaatgc acaattaatg    840

gccagtttct ccctgatttc catatccact ttcgagacca tggctgcagc ggctgtggat    900

cccaaaatgg ccgccaagtt cgtgcttctc atgctggtgg cattcattca actgtcgctt    960

tggtgcgtct ctggaacttt ggtttatact cagtcagtgg aggtggctca ggctgctttt   1020

gatatcaacg attggcacac caaatcgcca ggcatccaga gggatatatc ctttgtgata   1080

ctacgagccc agaaacccct gatgtatgtg gccgaaccat ttctgccctt caccctggga   1140

acctatatgc ttgtactgaa gaactgctat cgtttgctgg ccctgatgca agaatcgatg   1200

tag                                                                 1203
```

<210> SEQ ID NO 62
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR25

<400> SEQUENCE: 62

```
Met Asn Asp Ser Gly Tyr Gln Ser Asn Leu Ser Leu Leu Arg Val Phe
1               5                   10                  15

Leu Asp Glu Phe Arg Ser Val Leu Arg Gln Glu Ser Pro Gly Leu Ile
            20                  25                  30

Pro Arg Leu Ala Phe Tyr Tyr Val Arg Ala Phe Leu Ser Leu Pro Leu
        35                  40                  45

Tyr Arg Trp Ile Asn Leu Phe Ile Met Cys Asn Val Met Thr Ile Phe
    50                  55                  60

Trp Thr Met Phe Val Ala Leu Pro Glu Ser Lys Asn Val Ile Glu Met
65                  70                  75                  80

Gly Asp Asp Leu Val Trp Ile Ser Gly Met Ala Leu Val Phe Thr Lys
                85                  90                  95

Ile Phe Tyr Met His Leu Arg Cys Asp Glu Ile Asp Glu Leu Ile Ser
            100                 105                 110

Asp Phe Glu Tyr Tyr Asn Arg Glu Leu Arg Pro His Asn Ile Asp Glu
        115                 120                 125

Glu Val Leu Gly Trp Gln Arg Leu Cys Tyr Val Ile Glu Ser Gly Leu
    130                 135                 140

Tyr Ile Asn Cys Phe Cys Leu Val Asn Phe Phe Ser Ala Ala Ile Phe
145                 150                 155                 160

Leu Gln Pro Leu Leu Gly Glu Gly Lys Leu Pro Phe His Ser Val Tyr
                165                 170                 175

Pro Phe Gln Trp His Arg Leu Asp Leu His Pro Tyr Thr Phe Trp Phe
            180                 185                 190

Leu Tyr Ile Trp Gln Ser Leu Thr Ser Gln His Asn Leu Met Ser Ile
        195                 200                 205

Leu Met Val Asp Met Val Gly Ile Ser Thr Phe Leu Gln Thr Ala Leu
```

-continued

```
    210                 215                 220

Asn Leu Lys Leu Leu Cys Ile Glu Ile Arg Lys Leu Gly Asp Met Glu
225                 230                 235                 240

Val Ser Asp Lys Arg Phe His Glu Glu Phe Cys Arg Val Val Arg Phe
                245                 250                 255

His Gln His Ile Ile Lys Leu Val Gly Lys Ala Asn Arg Ala Phe Asn
            260                 265                 270

Gly Ala Phe Asn Ala Gln Leu Met Ala Ser Phe Ser Leu Ile Ser Ile
        275                 280                 285

Ser Thr Phe Glu Thr Met Ala Ala Ala Ala Val Asp Pro Lys Met Ala
    290                 295                 300

Ala Lys Phe Val Leu Leu Met Leu Val Ala Phe Ile Gln Leu Ser Leu
305                 310                 315                 320

Trp Cys Val Ser Gly Thr Leu Val Tyr Thr Gln Ser Val Glu Val Ala
                325                 330                 335

Gln Ala Ala Phe Asp Ile Asn Asp Trp His Thr Lys Ser Pro Gly Ile
            340                 345                 350

Gln Arg Asp Ile Ser Phe Val Ile Leu Arg Ala Gln Lys Pro Leu Met
        355                 360                 365

Tyr Val Ala Glu Pro Phe Leu Pro Phe Thr Leu Gly Thr Tyr Met Leu
    370                 375                 380

Val Leu Lys Asn Cys Tyr Arg Leu Leu Ala Leu Met Gln Glu Ser Met
385                 390                 395                 400
```

<210> SEQ ID NO 63
<211> LENGTH: 1368
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR28

<400> SEQUENCE: 63

```
atgtactcac cggaagaggc ggccgaactg aagaggcgca actatcgcag catcagggag     60

atgatccgac tctcctatac ggtgggcttc aacctgttgg atccttcccg atgcggacag    120

gtgctcagaa tctggacaat tgtccttagc gtgagtagct tggcatcgct ttatgggcac    180

tggcaaatgt tagccaggta cattcatgat attccacgca ttggagagac cgctggaact    240

gccctgcagt tcctaacatc gatagcaaag atgtggtact ttctgtttgc ccatagacag    300

atatacgaat tgctacgaaa ggcgcgctgc catgaattac tccaaaagtg tgagctcttt    360

gaaaggatgt cagatctacc tgttatcaaa gagattcgcc agcaggttga gtccacgatg    420

aatcggtact gggccagcac tcgtcggcaa attcttatct atttgtacag ctgtatttgt    480

attactacaa actactttat caactccttc gtaatcaacc tctatcgcta tttcactaaa    540

ccgaaaggat cctacgacat aatgttacct ctgccatctc tgtatcccgc ctgggagcac    600

aagggattag agtttcccta ctatcatata cagatgtacc tggaaacctg ttctctgtat    660

atctgcggca tgtgtgccgt tagctttgat ggagtcttta ttgtcctgtg ccttcatagc    720

gtgggactta tgaggtcact taaccaaatg gtggaacaag ccacatctga gttggttcct    780

ccagatcgca gggttgaata cttgcgatgc tgtatttatc agtaccaacg agtggcgaac    840

tttgcaaccg aggttaacaa ctgctttcgg cacatcactt tcacgcagtt cctgcttagc    900

cttttcaact ggggcctggc cttgttccaa atgagcgtcg gattgggcaa caacagcagc    960

atcaccatga tccggatgac catgtacctg gtggcagccg gctatcagat agttgtgtac   1020
```

-continued

```
tgctacaatg gccagcgatt tgcgactgct agcgaggaga ttgccaacgc cttttaccag   1080

gtgcgatggt acggagagtc cagggagttc cgccacctca tccgcatgat gctgatgcgc   1140

acgaaccggg gattcaggct ggacgtgtcc tggttcatgc aaatgtcctt gcccacactc   1200

atggcggtga gtagcggagc agagcagagc aggggtcctg caggtcctgc aggtcctgca   1260

ggtccacccc caagggtccc ctcctacagc cagttccact tgattgattc gcagatggtc   1320

cggacaagtg gacagtactt cctgctgctg cagaacgtca accagaaa                 1368


<210> SEQ ID NO 64
<211> LENGTH: 456
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR28

<400> SEQUENCE: 64

Met Tyr Ser Pro Glu Glu Ala Ala Glu Leu Lys Arg Arg Asn Tyr Arg
1               5                   10                  15

Ser Ile Arg Glu Met Ile Arg Leu Ser Tyr Thr Val Gly Phe Asn Leu
            20                  25                  30

Leu Asp Pro Ser Arg Cys Gly Gln Val Leu Arg Ile Trp Thr Ile Val
        35                  40                  45

Leu Ser Val Ser Ser Leu Ala Ser Leu Tyr Gly His Trp Gln Met Leu
    50                  55                  60

Ala Arg Tyr Ile His Asp Ile Pro Arg Ile Gly Glu Thr Ala Gly Thr
65                  70                  75                  80

Ala Leu Gln Phe Leu Thr Ser Ile Ala Lys Met Trp Tyr Phe Leu Phe
                85                  90                  95

Ala His Arg Gln Ile Tyr Glu Leu Leu Arg Lys Ala Arg Cys His Glu
            100                 105                 110

Leu Leu Gln Lys Cys Glu Leu Phe Glu Arg Met Ser Asp Leu Pro Val
        115                 120                 125

Ile Lys Glu Ile Arg Gln Gln Val Glu Ser Thr Met Asn Arg Tyr Trp
    130                 135                 140

Ala Ser Thr Arg Arg Gln Ile Leu Ile Tyr Leu Tyr Ser Cys Ile Cys
145                 150                 155                 160

Ile Thr Thr Asn Tyr Phe Ile Asn Ser Phe Val Ile Asn Leu Tyr Arg
                165                 170                 175

Tyr Phe Thr Lys Pro Lys Gly Ser Tyr Asp Ile Met Leu Pro Leu Pro
            180                 185                 190

Ser Leu Tyr Pro Ala Trp Glu His Lys Gly Leu Glu Phe Pro Tyr Tyr
        195                 200                 205

His Ile Gln Met Tyr Leu Glu Thr Cys Ser Leu Tyr Ile Cys Gly Met
    210                 215                 220

Cys Ala Val Ser Phe Asp Gly Val Phe Ile Val Leu Cys Leu His Ser
225                 230                 235                 240

Val Gly Leu Met Arg Ser Leu Asn Gln Met Val Glu Gln Ala Thr Ser
                245                 250                 255

Glu Leu Val Pro Pro Asp Arg Arg Val Glu Tyr Leu Arg Cys Cys Ile
            260                 265                 270

Tyr Gln Tyr Gln Arg Val Ala Asn Phe Ala Thr Glu Val Asn Asn Cys
        275                 280                 285

Phe Arg His Ile Thr Phe Thr Gln Phe Leu Leu Ser Leu Phe Asn Trp
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    290                 295                 300

Gly Leu Ala Leu Phe Gln Met Ser Val Gly Leu Gly Asn Asn Ser Ser
305                 310                 315                 320

Ile Thr Met Ile Arg Met Thr Met Tyr Leu Val Ala Ala Gly Tyr Gln
                325                 330                 335

Ile Val Val Tyr Cys Tyr Asn Gly Gln Arg Phe Ala Thr Ala Ser Glu
            340                 345                 350

Glu Ile Ala Asn Ala Phe Tyr Gln Val Arg Trp Tyr Gly Glu Ser Arg
        355                 360                 365

Glu Phe Arg His Leu Ile Arg Met Met Leu Met Arg Thr Asn Arg Gly
    370                 375                 380

Phe Arg Leu Asp Val Ser Trp Phe Met Gln Met Ser Leu Pro Thr Leu
385                 390                 395                 400

Met Ala Val Ser Ser Gly Ala Glu Gln Ser Arg Gly Pro Ala Gly Pro
                405                 410                 415

Ala Gly Pro Ala Gly Pro Pro Pro Arg Val Pro Ser Tyr Ser Gln Phe
            420                 425                 430

His Leu Ile Asp Ser Gln Met Val Arg Thr Ser Gly Gln Tyr Phe Leu
        435                 440                 445

Leu Leu Gln Asn Val Asn Gln Lys
    450                 455


<210> SEQ ID NO 65
<211> LENGTH: 1239
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DOR30

<400> SEQUENCE: 65

atggcggtga gcactcgtgt ggccacaaag caggaagtgc ccgaatcccg gcgagcgttt      60

aggaatctct tcaattgctt ctatgccctt ggcatgcagg caccggatgg cagtcgaccg     120

accacgagca gcacatggca acgcatctac gcctgcttct cggtggtcat gtacgtgtgg     180

caactgctgc tggtgcccac attctttgtg atcagctatc ggtacatggg cggcatggag     240

attacccagg tgctgacctc cgcccaggtg gccatcgatg cggtcattct gccggccaag     300

attgtggcac tggcgtggaa tttgccattg ctgcgcagag cagagcatca tctggccgcc     360

ttggatgcgc ggtgcaggga acaggaggag ttccaattga tcctcgatgc ggtgaggttt     420

tgcaactatc tggtatggtt ctaccagatc tgctatgcca tctactcctc gtcgacattt     480

gtgtgcgcct tcctgctggg ccaaccgcca tatgccctct atttgcctgg cctcgattgg     540

cagcgttccc agatgcagtt ctgcatccag gcctggattg agttccttat catgaactgg     600

acgtgcctgc accaagctag cgatgatgtg tacgccgtta tctatctgta tgtggtccgg     660

attcaagtgc aattgctggc caggcgggtg gagaagctgg gcacggatga tagtggccag     720

gtggagatct atcccgatga gcggcggcag gaggagcatt gcgcggaact gcagcgctgc     780

attgtagatc accagacgat gctgcagctg ctcgactgca ttagtcccgt catctcgcgt     840

accatattcg ttcagttcct gatcaccgcc gccatcatgg gcaccaccat gatcaacatt     900

ttcatttcg ccaatacgaa cacgaagatc gcatcgatca tttacctgct ggcggtgacc     960

ctgcagacgg ctccatgttg ctatcaggcc acctcgctga tgttggacaa cgagaggctg    1020

gccctggcca tcttccagtg ccagtggctg ggccagagtg cccggttccg taagatgctg    1080
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ctctactatc ttcatcgcgc ccagcagccc atcacgctga ccgccatgaa gctgtttccc   1140

atcaatctgg ccacgtactt cagtatagcc aagttctcgt tttcgctcta cacgctcatc   1200

aaggggatga atctcggcga gcgattcaac aggacaaat                           1239


<210> SEQ ID NO 66
<211> LENGTH: 413
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR30

<400> SEQUENCE: 66

Met Ala Val Ser Thr Arg Val Ala Thr Lys Gln Glu Val Pro Glu Ser
1               5                   10                  15

Arg Arg Ala Phe Arg Asn Leu Phe Asn Cys Phe Tyr Ala Leu Gly Met
            20                  25                  30

Gln Ala Pro Asp Gly Ser Arg Pro Thr Thr Ser Ser Thr Trp Gln Arg
        35                  40                  45

Ile Tyr Ala Cys Phe Ser Val Val Met Tyr Val Trp Gln Leu Leu Leu
    50                  55                  60

Val Pro Thr Phe Phe Val Ile Ser Tyr Arg Tyr Met Gly Gly Met Glu
65                  70                  75                  80

Ile Thr Gln Val Leu Thr Ser Ala Gln Val Ala Ile Asp Ala Val Ile
                85                  90                  95

Leu Pro Ala Lys Ile Val Ala Leu Ala Trp Asn Leu Pro Leu Leu Arg
            100                 105                 110

Arg Ala Glu His His Leu Ala Ala Leu Asp Ala Arg Cys Arg Glu Gln
        115                 120                 125

Glu Glu Phe Gln Leu Ile Leu Asp Ala Val Arg Phe Cys Asn Tyr Leu
    130                 135                 140

Val Trp Phe Tyr Gln Ile Cys Tyr Ala Ile Tyr Ser Ser Ser Thr Phe
145                 150                 155                 160

Val Cys Ala Phe Leu Leu Gly Gln Pro Pro Tyr Ala Leu Tyr Leu Pro
                165                 170                 175

Gly Leu Asp Trp Gln Arg Ser Gln Met Gln Phe Cys Ile Gln Ala Trp
            180                 185                 190

Ile Glu Phe Leu Ile Met Asn Trp Thr Cys Leu His Gln Ala Ser Asp
        195                 200                 205

Asp Val Tyr Ala Val Ile Tyr Leu Tyr Val Val Arg Ile Gln Val Gln
    210                 215                 220

Leu Leu Ala Arg Arg Val Glu Lys Leu Gly Thr Asp Asp Ser Gly Gln
225                 230                 235                 240

Val Glu Ile Tyr Pro Asp Glu Arg Arg Gln Glu Glu His Cys Ala Glu
                245                 250                 255

Leu Gln Arg Cys Ile Val Asp His Gln Thr Met Leu Gln Leu Leu Asp
            260                 265                 270

Cys Ile Ser Pro Val Ile Ser Arg Thr Ile Phe Val Gln Phe Leu Ile
        275                 280                 285

Thr Ala Ala Ile Met Gly Thr Thr Met Ile Asn Ile Phe Ile Phe Ala
    290                 295                 300

Asn Thr Asn Thr Lys Ile Ala Ser Ile Ile Tyr Leu Leu Ala Val Thr
305                 310                 315                 320

Leu Gln Thr Ala Pro Cys Cys Tyr Gln Ala Thr Ser Leu Met Leu Asp
                325                 330                 335
```

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```
Asn Glu Arg Leu Ala Leu Ala Ile Phe Gln Cys Gln Trp Leu Gly Gln
            340                 345                 350

Ser Ala Arg Phe Arg Lys Met Leu Leu Tyr Tyr Leu His Arg Ala Gln
        355                 360                 365

Gln Pro Ile Thr Leu Thr Ala Met Lys Leu Phe Pro Ile Asn Leu Ala
    370                 375                 380

Thr Tyr Phe Ser Ile Ala Lys Phe Ser Phe Ser Leu Tyr Thr Leu Ile
385                 390                 395                 400

Lys Gly Met Asn Leu Gly Glu Arg Phe Asn Arg Thr Asn
                405                 410


<210> SEQ ID NO 67
<211> LENGTH: 1191
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DOR31

<400> SEQUENCE: 67

atgattttta agtacattca agagccagtc cttggatcct tatttcgatc ccgggattcg      60

ctgatctact taaacagatc catagatcaa atgggatgga gactgccgcc acgaactaag     120

ccgtactggt ggctctatta catttggaca ttggtggtca tagtactcgt ctttatcttt     180

ataccctatg gactgataat gactggaata aaggagttca agaacttcac gaccacggat     240

ctgtttacgt atgtccaggt gccggttaac accaatgctt cgatcatgaa gggcattata     300

gtgttgttta tgcggcggcg attttcaagg gctcagaaga tgatggacgc catggacatt     360

cgatgcacca agatggagga gaaagtccag gtgcaccgag cagcagcctt atgcaatcgt     420

gttgttgtga tttaccattg catatacttc ggctatctat ccatggcctt aaccggagct     480

ctggtgattg ggaagactcc attctgtttg tacaatccac tggttaaccc cgacgatcat     540

ttctatctgg ccactgccat tgaatcggtc accatggctg gcattattct ggccaatctc     600

attttggacg tatatcccat catatatgtg gtcgttctgc ggatccacat ggagctcttg     660

agtgagcgaa tcaagacgct gcgtactgat gtggaaaaag gcgacgatca acattatgcc     720

gagctggtgg agtgtgtaaa ggatcacaag ctaattgtcg aatatggaaa cactctgcgt     780

cccatgatat ccgccacgat gttcatccaa ctactatccg ttggcttact tttgggtctg     840

gcagcggtgt ccatgcagtt ctataacacc gtaatggagc gtgttgtctc cggggtctac     900

accatagcca ttctatccca gacctttcca ttttgctatg tctgtgagca gctgagcagc     960

gattgcgaat ccctgaccaa cacactgttc cattccaagt ggattggagc tgagcgacga    1020

tacagaacca cgatgttgta cttcattcac aatgttcagc agtcgatttt gttcactgcg    1080

ggcggaattt tccccatatg tctaaacacc aatataaaga tggccaagtt cgctttctca    1140

gtggtgacca ttgtaaatga gatggacttg gccgagaaat tgagaaggga g             1191


<210> SEQ ID NO 68
<211> LENGTH: 397
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR31

<400> SEQUENCE: 68

Met Ile Phe Lys Tyr Ile Gln Glu Pro Val Leu Gly Ser Leu Phe Arg
1               5                   10                  15

Ser Arg Asp Ser Leu Ile Tyr Leu Asn Arg Ser Ile Asp Gln Met Gly
```

-continued

```
            20                  25                  30

Trp Arg Leu Pro Pro Arg Thr Lys Pro Tyr Trp Trp Leu Tyr Tyr Ile
        35                  40                  45

Trp Thr Leu Val Val Ile Val Leu Val Phe Ile Phe Ile Pro Tyr Gly
    50                  55                  60

Leu Ile Met Thr Gly Ile Lys Glu Phe Lys Asn Phe Thr Thr Thr Asp
65                  70                  75                  80

Leu Phe Thr Tyr Val Gln Val Pro Val Asn Thr Asn Ala Ser Ile Met
                85                  90                  95

Lys Gly Ile Ile Val Leu Phe Met Arg Arg Arg Phe Ser Arg Ala Gln
            100                 105                 110

Lys Met Met Asp Ala Met Asp Ile Arg Cys Thr Lys Met Glu Glu Lys
        115                 120                 125

Val Gln Val His Arg Ala Ala Ala Leu Cys Asn Arg Val Val Val Ile
    130                 135                 140

Tyr His Cys Ile Tyr Phe Gly Tyr Leu Ser Met Ala Leu Thr Gly Ala
145                 150                 155                 160

Leu Val Ile Gly Lys Thr Pro Phe Cys Leu Tyr Asn Pro Leu Val Asn
                165                 170                 175

Pro Asp Asp His Phe Tyr Leu Ala Thr Ala Ile Glu Ser Val Thr Met
            180                 185                 190

Ala Gly Ile Ile Leu Ala Asn Leu Ile Leu Asp Val Tyr Pro Ile Ile
        195                 200                 205

Tyr Val Val Val Leu Arg Ile His Met Glu Leu Leu Ser Glu Arg Ile
    210                 215                 220

Lys Thr Leu Arg Thr Asp Val Glu Lys Gly Asp Asp Gln His Tyr Ala
225                 230                 235                 240

Glu Leu Val Glu Cys Val Lys Asp His Lys Leu Ile Val Glu Tyr Gly
                245                 250                 255

Asn Thr Leu Arg Pro Met Ile Ser Ala Thr Met Phe Ile Gln Leu Leu
            260                 265                 270

Ser Val Gly Leu Leu Leu Gly Leu Ala Ala Val Ser Met Gln Phe Tyr
        275                 280                 285

Asn Thr Val Met Glu Arg Val Val Ser Gly Val Tyr Thr Ile Ala Ile
    290                 295                 300

Leu Ser Gln Thr Phe Pro Phe Cys Tyr Val Cys Glu Gln Leu Ser Ser
305                 310                 315                 320

Asp Cys Glu Ser Leu Thr Asn Thr Leu Phe His Ser Lys Trp Ile Gly
                325                 330                 335

Ala Glu Arg Arg Tyr Arg Thr Thr Met Leu Tyr Phe Ile His Asn Val
            340                 345                 350

Gln Gln Ser Ile Leu Phe Thr Ala Gly Gly Ile Phe Pro Ile Cys Leu
        355                 360                 365

Asn Thr Asn Ile Lys Met Ala Lys Phe Ala Phe Ser Val Val Thr Ile
    370                 375                 380

Val Asn Glu Met Asp Leu Ala Glu Lys Leu Arg Arg Glu
385                 390                 395
```

<210> SEQ ID NO 69
<211> LENGTH: 1176
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR32

-continued

<400> SEQUENCE: 69

atggaacctg tgcagtacag ctacgaggat ttcgctcgat tgcccacgac ggtgttctgg 60
atcatgggct acgacatgct gggcgttccg aagacccgct ctcgcaggat actatactgg 120
atatatcgtt tcctctgtct cgccagccat ggggtctgtg taggagtcat ggtatttcgt 180
atggtggagg caaagaccat tgacaatgtt tcgctgatca tgcggtatgc cactctggtc 240
acctatatca tcaactcgga tacgaaattc gcaactgtct tacaaaggag tgcaattcaa 300
agtctaaact caaaactggc cgaactatat ccgaagacca cgctggacag gatctatcac 360
cgggtgaatg atcactattg gaccaagtca tttgtatatt tggttattat ctacattggt 420
tcgtcgatta tggttgttat tggaccgatt attacgtcga ttatagctta cttcacgcac 480
aacgttttca cctacatgca ctgctatccg tactttttgt atgatcctga gaaggatccg 540
gtttggatct acatcagcat ctatgctctg gaatggttgc acagcacaca gatggtcatt 600
tcgaacattg gcgcggatat ctggctgctg tactttcagg tgcagataaa tctccacttc 660
aggggcatta tacgatcact ggcggatcac aagcccagtg tgaagcacga ccaggaggac 720
aggaaattca ttgcgaaaat tgtcgacaag caggtgcacc tggtcagttt gcaaaacgat 780
ctgaatggta tctttggaaa atcgctgctt ctaagcctgc tgaccaccgc agcggttatc 840
tgcacggtgg cggtgtacac tctgattcag ggtcccacct tggagggctt cacctatgtg 900
atcttcatcg ggacttctgt gatgcaggtc tacctggtgt gctattacgg tcagcaagtt 960
ctcgacttga gcggcgaggt ggcccacgcc gtgtacaatc atgattttca cgatgcttct 1020
atagcgtaca agaggtacct gctcataatc attatcaggg cgcagcagcc cgtggaactt 1080
aatgccatgg gctacctgtc catttcgctg gacaccttta aacagctgat gagcgtctcc 1140
taccgggtta taaccatgct catgcagatg attcag 1176

<210> SEQ ID NO 70
<211> LENGTH: 392
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR32

<400> SEQUENCE: 70

```
Met Glu Pro Val Gln Tyr Ser Tyr Glu Asp Phe Ala Arg Leu Pro Thr
1               5                   10                  15

Thr Val Phe Trp Ile Met Gly Tyr Asp Met Leu Gly Val Pro Lys Thr
            20                  25                  30

Arg Ser Arg Arg Ile Leu Tyr Trp Ile Tyr Arg Phe Leu Cys Leu Ala
        35                  40                  45

Ser His Gly Val Cys Val Gly Val Met Val Phe Arg Met Val Glu Ala
    50                  55                  60

Lys Thr Ile Asp Asn Val Ser Leu Ile Met Arg Tyr Ala Thr Leu Val
65                  70                  75                  80

Thr Tyr Ile Ile Asn Ser Asp Thr Lys Phe Ala Thr Val Leu Gln Arg
                85                  90                  95

Ser Ala Ile Gln Ser Leu Asn Ser Lys Leu Ala Glu Leu Tyr Pro Lys
            100                 105                 110

Thr Thr Leu Asp Arg Ile Tyr His Arg Val Asn Asp His Tyr Trp Thr
        115                 120                 125

Lys Ser Phe Val Tyr Leu Val Ile Ile Tyr Ile Gly Ser Ser Ile Met
```

-continued

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    130                 135                 140

Val Val Ile Gly Pro Ile Ile Thr Ser Ile Ile Ala Tyr Phe Thr His
145                 150                 155                 160

Asn Val Phe Thr Tyr Met His Cys Tyr Pro Tyr Phe Leu Tyr Asp Pro
                165                 170                 175

Glu Lys Asp Pro Val Trp Ile Tyr Ile Ser Ile Tyr Ala Leu Glu Trp
            180                 185                 190

Leu His Ser Thr Gln Met Val Ile Ser Asn Ile Gly Ala Asp Ile Trp
        195                 200                 205

Leu Leu Tyr Phe Gln Val Gln Ile Asn Leu His Phe Arg Gly Ile Ile
    210                 215                 220

Arg Ser Leu Ala Asp His Lys Pro Ser Val Lys His Asp Gln Glu Asp
225                 230                 235                 240

Arg Lys Phe Ile Ala Lys Ile Val Asp Lys Gln Val His Leu Val Ser
                245                 250                 255

Leu Gln Asn Asp Leu Asn Gly Ile Phe Gly Lys Ser Leu Leu Leu Ser
            260                 265                 270

Leu Leu Thr Thr Ala Ala Val Ile Cys Thr Val Ala Val Tyr Thr Leu
        275                 280                 285

Ile Gln Gly Pro Thr Leu Glu Gly Phe Thr Tyr Val Ile Phe Ile Gly
    290                 295                 300

Thr Ser Val Met Gln Val Tyr Leu Val Cys Tyr Tyr Gly Gln Gln Val
305                 310                 315                 320

Leu Asp Leu Ser Gly Glu Val Ala His Ala Val Tyr Asn His Asp Phe
                325                 330                 335

His Asp Ala Ser Ile Ala Tyr Lys Arg Tyr Leu Leu Ile Ile Ile Ile
            340                 345                 350

Arg Ala Gln Gln Pro Val Glu Leu Asn Ala Met Gly Tyr Leu Ser Ile
        355                 360                 365

Ser Leu Asp Thr Phe Lys Gln Leu Met Ser Val Ser Tyr Arg Val Ile
    370                 375                 380

Thr Met Leu Met Gln Met Ile Gln
385                 390


<210> SEQ ID NO 71
<211> LENGTH: 795
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DOR38

<400> SEQUENCE: 71

atgcgtttga tcaaaatttc atattcggca cttaatgagg tgtgcgtttg gctgaaactg     60

aatggttctt ggccattaac cgaatcatcg aggccatgga ggagccaatc cttattggcc    120

accgcctaca tcgtgtgggc gtggtacgtc attgcatctg tgggcataac aatcagctat    180

cagacggcct tttgctgaa caacctttcg gacattatta tcaccacgga aaattgttgc    240

accacccttta tgggtgtcct gaactttgtc cgactcatcc atcttcgcct caatcagagg    300

aaattccgcc agcttattga gaacttttcc tacgaaattt ggatacctaa ttcttccaaa    360

aacaatgttg ccgccgagtg tcgcagacgc atggttacct tcagcataat gacatccttg    420

ctagcgtgcc tgatcataat gtattgtgtc ctgccgctgg tggagatctt ctttggaccc    480

gccttcgatg cacagaacaa gccgtttccc tacaagatga tctttccgta cgatgcccag    540
```

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```
agcagttgga tccgatatgt gatgacctac atcttcacct cctacgcggg aatctgtgtg    600

gtcaccacct tgtttgcaga ggacaccatt cttggcttct tcataaccta cacttgtggc    660

caatttcatt tgctacacca acgaatcgca ggtttatttg cgggttccaa tgcggaattg    720

gccgagagca ttcagctgga gcgactcaaa cgtattgtgg aaaaacacaa caatattatc    780

agcgcaaatt ctgta                                                     795


<210> SEQ ID NO 72
<211> LENGTH: 265
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR38

<400> SEQUENCE: 72

Met Arg Leu Ile Lys Ile Ser Tyr Ser Ala Leu Asn Glu Val Cys Val
1               5                   10                  15

Trp Leu Lys Leu Asn Gly Ser Trp Pro Leu Thr Glu Ser Ser Arg Pro
            20                  25                  30

Trp Arg Ser Gln Ser Leu Leu Ala Thr Ala Tyr Ile Val Trp Ala Trp
        35                  40                  45

Tyr Val Ile Ala Ser Val Gly Ile Thr Ile Ser Tyr Gln Thr Ala Phe
    50                  55                  60

Leu Leu Asn Asn Leu Ser Asp Ile Ile Ile Thr Thr Glu Asn Cys Cys
65                  70                  75                  80

Thr Thr Phe Met Gly Val Leu Asn Phe Val Arg Leu Ile His Leu Arg
                85                  90                  95

Leu Asn Gln Arg Lys Phe Arg Gln Leu Ile Glu Asn Phe Ser Tyr Glu
            100                 105                 110

Ile Trp Ile Pro Asn Ser Ser Lys Asn Asn Val Ala Ala Glu Cys Arg
        115                 120                 125

Arg Arg Met Val Thr Phe Ser Ile Met Thr Ser Leu Leu Ala Cys Leu
    130                 135                 140

Ile Ile Met Tyr Cys Val Leu Pro Leu Val Glu Ile Phe Phe Gly Pro
145                 150                 155                 160

Ala Phe Asp Ala Gln Asn Lys Pro Phe Pro Tyr Lys Met Ile Phe Pro
                165                 170                 175

Tyr Asp Ala Gln Ser Ser Trp Ile Arg Tyr Val Met Thr Tyr Ile Phe
            180                 185                 190

Thr Ser Tyr Ala Gly Ile Cys Val Val Thr Thr Leu Phe Ala Glu Asp
        195                 200                 205

Thr Ile Leu Gly Phe Phe Ile Thr Tyr Thr Cys Gly Gln Phe His Leu
    210                 215                 220

Leu His Gln Arg Ile Ala Gly Leu Phe Ala Gly Ser Asn Ala Glu Leu
225                 230                 235                 240

Ala Glu Ser Ile Gln Leu Glu Arg Leu Lys Arg Ile Val Glu Lys His
                245                 250                 255

Asn Asn Ile Ile Ser Ala Asn Ser Val
            260                 265


<210> SEQ ID NO 73
<211> LENGTH: 1409
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DOR48

<400> SEQUENCE: 73
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```
atggagcgcc attatttcat ggtgccaaag tttgcattat cgctgattgg tttttatccc     60
gaacagaagc gaacggtttt ggtgaaactt tggagtttct tcaacttttt catcctcacc    120
tacggctgtt atgcagaggc ttactatggc atacactata taccgattaa catagccact    180
gcattggatg ccctttgtcc tgtggcctcc agcattttgt cgctggtgaa aatggtcgcc    240
atttggtggt atcaagatga attaaggagt ttgatagagc gggtaagatt tttaacagag    300
caacagaagt ccaagaggaa actgggctat aagaagaggt tctatacact ggcaacgcaa    360
ctaacattcc tgctactatg ctgtggattt tgcaccagta cttcctattc cgtcagacat    420
ttgattgata atatcctgag acgcacccat ggcaaggact ggatctacga gactccgttc    480
aagatgatgt aaggaaaggg aagaatggtt tatatatact tttggaacga aataatgatg    540
tgatctaaac aagatgcact ttttttagg ttccccgatc ttctcctgcg tttgccactc     600
tatcccatca cctatatact cgtgcattgg catggctaca ttactgtggt ttgttttgtc    660
ggcgcggatg gtttcttcct ggggttctgt ttgtacttca ctgttttgct gctctgtctg    720
caggacgatg tttgtgattt actagaggtt gaaaacatcg agaagagtcc ctccgaagcg    780
gaggaagctc gcatagttcg ggaaatggaa aaactggtgg accggcataa cgaggtggcc    840
gagctgacag aaagattgtc gggtgttatg gtggaaataa cactggccca ctttgttact    900
tcgagtttga taatcggaac cagcgtggtg gatattttat tagtgggtat ttacatttga    960
ttagatcctt tcgatatatg ttcttaaatt ctagttttcc ggcctgggaa tcattgtgta   1020
tgtggtctac acttgtgccg taggtgtgga aatatttcta tactgtttag gaggatctca   1080
tattatggaa gcggtatatt cataagaaac tactataaag ttacttttaa attcattgca   1140
tttcttagtg ttccaatcta gcgcgctcca catttccag ccactggtat ggccacagtg    1200
ttcgggtcca aaagatgacc cttttgatgg tagctcgtgc tcaacgagtt ctcacaatta   1260
aaattccttt cttttcccca tcattagaga ctctaacttc ggtaagctta tgcgaaaatg   1320
ttatggtaca cacaagtcta catttctatg aggtcttgta gattttgcgc ttcactggat   1380
ctctgattgc cctggcaaag tcggttata                                     1409
```

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<210> SEQ ID NO 74
<211> LENGTH: 369
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR48

<400> SEQUENCE: 74

Met Glu Arg His Tyr Phe Met Val Pro Lys Phe Ala Leu Ser Leu Ile
1               5                   10                  15

Gly Phe Tyr Pro Glu Gln Lys Arg Thr Val Leu Val Lys Leu Trp Ser
            20                  25                  30

Phe Phe Asn Phe Phe Ile Leu Thr Tyr Gly Cys Tyr Ala Glu Ala Tyr
        35                  40                  45

Tyr Gly Ile His Tyr Ile Pro Ile Asn Ile Ala Thr Ala Leu Asp Ala
    50                  55                  60

Leu Cys Pro Val Ala Ser Ser Ile Leu Ser Leu Val Lys Met Val Ala
65                  70                  75                  80

Ile Trp Trp Tyr Gln Asp Glu Leu Arg Ser Leu Ile Glu Arg Arg Phe
                85                  90                  95

Tyr Thr Leu Ala Thr Gln Leu Thr Phe Leu Leu Leu Cys Cys Gly Phe
```

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```
            100                 105                 110

Cys Thr Ser Thr Ser Tyr Ser Val Arg His Leu Ile Asp Asn Ile Leu
        115                 120                 125

Arg Arg Thr His Gly Lys Asp Trp Ile Tyr Glu Thr Pro Phe Lys Met
    130                 135                 140

Met Phe Pro Asp Leu Leu Leu Arg Leu Pro Leu Tyr Pro Ile Thr Tyr
145                 150                 155                 160

Ile Leu Val His Trp His Gly Tyr Ile Thr Val Val Cys Phe Val Gly
                165                 170                 175

Ala Asp Gly Phe Phe Leu Gly Phe Cys Leu Tyr Phe Thr Val Leu Leu
            180                 185                 190

Leu Cys Leu Gln Asp Asp Val Cys Asp Leu Leu Glu Val Glu Asn Ile
        195                 200                 205

Glu Lys Ser Pro Ser Glu Ala Glu Glu Ala Arg Ile Val Arg Glu Met
    210                 215                 220

Glu Lys Leu Val Asp Arg His Asn Glu Val Ala Glu Leu Thr Glu Arg
225                 230                 235                 240

Leu Ser Gly Val Met Val Glu Ile Thr Leu Ala His Phe Val Thr Ser
                245                 250                 255

Ser Leu Ile Ile Gly Thr Ser Val Val Asp Ile Leu Leu Phe Ser Gly
            260                 265                 270

Leu Gly Ile Ile Val Tyr Val Val Tyr Thr Cys Ala Val Gly Val Glu
        275                 280                 285

Ile Phe Leu Tyr Cys Leu Gly Gly Ser His Ile Met Glu Ala Cys Ser
    290                 295                 300

Asn Leu Ala Arg Ser Thr Phe Ser Ser His Trp Tyr Gly His Ser Val
305                 310                 315                 320

Arg Val Gln Lys Met Thr Leu Leu Met Val Ala Arg Ala Gln Arg Val
                325                 330                 335

Leu Thr Ile Lys Ile Pro Phe Phe Ser Pro Ser Leu Glu Thr Leu Thr
            340                 345                 350

Ser Ile Leu Arg Phe Thr Gly Ser Leu Ile Ala Leu Ala Lys Ser Val
        355                 360                 365

Ile
```

<210> SEQ ID NO 75
<211> LENGTH: 891
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR56

<400> SEQUENCE: 75

```
atggatccgg tggagatgcc catttttggt agcactctga agctaatgaa gttctggtca      60

tatctgtttg ttcacaactg gcgccgctat gtcgcaatga ctccgtacat cattatcaac     120

tgtactcagt atgtggatat atatctgagc accgaatcct tggactttat catcagaaat     180

gtatacctgg ctgtattgtt taccaacacg gtggtcagag gtgtattgtt atgcgtacag     240

cggtttagct acgagcgttt cattaatatt ttgaaaagct tttacattga gttgttggtg     300

agtaccgaaa gattatctca aaaatgcata ttgcataaat gggcagttct gccatatggc     360

atgtatttgc ccactattga tgaatacaaa tacgcatcac cttactacga gattttcttt     420

gtgattcaag ccattatggc tccaatgggg tgttgcatgt acataccata cacaaacatg     480
```

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```
gtagtgacat ttacccttt cgccattctc atgtgtcgag tgttgcaaca taagttgaga    540

agcctagaaa agctgaaaaa tgaacaagta cgtggtgaaa tcgctcaaac aattgctcag    600

accgtcatag tcatcgcata catggtaatg atatttgcca acagtgtagt cctttactac    660

gtggccaatg agctatactt tcaaagcttt gatattgcca ttgctgccta tgagagcaat    720

tggatggact ttgatgtgga cacacaaaag actttgaagt tcctcatcat gcgctcgcaa    780

aagcccttgg cgagtctggt gggtggcaca tatcccatga acttgaaaat gcttcagtca    840

ctactaaatg ccatttactc cttcttcacc cttctgcgtc gcgtttacgg c             891
```

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<210> SEQ ID NO 76
<211> LENGTH: 297
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR56

<400> SEQUENCE: 76

Met Asp Pro Val Glu Met Pro Ile Phe Gly Ser Thr Leu Lys Leu Met
1               5                   10                  15

Lys Phe Trp Ser Tyr Leu Phe Val His Asn Trp Arg Arg Tyr Val Ala
            20                  25                  30

Met Thr Pro Tyr Ile Ile Ile Asn Cys Thr Gln Tyr Val Asp Ile Tyr
        35                  40                  45

Leu Ser Thr Glu Ser Leu Asp Phe Ile Ile Arg Asn Val Tyr Leu Ala
    50                  55                  60

Val Leu Phe Thr Asn Thr Val Val Arg Gly Val Leu Leu Cys Val Gln
65                  70                  75                  80

Arg Phe Ser Tyr Glu Arg Phe Ile Asn Ile Leu Lys Ser Phe Tyr Ile
                85                  90                  95

Glu Leu Leu Val Ser Thr Glu Arg Leu Ser Gln Lys Cys Ile Leu His
            100                 105                 110

Lys Trp Ala Val Leu Pro Tyr Gly Met Tyr Leu Pro Thr Ile Asp Glu
        115                 120                 125

Tyr Lys Tyr Ala Ser Pro Tyr Tyr Glu Ile Phe Phe Val Ile Gln Ala
    130                 135                 140

Ile Met Ala Pro Met Gly Cys Cys Met Tyr Ile Pro Tyr Thr Asn Met
145                 150                 155                 160

Val Val Thr Phe Thr Leu Phe Ala Ile Leu Met Cys Arg Val Leu Gln
                165                 170                 175

His Lys Leu Arg Ser Leu Glu Lys Leu Lys Asn Glu Gln Val Arg Gly
            180                 185                 190

Glu Ile Ala Gln Thr Ile Ala Gln Thr Val Ile Val Ile Ala Tyr Met
        195                 200                 205

Val Met Ile Phe Ala Asn Ser Val Val Leu Tyr Tyr Val Ala Asn Glu
    210                 215                 220

Leu Tyr Phe Gln Ser Phe Asp Ile Ala Ile Ala Ala Tyr Glu Ser Asn
225                 230                 235                 240

Trp Met Asp Phe Asp Val Asp Thr Gln Lys Thr Leu Lys Phe Leu Ile
                245                 250                 255

Met Arg Ser Gln Lys Pro Leu Ala Ser Leu Val Gly Gly Thr Tyr Pro
            260                 265                 270

Met Asn Leu Lys Met Leu Gln Ser Leu Leu Asn Ala Ile Tyr Ser Phe
        275                 280                 285
```

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```
Phe Thr Leu Leu Arg Arg Val Tyr Gly
    290                 295


<210> SEQ ID NO 77
<211> LENGTH: 1134
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DOR58

<400> SEQUENCE: 77

atggacgcca gctactttgc cgtccagaga agagctctgg aaatagttgg attcgatccc     60

agtactccgc aactgagtct gaaacatccc atctgggccg ggattctcat cctgtccttg    120

atctctcaca actggcccat ggtagtctat gccctgcagg atctctccga cttgacccgt    180

ctgacggaca actttgcggt gtttatgcaa ggatcacaga gcaccttcaa gttcctggtc    240

atgatggcga aacgaaggcg cattggatcg ttgattcacc gtttgcataa gctaaaccag    300

gcggccagtg ccacgcccaa tcacctggag aagatcgaga gggaaaacca actggatagg    360

tatgtcgcca ggtcctttag aaatgccgcc tacggagtga tttgtgcctc ggccatagcg    420

cccatgttgc ttggcctgtg gggatatgtg gagacgggtg tatttacccc caccacaccc    480

atggagttca acttctggct ggacgagcga aagcctcact tttattggcc catctacgtt    540

tggggcgtac tgggcgtggc agctgccgcc tggttggcca ttgcaacgga caccctgttc    600

tcctggctga ctcacaatgt ggtgattcag ttccaactac tggagcttgt tctcgaagag    660

aaggatctga atggcggaga ctctcgcctg accgggtttg ttagtcgtca tcgtatagct    720

ctggatttgg ccaaggaact aagttcgatt ttcggggaga tcgtctttgt gaaatacatg    780

ctcagttacc tgcaactctg catgttggcc tttcgcttca gccgcagtgg ctggagtgcc    840

caggtgccat ttagagccac cttcctagtg gccatcatca tccaactgag ttcgtattgc    900

tatggaggcg agtatataaa gcagcaaagt ttggccatcg cacaagccgt ttatggtcaa    960

atcaattggc cagaaatgac gccaaagaaa agaagactct ggcaaatggt gatcatgagg   1020

gcgcagcgac cggctaagat ttttggattc atgttcgttg tggacttgcc actgctgctt   1080

tgggtcatca gaactgcggg ctcatttctg gccatgctta ggactttcga gcgt         1134


<210> SEQ ID NO 78
<211> LENGTH: 378
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR58

<400> SEQUENCE: 78

Met Asp Ala Ser Tyr Phe Ala Val Gln Arg Arg Ala Leu Glu Ile Val
1               5                   10                  15

Gly Phe Asp Pro Ser Thr Pro Gln Leu Ser Leu Lys His Pro Ile Trp
            20                  25                  30

Ala Gly Ile Leu Ile Leu Ser Leu Ile Ser His Asn Trp Pro Met Val
        35                  40                  45

Val Tyr Ala Leu Gln Asp Leu Ser Asp Leu Thr Arg Leu Thr Asp Asn
    50                  55                  60

Phe Ala Val Phe Met Gln Gly Ser Gln Ser Thr Phe Lys Phe Leu Val
65                  70                  75                  80

Met Met Ala Lys Arg Arg Arg Ile Gly Ser Leu Ile His Arg Leu His
                85                  90                  95

Lys Leu Asn Gln Ala Ala Ser Ala Thr Pro Asn His Leu Glu Lys Ile
```

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```
            100                 105                 110

Glu Arg Glu Asn Gln Leu Asp Arg Tyr Val Ala Arg Ser Phe Arg Asn
        115                 120                 125

Ala Ala Tyr Gly Val Ile Cys Ala Ser Ala Ile Ala Pro Met Leu Leu
    130                 135                 140

Gly Leu Trp Gly Tyr Val Glu Thr Gly Val Phe Thr Pro Thr Thr Pro
145                 150                 155                 160

Met Glu Phe Asn Phe Trp Leu Asp Glu Arg Lys Pro His Phe Tyr Trp
                165                 170                 175

Pro Ile Tyr Val Trp Gly Val Leu Gly Val Ala Ala Ala Ala Trp Leu
            180                 185                 190

Ala Ile Ala Thr Asp Thr Leu Phe Ser Trp Leu Thr His Asn Val Val
        195                 200                 205

Ile Gln Phe Gln Leu Leu Glu Leu Val Leu Glu Glu Lys Asp Leu Asn
    210                 215                 220

Gly Gly Asp Ser Arg Leu Thr Gly Phe Val Ser Arg His Arg Ile Ala
225                 230                 235                 240

Leu Asp Leu Ala Lys Glu Leu Ser Ser Ile Phe Gly Glu Ile Val Phe
                245                 250                 255

Val Lys Tyr Met Leu Ser Tyr Leu Gln Leu Cys Met Leu Ala Phe Arg
            260                 265                 270

Phe Ser Arg Ser Gly Trp Ser Ala Gln Val Pro Phe Arg Ala Thr Phe
        275                 280                 285

Leu Val Ala Ile Ile Ile Gln Leu Ser Ser Tyr Cys Tyr Gly Gly Glu
    290                 295                 300

Tyr Ile Lys Gln Gln Ser Leu Ala Ile Ala Gln Ala Val Tyr Gly Gln
305                 310                 315                 320

Ile Asn Trp Pro Glu Met Thr Pro Lys Lys Arg Arg Leu Trp Gln Met
                325                 330                 335

Val Ile Met Arg Ala Gln Arg Pro Ala Lys Ile Phe Gly Phe Met Phe
            340                 345                 350

Val Val Asp Leu Pro Leu Leu Leu Trp Val Ile Arg Thr Ala Gly Ser
        355                 360                 365

Phe Leu Ala Met Leu Arg Thr Phe Glu Arg
    370                 375
```

<210> SEQ ID NO 79
<211> LENGTH: 807
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DOR59

<400> SEQUENCE: 79

```
atgcacgaag cagataatcg ggagatggaa cttttggtcg ccactcaggc ttatacacga      60

accattaccc tgttgatctg gataccatcg gttattgctg gcctaatggc ctattcagac     120

tgcatctaca ggagtctgtt tctgccgaaa tcggttttca atgtgccagc tgtgcgacgt     180

ggtgaggagc atcccattct gctatttcag ctgtttccct tcggagaact ttgcgataac     240

ttcgttgttg gatacttggg accttggtat gctctgggcc tgggaatcac ggctatccca     300

ttgtggcaca cctttatcac ttgcctcatg aagtacgtaa atctcaagct gcaaatactc     360

aacaagcgag tggaggagat ggatattacc cgacttaatt ccaaattggt aattggtcgc     420

ctaactgcca gtgagttaac cttctggcaa atgcaactct tcaaggaatt tgtaaaggaa     480
```

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```
cagctgagga ttcgaaaatt tgtccaggaa ctacagtatc tgatttgcgt gcctgtgatg    540

gcagatttca ttatcttctc ggttctcatt tgctttctct tttttgcctt gacagttggc    600

cacgatgaac tgagccttgc ttacttttct tgcggatggt acaacttcga aatgcctttg    660

cagaaaatgc tggtttttat gatgatgcat gcccaaaggc cgatgaagat gcgcgccctg    720

ctggtcgatt tgaatctgag gaccttcata gacattggcc gtggagccta cagctacttc    780

aatttgctgc gtagctccca cttgtat                                        807
```

```
<210> SEQ ID NO 80
<211> LENGTH: 269
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR59

<400> SEQUENCE: 80

Met His Glu Ala Asp Asn Arg Glu Met Glu Leu Leu Val Ala Thr Gln
1               5                   10                  15

Ala Tyr Thr Arg Thr Ile Thr Leu Leu Ile Trp Ile Pro Ser Val Ile
            20                  25                  30

Ala Gly Leu Met Ala Tyr Ser Asp Cys Ile Tyr Arg Ser Leu Phe Leu
        35                  40                  45

Pro Lys Ser Val Phe Asn Val Pro Ala Val Arg Arg Gly Glu Glu His
    50                  55                  60

Pro Ile Leu Leu Phe Gln Leu Phe Pro Phe Gly Glu Leu Cys Asp Asn
65                  70                  75                  80

Phe Val Val Gly Tyr Leu Gly Pro Trp Tyr Ala Leu Gly Leu Gly Ile
                85                  90                  95

Thr Ala Ile Pro Leu Trp His Thr Phe Ile Thr Cys Leu Met Lys Tyr
            100                 105                 110

Val Asn Leu Lys Leu Gln Ile Leu Asn Lys Arg Val Glu Glu Met Asp
        115                 120                 125

Ile Thr Arg Leu Asn Ser Lys Leu Val Ile Gly Arg Leu Thr Ala Ser
    130                 135                 140

Glu Leu Thr Phe Trp Gln Met Gln Leu Phe Lys Glu Phe Val Lys Glu
145                 150                 155                 160

Gln Leu Arg Ile Arg Lys Phe Val Gln Glu Leu Gln Tyr Leu Ile Cys
                165                 170                 175

Val Pro Val Met Ala Asp Phe Ile Ile Phe Ser Val Leu Ile Cys Phe
            180                 185                 190

Leu Phe Phe Ala Leu Thr Val Gly His Asp Glu Leu Ser Leu Ala Tyr
        195                 200                 205

Phe Ser Cys Gly Trp Tyr Asn Phe Glu Met Pro Leu Gln Lys Met Leu
    210                 215                 220

Val Phe Met Met Met His Ala Gln Arg Pro Met Lys Met Arg Ala Leu
225                 230                 235                 240

Leu Val Asp Leu Asn Leu Arg Thr Phe Ile Asp Ile Gly Arg Gly Ala
                245                 250                 255

Tyr Ser Tyr Phe Asn Leu Leu Arg Ser Ser His Leu Tyr
            260                 265

<210> SEQ ID NO 81
<211> LENGTH: 1143
<212> TYPE: DNA
```

-continued

<213> ORGANISM: Drosophila Melanogaster DOR68

<400> SEQUENCE: 81

```
atgtcaaagc taatcgaggt gtttctgggt aatctgtgga cccagcgttt taccttcgcc      60
cgaatgggtt tggatttgca gcccgataaa aagggcaatg ttttgcgatc tccgcttctt     120
tattgtatta tgtgtctgac aacaagcttt gagctctgca ccgtgtgcgc ctttatggtc     180
caaaatcgca accaaatcgt gctttgttcc gaggccctga tgcacggact acagatggtc     240
tcctcgctac tgaagatggc tatattcttg gccaaatctc acgacctggt ggacctaatt     300
caacagattc agtcgccttt tacagaggag gatcttgtag gtacagagtg gagatcccaa     360
aatcaaaggg gacaactaat ggctgccatt tactttatga tgtgtgccgg tacgagtgtg     420
tcatttctgt tgatgccagt ggctttgacc atgcttaagt accattccac tggggaattc     480
gcgcctgtca gctcgttccg ggttctgctt ccatacgatg tgacacaacc gcatgtttat     540
gccatggact gctgcttgat ggtatttgtg ttaagttttt tttgctgctc caccaccgga     600
gtggatacct tatatggatg gtgtgcttta ggcgtgagtt tacaataccg tcgcctcggt     660
caacaactta aaaggatacc ctcctgtttc aatccatctc ggtctgactt tggattaagt     720
gggatttttg tggagcatgc tcgtctgctt aaaatagtcc aacattttaa ttatagtttt     780
atggagatcg catttgtgga ggttgttata atctgtggac tctattgctc agtaatttgt     840
cagtatataa tgccacacac caaccaaaac ttcgcctttc tgggtttctt ttcattggta     900
gttaccacac agctgtgcat ctatcttttc ggtgccgaac aggtccgttt ggaggctgag     960
cgattttccc ggctgctata cgaagtaatt ccttggcaaa accttcctcc taaacaccgg    1020
aaacttttcc tttttccaat tgagcgcgcc caacgagaaa ctgttctcgg tgcttatttc    1080
ttcgaactag gcagacctct tcttgtttgg gtaagcatat tcctttttat tgtattatta    1140
ttt                                                                  1143
```

<210> SEQ ID NO 82
<211> LENGTH: 381
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR68

<400> SEQUENCE: 82

```
Met Ser Lys Leu Ile Glu Val Phe Leu Gly Asn Leu Trp Thr Gln Arg
1               5                   10                  15

Phe Thr Phe Ala Arg Met Gly Leu Asp Leu Gln Pro Asp Lys Lys Gly
            20                  25                  30

Asn Val Leu Arg Ser Pro Leu Leu Tyr Cys Ile Met Cys Leu Thr Thr
        35                  40                  45

Ser Phe Glu Leu Cys Thr Val Cys Ala Phe Met Val Gln Asn Arg Asn
    50                  55                  60

Gln Ile Val Leu Cys Ser Glu Ala Leu Met His Gly Leu Gln Met Val
65                  70                  75                  80

Ser Ser Leu Leu Lys Met Ala Ile Phe Leu Ala Lys Ser His Asp Leu
                85                  90                  95

Val Asp Leu Ile Gln Gln Ile Gln Ser Pro Phe Thr Glu Glu Asp Leu
            100                 105                 110

Val Gly Thr Glu Trp Arg Ser Gln Asn Gln Arg Gly Gln Leu Met Ala
        115                 120                 125
```

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```
Ala Ile Tyr Phe Met Met Cys Ala Gly Thr Ser Val Ser Phe Leu Leu
    130                 135                 140

Met Pro Val Ala Leu Thr Met Leu Lys Tyr His Ser Thr Gly Glu Phe
145                 150                 155                 160

Ala Pro Val Ser Ser Phe Arg Val Leu Leu Pro Tyr Asp Val Thr Gln
                165                 170                 175

Pro His Val Tyr Ala Met Asp Cys Cys Leu Met Val Phe Val Leu Ser
            180                 185                 190

Phe Phe Cys Cys Ser Thr Thr Gly Val Asp Thr Leu Tyr Gly Trp Cys
        195                 200                 205

Ala Leu Gly Val Ser Leu Gln Tyr Arg Arg Leu Gly Gln Gln Leu Lys
    210                 215                 220

Arg Ile Pro Ser Cys Phe Asn Pro Ser Arg Ser Asp Phe Gly Leu Ser
225                 230                 235                 240

Gly Ile Phe Val Glu His Ala Arg Leu Leu Lys Ile Val Gln His Phe
                245                 250                 255

Asn Tyr Ser Phe Met Glu Ile Ala Phe Val Glu Val Val Ile Ile Cys
            260                 265                 270

Gly Leu Tyr Cys Ser Val Ile Cys Gln Tyr Ile Met Pro His Thr Asn
        275                 280                 285

Gln Asn Phe Ala Phe Leu Gly Phe Phe Ser Leu Val Val Thr Thr Gln
    290                 295                 300

Leu Cys Ile Tyr Leu Phe Gly Ala Glu Gln Val Arg Leu Glu Ala Glu
305                 310                 315                 320

Arg Phe Ser Arg Leu Leu Tyr Glu Val Ile Pro Trp Gln Asn Leu Pro
                325                 330                 335

Pro Lys His Arg Lys Leu Phe Leu Phe Pro Ile Glu Arg Ala Gln Arg
            340                 345                 350

Glu Thr Val Leu Gly Ala Tyr Phe Phe Glu Leu Gly Arg Pro Leu Leu
        355                 360                 365

Val Trp Val Ser Ile Phe Leu Phe Ile Val Leu Leu Phe
    370                 375                 380
```

```
<210> SEQ ID NO 83
<211> LENGTH: 927
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster  DOR77

<400> SEQUENCE: 83

atggaattga tgcgagtgcc agtacagttt tacagaacga ttggagagga tatctacgcc      60

catcgatcca cgaatcccct aaaatcgctt ctcttcaaga tctatctata tgcgggattc     120

ataaatttta atctgttggt aatcggtgaa ctggtgttct tctacaactc aattcaggac     180

tttgaaacca ttcgattggc catcgcggtg gctccatgta tcggattttc tctggttgct     240

gattttaaac aagctgccat gattagaggc aagaaaacac taattatgct actcgatgat     300

ttggagaaca tgcatccgaa aaccctggca aagcaaatgg aatacaaatt gccggacttt     360

gaaaagacca tgaaacgtgt gatcaatata ttcacctttc tctgcttggc ctatacgact     420

acgttctcct tttatccggc catcaaggca tccgtgaaat ttaatttctt gggctacgac     480

acctttgatc gaaattttgg tttcctcatc tggtttccct tcgatgcaac aaggaataat     540

ttgatatact ggatcatgta ctgggacata gcccatgggg cctatctagc ggcctttcag     600
```

-continued

```
gtcaccgaat caacagtgga agtgattatt atttactgca ttttttgat gacctcgatg    660

gttcaggtat ttatggtgtg ctactatggg gatactttaa ttgccgcgag cttgaaagtg    720

ggcgatgccg cttacaacca aaagtggttt cagtgcagca aatcctattg caccatgttg    780

aagttgctaa tcatgaggag tcagaaacca gcttcaataa gaccgccgac ttttcccccc    840

atatccttgg ttacctatat gaagaatccc ttcaacaatc tacccaaaca cagctcttcc    900

ctgcaaatca acgccaatcg ctatatc                                        927


<210> SEQ ID NO 84
<211> LENGTH: 309
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR77

<400> SEQUENCE: 84

Met Glu Leu Met Arg Val Pro Val Gln Phe Tyr Arg Thr Ile Gly Glu
1               5                   10                  15

Asp Ile Tyr Ala His Arg Ser Thr Asn Pro Leu Lys Ser Leu Leu Phe
            20                  25                  30

Lys Ile Tyr Leu Tyr Ala Gly Phe Ile Asn Phe Asn Leu Leu Val Ile
        35                  40                  45

Gly Glu Leu Val Phe Phe Tyr Asn Ser Ile Gln Asp Phe Glu Thr Ile
    50                  55                  60

Arg Leu Ala Ile Ala Val Ala Pro Cys Ile Gly Phe Ser Leu Val Ala
65                  70                  75                  80

Asp Phe Lys Gln Ala Ala Met Ile Arg Gly Lys Lys Thr Leu Ile Met
                85                  90                  95

Leu Leu Asp Asp Leu Glu Asn Met His Pro Lys Thr Leu Ala Lys Gln
            100                 105                 110

Met Glu Tyr Lys Leu Pro Asp Phe Glu Lys Thr Met Lys Arg Val Ile
        115                 120                 125

Asn Ile Phe Thr Phe Leu Cys Leu Ala Tyr Thr Thr Thr Phe Ser Phe
    130                 135                 140

Tyr Pro Ala Ile Lys Ala Ser Val Lys Phe Asn Phe Leu Gly Tyr Asp
145                 150                 155                 160

Thr Phe Asp Arg Asn Phe Gly Phe Leu Ile Trp Phe Pro Phe Asp Ala
                165                 170                 175

Thr Arg Asn Asn Leu Ile Tyr Trp Ile Met Tyr Trp Asp Ile Ala His
            180                 185                 190

Gly Ala Tyr Leu Ala Ala Phe Gln Val Thr Glu Ser Thr Val Glu Val
        195                 200                 205

Ile Ile Ile Tyr Cys Ile Phe Leu Met Thr Ser Met Val Gln Val Phe
    210                 215                 220

Met Val Cys Tyr Tyr Gly Asp Thr Leu Ile Ala Ala Ser Leu Lys Val
225                 230                 235                 240

Gly Asp Ala Ala Tyr Asn Gln Lys Trp Phe Gln Cys Ser Lys Ser Tyr
                245                 250                 255

Cys Thr Met Leu Lys Leu Leu Ile Met Arg Ser Gln Lys Pro Ala Ser
            260                 265                 270

Ile Arg Pro Pro Thr Phe Pro Pro Ile Ser Leu Val Thr Tyr Met Lys
        275                 280                 285

Asn Pro Phe Asn Asn Leu Pro Lys His Ser Ser Ser Leu Gln Ile Asn
    290                 295                 300
```

-continued

```
Ala Asn Arg Tyr Ile
305

<210> SEQ ID NO 85
<211> LENGTH: 1152
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DOR78

<400> SEQUENCE: 85

atgaagttca tgaagtacgc agttttcttt tacacatcgg tgggcattga gccgtatacg     60

attgactcgc ggtccaaaaa agcgagccta tggtcacatc ttctcttctg ggccaatgtg    120

atcaatttaa gtgtcattgt tttcggagag atcctctatc tgggagtggc ctattccgat    180

ggaaagttca ttgatgccgt cactgtactg tcatatatcg gattcgtaat cgtgggcatg    240

agcaagatgt tcttcatatg gtggaagaag accgatctaa gcgatttggt taaggaattg    300

gagcacatct atccaaatgg caaagctgag gaggagatgt atcggttgga taggtatctg    360

cgatcttgtt cacgaattag cattacctat gcactactct actccgtact catctggacc    420

ttcaatctgt tcagtatcat gcaattcctt gtctatgaaa agttgcttaa aatccgagtg    480

gtcggccaaa cgctgccata tttgatgtac tttccctgga actggcatga aaactggacg    540

tattatgtgc tgctgttctg tcaaaacttc gcaggacata cttcggcatc gggacagatc    600

tctacggatc ttttgctttg tgctgttgct acccaggtgg taatgcactt cgattacttg    660

gccagagtgg tggaaaaaca agtgttagat cgcgattgga gcgaaaactc cagatttttg    720

gcaaaaactg tacaatatca tcagcgcatt cttcggctaa tggacgttct caacgatata    780

ttcgggatac cgctactgct taactttatg gtctccacat ttgtcatctg ctttgtggga    840

ttccaaatga ccgtgggtgt cccgccggac atcatgatta agctcttctt gttcctgttc    900

tcgtccttgt cgcaagtgta cttgatatgc cactacggcc agctgattgc cgatgcggta    960

agagactttc gaagctctag cttatcgatt tctgcatata agcagaattg gcaaaatgct   1020

gacattcgct atcgtcgggc tctggtattc tttatagctc gacctcagag gacaacttat   1080

ctaaaagcta caattttcat gaatataaca agggccacca tgacggacgt aagatacaat   1140

ttgaaatgtc at                                                        1152

<210> SEQ ID NO 86
<211> LENGTH: 384
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster    DOR78

<400> SEQUENCE: 86

Met Lys Phe Met Lys Tyr Ala Val Phe Phe Tyr Thr Ser Val Gly Ile
1               5                   10                  15

Glu Pro Tyr Thr Ile Asp Ser Arg Ser Lys Lys Ala Ser Leu Trp Ser
            20                  25                  30

His Leu Leu Phe Trp Ala Asn Val Ile Asn Leu Ser Val Ile Val Phe
        35                  40                  45

Gly Glu Ile Leu Tyr Leu Gly Val Ala Tyr Ser Asp Gly Lys Phe Ile
    50                  55                  60

Asp Ala Val Thr Val Leu Ser Tyr Ile Gly Phe Val Ile Val Gly Met
65                  70                  75                  80

Ser Lys Met Phe Phe Ile Trp Trp Lys Lys Thr Asp Leu Ser Asp Leu
```

-continued

```
                85                  90                  95

Val Lys Glu Leu Glu His Ile Tyr Pro Asn Gly Lys Ala Glu Glu Glu
            100                 105                 110

Met Tyr Arg Leu Asp Arg Tyr Leu Arg Ser Cys Ser Arg Ile Ser Ile
        115                 120                 125

Thr Tyr Ala Leu Leu Tyr Ser Val Leu Ile Trp Thr Phe Asn Leu Phe
    130                 135                 140

Ser Ile Met Gln Phe Leu Val Tyr Glu Lys Leu Leu Lys Ile Arg Val
145                 150                 155                 160

Val Gly Gln Thr Leu Pro Tyr Leu Met Tyr Phe Pro Trp Asn Trp His
                165                 170                 175

Glu Asn Trp Thr Tyr Tyr Val Leu Leu Phe Cys Gln Asn Phe Ala Gly
            180                 185                 190

His Thr Ser Ala Ser Gly Gln Ile Ser Thr Asp Leu Leu Leu Cys Ala
        195                 200                 205

Val Ala Thr Gln Val Val Met His Phe Asp Tyr Leu Ala Arg Val Val
    210                 215                 220

Glu Lys Gln Val Leu Asp Arg Asp Trp Ser Glu Asn Ser Arg Phe Leu
225                 230                 235                 240

Ala Lys Thr Val Gln Tyr His Gln Arg Ile Leu Arg Leu Met Asp Val
                245                 250                 255

Leu Asn Asp Ile Phe Gly Ile Pro Leu Leu Leu Asn Phe Met Val Ser
            260                 265                 270

Thr Phe Val Ile Cys Phe Val Gly Phe Gln Met Thr Val Gly Val Pro
        275                 280                 285

Pro Asp Ile Met Ile Lys Leu Phe Leu Phe Leu Phe Ser Ser Leu Ser
    290                 295                 300

Gln Val Tyr Leu Ile Cys His Tyr Gly Gln Leu Ile Ala Asp Ala Val
305                 310                 315                 320

Arg Asp Phe Arg Ser Ser Ser Leu Ser Ile Ser Ala Tyr Lys Gln Asn
                325                 330                 335

Trp Gln Asn Ala Asp Ile Arg Tyr Arg Arg Ala Leu Val Phe Phe Ile
            340                 345                 350

Ala Arg Pro Gln Arg Thr Thr Tyr Leu Lys Ala Thr Ile Phe Met Asn
        355                 360                 365

Ile Thr Arg Ala Thr Met Thr Asp Val Arg Tyr Asn Leu Lys Cys His
    370                 375                 380
```

<210> SEQ ID NO 87
<211> LENGTH: 1203
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR81

<400> SEQUENCE: 87

```
atgatggaga cgctgcgaaa ttcgggcttg aatttgaaga acgatttcgg tataggccgc     60

aagatttgga gggtgttttc gttcacctac aatatggtga tacttcccgt aagtttccca    120

atcaactatg tgatacatct ggcggagttc ccgccggagc tgctgctgca atccctgcaa    180

ctgtgcctca acacttggtg cttcgctctg aagttcttca ctctgatcgt ctatacgcac    240

cgcttggagc tggccaacaa gcactttgac gaattggata agtactgcgt gaagccggcg    300

gagaagcgca aggttcgcga catggtggcc actattacaa gactgtacct gaccttcgtc    360
```

-continued

```
gtggtctacg tcctctacgc cacctccacg ctactggacg gactactgca ccaccgtgtt    420

ccctacaata cgtactatcc gttcataaac tggcgagtcg atcggaccca gatgtacatc    480

cagagttttc tggagtactt caccgtgggt tatgccatat atgtggccac cgccaccgat    540

tcctaccctg tgatttacgt ggcagccctg cgaactcata ttctcttgct caaggaccgt    600

atcatttact tgggcgatcc cagcaacgag ggtagcagcg acccgagcta catgtttaaa    660

tcgttggtgg attgtatcaa ggcacacaga accatgctaa agtgcagttt ttgtgatgcc    720

attcaaccaa tcatctctgg cacgatattt gcccaattca tcatatgcgg atcgatcctg    780

ggcataatta tgatcaacat ggtattgttc gctgatcaat cgacccgatt cggcatagtc    840

atctacgtta tggccgtcct tctgcagact tttccgcttt gcttctactg caacgccatc    900

gtggacgact gcaaagaact ggcccacgca cttttccatt ccgcctggtg ggtgcaggac    960

aagcgatacc agcggactgt catccagttc ctgcagaaac tgcagcagcc catgaccttc   1020

accgccatga acatatttaa cattaatttg gccactaaca tcaatgtaag tccactgctc   1080

tcggttagaa cggggaagga agcaaagtcc gaacttcaat ccttgcaggt agccaagttc   1140

gccttcaccg tgtacgccat cgcgagcggt atgaacctgg accaaaagtt aagcattaag   1200

gaa                                                                 1203
```

```
<210> SEQ ID NO 88
<211> LENGTH: 399
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DOR81

<400> SEQUENCE: 88

Met Met Glu Thr Leu Arg Asn Ser Gly Leu Asn Leu Lys Asn Asp Phe
1               5                   10                  15

Gly Ile Gly Arg Lys Ile Trp Arg Val Phe Ser Phe Thr Tyr Asn Met
            20                  25                  30

Val Ile Leu Pro Val Ser Phe Pro Ile Asn Tyr Val Ile His Leu Ala
        35                  40                  45

Glu Phe Pro Pro Glu Leu Leu Leu Gln Ser Leu Gln Leu Cys Leu Asn
    50                  55                  60

Thr Trp Cys Phe Ala Leu Lys Phe Phe Thr Leu Ile Val Tyr Thr His
65                  70                  75                  80

Arg Leu Glu Leu Ala Asn Lys His Phe Asp Glu Leu Asp Lys Tyr Cys
                85                  90                  95

Val Lys Pro Ala Glu Lys Arg Lys Val Arg Asp Met Val Ala Thr Ile
            100                 105                 110

Thr Arg Leu Tyr Leu Thr Phe Val Val Val Tyr Val Leu Tyr Ala Thr
        115                 120                 125

Ser Thr Leu Leu Asp Gly Leu Leu His His Arg Val Pro Tyr Asn Thr
    130                 135                 140

Tyr Tyr Pro Phe Ile Asn Trp Arg Val Asp Arg Thr Gln Met Tyr Ile
145                 150                 155                 160

Gln Ser Phe Leu Glu Tyr Phe Thr Val Gly Tyr Ala Ile Tyr Val Ala
                165                 170                 175

Thr Ala Thr Asp Ser Tyr Pro Val Ile Tyr Val Ala Ala Leu Arg Thr
            180                 185                 190

His Ile Leu Leu Leu Lys Asp Arg Ile Ile Tyr Leu Gly Asp Pro Ser
        195                 200                 205
```

-continued

```
Asn Glu Gly Ser Ser Asp Pro Ser Tyr Met Phe Lys Ser Leu Val Asp
    210                 215                 220

Cys Ile Lys Ala His Arg Thr Met Leu Asn Phe Cys Asp Ala Ile Gln
225                 230                 235                 240

Pro Ile Ile Ser Gly Thr Ile Phe Ala Gln Phe Ile Ile Cys Gly Ser
                245                 250                 255

Ile Leu Gly Ile Ile Met Ile Asn Met Val Leu Phe Ala Asp Gln Ser
            260                 265                 270

Thr Arg Phe Gly Ile Val Ile Tyr Val Met Ala Val Leu Leu Gln Thr
        275                 280                 285

Phe Pro Leu Cys Phe Tyr Cys Asn Ala Ile Val Asp Asp Cys Lys Glu
    290                 295                 300

Leu Ala His Ala Leu Phe His Ser Ala Trp Trp Val Gln Asp Lys Arg
305                 310                 315                 320

Tyr Gln Arg Thr Val Ile Gln Phe Leu Gln Lys Leu Gln Gln Pro Met
                325                 330                 335

Thr Phe Thr Ala Met Asn Ile Phe Asn Ile Asn Leu Ala Thr Asn Ile
            340                 345                 350

Asn Val Ser Pro Leu Leu Ser Val Arg Thr Gly Lys Glu Ala Lys Ser
        355                 360                 365

Glu Leu Gln Ser Leu Gln Val Ala Lys Phe Ala Phe Thr Val Tyr Ala
    370                 375                 380

Ile Ala Ser Gly Met Asn Leu Asp Gln Lys Leu Ser Ile Lys Glu
385                 390                 395
```

<210> SEQ ID NO 89
<211> LENGTH: 1179
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR82

<400> SEQUENCE: 89

```
atggcatgca taccaagata tcaatggaaa ggacgcccta ctgaaagaca gttctacgct      60

tcggagcaaa ggatagtgtt ccttcttgga accatttgcc agatattcca gattactgga     120

gtgcttatct attggtattg caatggccgt cttgccacgg aaacgggcac ctttgtggca     180

caattatctg aaatgtgcag ttctttttgt ctaacatttg tgggattctg taacgtttat     240

gcgatctcta caaaccgcaa tcaaattgaa acattactcg aggagcttca tcagatatat     300

ccgagataca ggaaaaatca ctatcgctgc cagcattatt ttgacatggc catgacaata     360

atgagaattg agtttctttt ctatatgatc ttgtacgtgt actacaatag tgcaccatta     420

tgggtgcttc tttgggaaca cttgcacgag gaatatgatc ttagcttcaa gacgcagacc     480

aacacttggt ttccatggaa agtccatggg tcggcacttg gatttggtat ggctgtacta     540

agcataaccg tgggatcctt tgtgggcgta ggtttcagta ttgtcaccca gaatcttatc     600

tgtttgttaa ccttccaact aaagttgcac tacgatggaa tatccagtca gttagtatct     660

ctcgattgcc gtcgtcctgg agctcataag gagttgagca tcctcatcgc ccaccacagc     720

cgaatccttc agctgggcga ccaagtcaat gacataatga actttgtatt cggctctagc     780

ctagtaggtg ccactattgc catttgtatg tcaagtgttt ctataatgct actggactta     840

gcatctgcct tcaaatatgc cagtggtcta gtggcattcg tcctctacaa ctttgtcatc     900

tgctacatgg gaaccgaggt cactttagct gtgaagattg gttcatatat ggacggaagg     960
```

-continued

```
cggtggatac ccaaagattc gttgctgaga tctcagaggc tacaggtgct cgtcgcagtt   1020

ggatttttta atatatgtgt cctctcgaat cgtcgtccta aaattgaaat tttgcttaga   1080

tattattacc atattatgtt ttattcattt aaattatatt tttctttaag gaaaggtagc   1140

ctttggaaaa tcttgtcttc tttcacctta ttgaggatc                          1179


&lt;210&gt; SEQ ID NO 90
&lt;211&gt; LENGTH: 393
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Drosophila Melanogaster   DOR82

&lt;400&gt; SEQUENCE: 90

Met Ala Cys Ile Pro Arg Tyr Gln Trp Lys Gly Arg Pro Thr Glu Arg
1               5                   10                  15

Gln Phe Tyr Ala Ser Glu Gln Arg Ile Val Phe Leu Leu Gly Thr Ile
            20                  25                  30

Cys Gln Ile Phe Gln Ile Thr Gly Val Leu Ile Tyr Trp Tyr Cys Asn
        35                  40                  45

Gly Arg Leu Ala Thr Glu Thr Gly Thr Phe Val Ala Gln Leu Ser Glu
    50                  55                  60

Met Cys Ser Ser Phe Cys Leu Thr Phe Val Gly Phe Cys Asn Val Tyr
65                  70                  75                  80

Ala Ile Ser Thr Asn Arg Asn Gln Ile Glu Thr Leu Leu Glu Glu Leu
                85                  90                  95

His Gln Ile Tyr Pro Arg Tyr Arg Lys Asn His Tyr Arg Cys Gln His
            100                 105                 110

Tyr Phe Asp Met Ala Met Thr Ile Met Arg Ile Glu Phe Leu Phe Tyr
        115                 120                 125

Met Ile Leu Tyr Val Tyr Tyr Asn Ser Ala Pro Leu Trp Val Leu Leu
    130                 135                 140

Trp Glu His Leu His Glu Glu Tyr Asp Leu Ser Phe Lys Thr Gln Thr
145                 150                 155                 160

Asn Thr Trp Phe Pro Trp Lys Val His Gly Ser Ala Leu Gly Phe Gly
                165                 170                 175

Met Ala Val Leu Ser Ile Thr Val Gly Ser Phe Val Gly Val Gly Phe
            180                 185                 190

Ser Ile Val Thr Gln Asn Leu Ile Cys Leu Leu Thr Phe Gln Leu Lys
        195                 200                 205

Leu His Tyr Asp Gly Ile Ser Ser Gln Leu Val Ser Leu Asp Cys Arg
    210                 215                 220

Arg Pro Gly Ala His Lys Glu Leu Ser Ile Leu Ile Ala His His Ser
225                 230                 235                 240

Arg Ile Leu Gln Leu Gly Asp Gln Val Asn Asp Ile Met Asn Phe Val
                245                 250                 255

Phe Gly Ser Ser Leu Val Gly Ala Thr Ile Ala Ile Cys Met Ser Ser
            260                 265                 270

Val Ser Ile Met Leu Leu Asp Leu Ala Ser Ala Phe Lys Tyr Ala Ser
        275                 280                 285

Gly Leu Val Ala Phe Val Leu Tyr Asn Phe Val Ile Cys Tyr Met Gly
    290                 295                 300

Thr Glu Val Thr Leu Ala Val Lys Ile Gly Ser Tyr Met Asp Gly Arg
305                 310                 315                 320
```

-continued

```
Arg Trp Ile Pro Lys Asp Ser Leu Leu Arg Ser Gln Arg Leu Gln Val
                325                 330                 335

Leu Val Ala Val Gly Phe Phe Asn Ile Cys Val Leu Ser Asn Arg Arg
            340                 345                 350

Pro Lys Ile Glu Ile Leu Leu Arg Tyr Tyr Tyr His Ile Met Phe Tyr
        355                 360                 365

Ser Phe Lys Leu Tyr Phe Ser Leu Arg Lys Gly Ser Leu Trp Lys Ile
    370                 375                 380

Leu Ser Ser Phe Thr Leu Leu Arg Ile
385                 390
```

<210> SEQ ID NO 91
<211> LENGTH: 1209
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR83

<400> SEQUENCE: 91

```
atgcagttgg aggactttat gcggtacccg gacctcgtgt gtcaagcggc ccaacttccc     60

agatacacgt ggaatggcag acgatccttg gaagttaaac gcaacttggc aaaacgcatt    120

atcttctggc ttggagcagt aaatttggtt tatcacaata ttggctgcgt catgtatggc    180

tatttcggtg atggaagaac aaaggatcca attgcgtatt tagctgaatt ggcatctgtg    240

gccagcatgc ttggtttcac cattgtgggc accctcaact tgtggaagat gctgagcctt    300

aagacccatt ttgagaacct actaaatgaa ttcgaggaat tatttcaact aatcaagcac    360

agggcgtatc gcatacacca ctatcaagaa aagtatacgc gtcatatacg aaatacattt    420

attttccata cctctgccgt tgtctactac aactcactac caattcttct aatgattcgg    480

gaacatttct cgaactcaca gcagttgggc tatagaattc agagtaatac ctggtatccc    540

tggcaggttc agggatcaat tcctggattt tttgctgcag tcgcctgtca aatcttttcg    600

tgccaaacca atatgtgcgt caatatgttt atccagtttc tgatcaactt ttttggtatc    660

cagctagaaa tacacttcga tggtttggcc aggcagctgg agaccatcga tgcccgcaat    720

ccccatgcca aggatcaatt gaagtatctg attgtatatc acacaaaatt gcttaatcta    780

gccgacagag ttaatcgatc gtttaacttt acgtttctca taagtctgtc ggtatccatg    840

atatccaact gttttctggc attttccatg accatgttcg actttggcac ctctctaaaa    900

catttactcg gacttttgct attcatcaca tataattttt caatgtgccg cagtggtacg    960

cacttgattt taacgagtgg caaagtattg ccagcggcct tttataacaa ttggtatgaa   1020

ggcgatcttg tttatcgaag gatgctcctc atcctgatga tgcgtgctac gaaaccttat   1080

atgtggaaaa cctacaagct ggcacctgta tccataacta catatatggc agaatgcaaa   1140

acaaaagaag cccatgaaca acgccatttt agacgccatg aaagacaaaa acctcgggtt   1200

gcacgaata                                                           1209
```

<210> SEQ ID NO 92
<211> LENGTH: 403
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR83

<400> SEQUENCE: 92

```
Met Gln Leu Glu Asp Phe Met Arg Tyr Pro Asp Leu Val Cys Gln Ala
1               5                   10                  15
```

-continued

```
Ala Gln Leu Pro Arg Tyr Thr Trp Asn Gly Arg Arg Ser Leu Glu Val
            20                  25                  30

Lys Arg Asn Leu Ala Lys Arg Ile Ile Phe Trp Leu Gly Ala Val Asn
        35                  40                  45

Leu Val Tyr His Asn Ile Gly Cys Val Met Tyr Gly Tyr Phe Gly Asp
    50                  55                  60

Gly Arg Thr Lys Asp Pro Ile Ala Tyr Leu Ala Glu Leu Ala Ser Val
65                  70                  75                  80

Ala Ser Met Leu Gly Phe Thr Ile Val Gly Thr Leu Asn Leu Trp Lys
                85                  90                  95

Met Leu Ser Leu Lys Thr His Phe Glu Asn Leu Leu Asn Glu Phe Glu
            100                 105                 110

Glu Leu Phe Gln Leu Ile Lys His Arg Ala Tyr Arg Ile His His Tyr
        115                 120                 125

Gln Glu Lys Tyr Thr Arg His Ile Arg Asn Thr Phe Ile Phe His Thr
    130                 135                 140

Ser Ala Val Val Tyr Tyr Asn Ser Leu Pro Ile Leu Leu Met Ile Arg
145                 150                 155                 160

Glu His Phe Ser Asn Ser Gln Gln Leu Gly Tyr Arg Ile Gln Ser Asn
                165                 170                 175

Thr Trp Tyr Pro Trp Gln Val Gln Gly Ser Ile Pro Gly Phe Phe Ala
            180                 185                 190

Ala Val Ala Cys Gln Ile Phe Ser Cys Gln Thr Asn Met Cys Val Asn
        195                 200                 205

Met Phe Ile Gln Phe Leu Ile Asn Phe Phe Gly Ile Gln Leu Glu Ile
    210                 215                 220

His Phe Asp Gly Leu Ala Arg Gln Leu Glu Thr Ile Asp Ala Arg Asn
225                 230                 235                 240

Pro His Ala Lys Asp Gln Leu Lys Tyr Leu Ile Val Tyr His Thr Lys
                245                 250                 255

Leu Leu Asn Leu Ala Asp Arg Val Asn Arg Ser Phe Asn Phe Thr Phe
            260                 265                 270

Leu Ile Ser Leu Ser Val Ser Met Ile Ser Asn Cys Phe Leu Ala Phe
        275                 280                 285

Ser Met Thr Met Phe Asp Phe Gly Thr Ser Leu Lys His Leu Leu Gly
    290                 295                 300

Leu Leu Leu Phe Ile Thr Tyr Asn Phe Ser Met Cys Arg Ser Gly Thr
305                 310                 315                 320

His Leu Ile Leu Thr Ser Gly Lys Val Leu Pro Ala Ala Phe Tyr Asn
                325                 330                 335

Asn Trp Tyr Glu Gly Asp Leu Val Tyr Arg Arg Met Leu Leu Ile Leu
            340                 345                 350

Met Met Arg Ala Thr Lys Pro Tyr Met Trp Lys Thr Tyr Lys Leu Ala
        355                 360                 365

Pro Val Ser Ile Thr Thr Tyr Met Ala Glu Cys Lys Thr Lys Glu Ala
    370                 375                 380

His Glu Gln Arg His Phe Arg Arg His Glu Arg Gln Lys Pro Arg Val
385                 390                 395                 400

Ala Arg Ile
```

-continued

<210> SEQ ID NO 93
<211> LENGTH: 858
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR84

<400> SEQUENCE: 93

```
atggtgttta gtttttatgc cgaggtagcg actctggtgg acaggttacg cgataatgaa      60
aattttctcg agagctgcat cttactgagc tacgtgtcct ttgtggtcat gggcctctcc     120
aagataggtg ctgtaatgaa aaaaaagcca aaaatgacag ctttggtcag gcaattggag     180
acctgctttc cgtcgccaag tgcaaaggtt caagaggaat atgctgtgaa gtcctggctg     240
aaacgctgcc atatatacac aaagggattt ggtggtctct tcatgatcat gtatttcgct     300
cacgctctga ttcccttatt catatacttc attcaaagag tgctgctcca ctatccggat     360
gccaagcaga ttatgccgtt ttaccaactc gaaccttggg aatttcgcga ctcctggttg     420
ttttatccaa gctattttca ccagtcgtcg gccggatata cggctacatg tggatccatt     480
gccggtgacc taatgatctt cgctgtggtc ctgcaggtca tcatgcacta cgaaagactg     540
gccaaggttc ttagggagtt taagattcaa gcccataacg cacccaatgg agctaaggag     600
gatataagga agttgcagtc cctagtcgcc aatcacattg atatacttcg actcactgat     660
ctgatgaacg aggtctttgg aattcccttg ttgctaaact ttattgcatc tgcgctgctg     720
gtctgcctgg tgggagttca attaaccatc gctttaagtc cagagtattt ttgcaagcag     780
atgctatttc tgatttccgt actgcttgag gtctatctcc tttgctcctt cagccagagg     840
ttaatagatg ctgtatgt                                                   858
```

<210> SEQ ID NO 94
<211> LENGTH: 286
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR84

<400> SEQUENCE: 94

```
Met Val Phe Ser Phe Tyr Ala Glu Val Ala Thr Leu Val Asp Arg Leu
1               5                   10                  15

Arg Asp Asn Glu Asn Phe Leu Glu Ser Cys Ile Leu Leu Ser Tyr Val
            20                  25                  30

Ser Phe Val Val Met Gly Leu Ser Lys Ile Gly Ala Val Met Lys Lys
        35                  40                  45

Lys Pro Lys Met Thr Ala Leu Val Arg Gln Leu Glu Thr Cys Phe Pro
    50                  55                  60

Ser Pro Ser Ala Lys Val Gln Glu Glu Tyr Ala Val Lys Ser Trp Leu
65                  70                  75                  80

Lys Arg Cys His Ile Tyr Thr Lys Gly Phe Gly Gly Leu Phe Met Ile
                85                  90                  95

Met Tyr Phe Ala His Ala Leu Ile Pro Leu Phe Ile Tyr Phe Ile Gln
            100                 105                 110

Arg Val Leu Leu His Tyr Pro Asp Ala Lys Gln Ile Met Pro Phe Tyr
        115                 120                 125

Gln Leu Glu Pro Trp Glu Phe Arg Asp Ser Trp Leu Phe Tyr Pro Ser
    130                 135                 140

Tyr Phe His Gln Ser Ser Ala Gly Tyr Thr Ala Thr Cys Gly Ser Ile
145                 150                 155                 160

Ala Gly Asp Leu Met Ile Phe Ala Val Val Leu Gln Val Ile Met His
```

-continued

```
                165                 170                 175

Tyr Glu Arg Leu Ala Lys Val Leu Arg Glu Phe Lys Ile Gln Ala His
            180                 185                 190

Asn Ala Pro Asn Gly Ala Lys Glu Asp Ile Arg Lys Leu Gln Ser Leu
        195                 200                 205

Val Ala Asn His Ile Asp Ile Leu Arg Leu Thr Asp Leu Met Asn Glu
    210                 215                 220

Val Phe Gly Ile Pro Leu Leu Leu Asn Phe Ile Ala Ser Ala Leu Leu
225                 230                 235                 240

Val Cys Leu Val Gly Val Gln Leu Thr Ile Ala Leu Ser Pro Glu Tyr
                245                 250                 255

Phe Cys Lys Gln Met Leu Phe Leu Ile Ser Val Leu Leu Glu Val Tyr
            260                 265                 270

Leu Leu Cys Ser Phe Ser Gln Arg Leu Ile Asp Ala Val Cys
        275                 280                 285
```

<210> SEQ ID NO 95
<211> LENGTH: 1155
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR91

<400> SEQUENCE: 95

```
atggttcgtt acgtgccccg gttcgctgat ggtcagaaag taaagttggc ttggcccttg     60

gcggtttttc ggttaaatca catattctgg ccattggatc cgagcacagg gaaatggggc    120

cgatatctgg acaaggttct agctgttgcg atgtccttgg tttttatgca acacaacgat    180

gcagagctga ggtacttgcg cttcgaggca agtaatcgga atttggatgc ctttctcaca    240

ggaatgccaa cgtatttaat cctcgtggag gctcaattta gaagtcttca cattctactg    300

cacttcgaga agcttcagaa gtttttagaa atattctacg caaatattta tattgatccc    360

cgtaaggaac ccgaaatgtt tcgaaaagtg gatggaaaga tgataattaa cagattagtt    420

tcggccatgt acggtgcagt tatctctctg tatctaatcg cacccgtttt ttccatcatt    480

aaccaaagca aagattttct atactctatg atctttccgt tcgattcgga tcccttgtac    540

atatttgtgc cactgctttt gacaaacgta tgggttggca ttgtaataga taccatgatg    600

ttcggggaga cgaatttgtt gtgtgaacta attgtccacc taaatggtag ttatatgttg    660

ctcaagaggg acttgcagtt ggccattgaa aagatattag ttgcaaggga ccgtccgcat    720

atggccaaac agctaaaggt tttaattaca aaaactctcc gaaagaatgt ggctctaaat    780

cagtttggcc agcagctgga ggctcagtat actgtgcggg tttttattat gtttgcattc    840

gctgcgggcc ttttatgtgc tctttctttt aaggcttata cgacggattc cctcagcaca    900

atgtactacc ttacccattg ggagcaaatc ctgcagtact ctacaaatcc cagcgaaaat    960

ctgcgattac taaagctcat taacttggcc attgagatga acagcaagcc cttctatgtg   1020

acagggctaa aatattttcg cgttagtctg caggctggct taaaacgtca aaagtttctg   1080

cggtctgcca gctcatccac ccttagcacc gctgatgtgt tggcatttgc ttttgctttt   1140

actcgctggc tgctt                                                    1155
```

<210> SEQ ID NO 96
<211> LENGTH: 385
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR91

-continued

<400> SEQUENCE: 96

```
Met Val Arg Tyr Val Pro Arg Phe Ala Asp Gly Gln Lys Val Lys Leu
1               5                   10                  15

Ala Trp Pro Leu Ala Val Phe Arg Leu Asn His Ile Phe Trp Pro Leu
            20                  25                  30

Asp Pro Ser Thr Gly Lys Trp Gly Arg Tyr Leu Asp Lys Val Leu Ala
        35                  40                  45

Val Ala Met Ser Leu Val Phe Met Gln His Asn Asp Ala Glu Leu Arg
    50                  55                  60

Tyr Leu Arg Phe Glu Ala Ser Asn Arg Asn Leu Asp Ala Phe Leu Thr
65                  70                  75                  80

Gly Met Pro Thr Tyr Leu Ile Leu Val Glu Ala Gln Phe Arg Ser Leu
                85                  90                  95

His Ile Leu Leu His Phe Glu Lys Leu Gln Lys Phe Leu Glu Ile Phe
            100                 105                 110

Tyr Ala Asn Ile Tyr Ile Asp Pro Arg Lys Glu Pro Glu Met Phe Arg
        115                 120                 125

Lys Val Asp Gly Lys Met Ile Ile Asn Arg Leu Val Ser Ala Met Tyr
    130                 135                 140

Gly Ala Val Ile Ser Leu Tyr Leu Ile Ala Pro Val Phe Ser Ile Ile
145                 150                 155                 160

Asn Gln Ser Lys Asp Phe Leu Tyr Ser Met Ile Phe Pro Phe Asp Ser
                165                 170                 175

Asp Pro Leu Tyr Ile Phe Val Pro Leu Leu Leu Thr Asn Val Trp Val
            180                 185                 190

Gly Ile Val Ile Asp Thr Met Met Phe Gly Glu Thr Asn Leu Leu Cys
        195                 200                 205

Glu Leu Ile Val His Leu Asn Gly Ser Tyr Met Leu Leu Lys Arg Asp
    210                 215                 220

Leu Gln Leu Ala Ile Glu Lys Ile Leu Val Ala Arg Asp Arg Pro His
225                 230                 235                 240

Met Ala Lys Gln Leu Lys Val Leu Ile Thr Lys Thr Leu Arg Lys Asn
                245                 250                 255

Val Ala Leu Asn Gln Phe Gly Gln Gln Leu Glu Ala Gln Tyr Thr Val
            260                 265                 270

Arg Val Phe Ile Met Phe Ala Phe Ala Ala Gly Leu Leu Cys Ala Leu
        275                 280                 285

Ser Phe Lys Ala Tyr Thr Thr Asp Ser Leu Ser Thr Met Tyr Tyr Leu
    290                 295                 300

Thr His Trp Glu Gln Ile Leu Gln Tyr Ser Thr Asn Pro Ser Glu Asn
305                 310                 315                 320

Leu Arg Leu Leu Lys Leu Ile Asn Leu Ala Ile Glu Met Asn Ser Lys
                325                 330                 335

Pro Phe Tyr Val Thr Gly Leu Lys Tyr Phe Arg Val Ser Leu Gln Ala
            340                 345                 350

Gly Leu Lys Arg Gln Lys Phe Leu Arg Ser Ala Ser Ser Ser Thr Leu
        355                 360                 365

Ser Thr Ala Asp Val Leu Ala Phe Ala Phe Ala Phe Thr Arg Trp Leu
    370                 375                 380

Leu
```

-continued

385

<210> SEQ ID NO 97
<211> LENGTH: 1218
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster DOR92

<400> SEQUENCE: 97

```
atgtccgagt ggttacgctt tctgaaacgc gatcaacagc tggatgtgta ctttttgca     60

gtgccccgct tgagtttaga cataatgggc tattggccgg gcaaaactgg tgatacatgg    120

ccctggagat ccctgattca cttcgcaatc ctggccattg gcgtggccac cgaactgcat    180

gctggcatgt gttttctaga ccgacagcag attaccttgg cactggagac cctctgtcca    240

gctggcacat cggcggtcac gctgctcaag atgttcctaa tgctgcgctt tcgtcaggat    300

ctctccatta tgtggaaccg cctgaggggc ctgctcttcg atcccaactg ggagcgaccc    360

gagcagcggg acatccggct aaagcactcg gccatggcgg ctcgcatcaa tttctggccc    420

ctgtcagccg gattcttcac atgcaccacc tacaacctaa agccgatact gatcgcaatg    480

atattgtatc tccagaatcg ttacgaggac ttcgtttggt ttacaccctt caatatgact    540

atgcccaaag ttctgctaaa ctatccattt tttcccctga cctacatatt tattgcctat    600

acgggctatg tgaccatctt tatgttcggc ggctgtgatg gtttttattt cgagttctgt    660

gcccacctat cagctctttt cgaagtgctc caggcggaga tagaatcaat gtttagaccc    720

tacactgatc acttggaact gtcgccagtg cagctttaca ttttagagca aaagatgcga    780

tcagtaatca ttaggcacaa tgccatcatc gatttgacca gattttttcg tgatcgctat    840

accattatta ccctggccca ttttgtgtcc gccgccatgg tgattggatt cagcatggtt    900

aatctcctga cattgggcaa taatggtctg ggcgcaatgc tctatgtggc ctacacggtt    960

gccgctttga gccaactgct ggtttattgc tatggcggaa ctctggtggc cgaaagtagc   1020

actggtctgt gccgagccat gttctcctgt ccgtggcagc tttttaagcc taaacaacgt   1080

cgactcgttc agcttttgat tctcagatcg cagcgtcctg tttccatggc agtgccattc   1140

ttttcgccat cgttggctac ctttgctgcg attcttcaaa cttcgggttc cataattgcg   1200

ctggttaagt cctttcag                                                 1218
```

<210> SEQ ID NO 98
<211> LENGTH: 406
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR92

<400> SEQUENCE: 98

```
Met Ser Glu Trp Leu Arg Phe Leu Lys Arg Asp Gln Gln Leu Asp Val
1               5                   10                  15

Tyr Phe Phe Ala Val Pro Arg Leu Ser Leu Asp Ile Met Gly Tyr Trp
            20                  25                  30

Pro Gly Lys Thr Gly Asp Thr Trp Pro Trp Arg Ser Leu Ile His Phe
        35                  40                  45

Ala Ile Leu Ala Ile Gly Val Ala Thr Glu Leu His Ala Gly Met Cys
    50                  55                  60

Phe Leu Asp Arg Gln Gln Ile Thr Leu Ala Leu Glu Thr Leu Cys Pro
65                  70                  75                  80

Ala Gly Thr Ser Ala Val Thr Leu Leu Lys Met Phe Leu Met Leu Arg
```

-continued

```
                85                  90                  95

Phe Arg Gln Asp Leu Ser Ile Met Trp Asn Arg Leu Arg Gly Leu Leu
            100                 105                 110

Phe Asp Pro Asn Trp Glu Arg Pro Glu Gln Arg Asp Ile Arg Leu Lys
        115                 120                 125

His Ser Ala Met Ala Ala Arg Ile Asn Phe Trp Pro Leu Ser Ala Gly
    130                 135                 140

Phe Phe Thr Cys Thr Thr Tyr Asn Leu Lys Pro Ile Leu Ile Ala Met
145                 150                 155                 160

Ile Leu Tyr Leu Gln Asn Arg Tyr Glu Asp Phe Val Trp Phe Thr Pro
                165                 170                 175

Phe Asn Met Thr Met Pro Lys Val Leu Leu Asn Tyr Pro Phe Phe Pro
            180                 185                 190

Leu Thr Tyr Ile Phe Ile Ala Tyr Thr Gly Tyr Val Thr Ile Phe Met
        195                 200                 205

Phe Gly Gly Cys Asp Gly Phe Tyr Phe Glu Phe Cys Ala His Leu Ser
    210                 215                 220

Ala Leu Phe Glu Val Leu Gln Ala Glu Ile Glu Ser Met Phe Arg Pro
225                 230                 235                 240

Tyr Thr Asp His Leu Glu Leu Ser Pro Val Gln Leu Tyr Ile Leu Glu
                245                 250                 255

Gln Lys Met Arg Ser Val Ile Ile Arg His Asn Ala Ile Ile Asp Leu
            260                 265                 270

Thr Arg Phe Phe Arg Asp Arg Tyr Thr Ile Ile Thr Leu Ala His Phe
        275                 280                 285

Val Ser Ala Ala Met Val Ile Gly Phe Ser Met Val Asn Leu Leu Thr
    290                 295                 300

Leu Gly Asn Asn Gly Leu Gly Ala Met Leu Tyr Val Ala Tyr Thr Val
305                 310                 315                 320

Ala Ala Leu Ser Gln Leu Leu Val Tyr Cys Tyr Gly Gly Thr Leu Val
                325                 330                 335

Ala Glu Ser Ser Thr Gly Leu Cys Arg Ala Met Phe Ser Cys Pro Trp
            340                 345                 350

Gln Leu Phe Lys Pro Lys Gln Arg Arg Leu Val Gln Leu Leu Ile Leu
        355                 360                 365

Arg Ser Gln Arg Pro Val Ser Met Ala Val Pro Phe Phe Ser Pro Ser
    370                 375                 380

Leu Ala Thr Phe Ala Ala Ile Leu Gln Thr Ser Gly Ser Ile Ile Ala
385                 390                 395                 400

Leu Val Lys Ser Phe Gln
                405
```

```
<210> SEQ ID NO 99
<211> LENGTH: 1176
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DOR95

<400> SEQUENCE: 99

atgagcgaca aggtgaaggg aaaaaagcag gaggaaaagg atcaatcctt gcgggtgcaa      60

attctcgttt atcgctgcat gggcatcgat ttgtggagcc ccacgatggc gaatgaccgc     120

ccgtggctga cctttgtcac aatgggacca cttttcctgt ttatggtgcc catgttcctg     180
```

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```
gccgcccacg agtacatcac ccaggtgagc ctgctctccg acaccctggg ctccaccttc    240

gccagcatgc tcaccctggt caaattcctg ctcttctgct atcatcgcaa ggagttcgtc    300

ggcctgatct accacatcag ggccattctg gctaaagaaa tcgaagtgtg gcctgatgcg    360

cgggaaatca tcgaggtgga gaaccaaagt gaccaaatgc tcagtcttac gtacactcgc    420

tgttttggac tggctggaat ctttgcggcc ctgaagccct ttgtgggcat catactctcc    480

tcgattcgcg gcgacgagat tcacctggag ctgccccaca acggcgttta cccgtacgat    540

ctccaggtgg tcatgtttta tgtgcccacc tatctgtgga atgtgatggc cagctatagt    600

gctgtaacca tggcactctg cgtggactcg ctgctcttct ttttcaccta caacgtgtgc    660

gccattttca agatcgccaa gcaccggatg atccatctgc cggcggtggg cggaaaggag    720

gagctggagg ggctcgtcca ggtgctgctg ctgcaccaga agggcctcca gatcgccgat    780

cacattgcgg acaagtaccg gccgctgatc tttttgcagt tctttctgtc cgccttgcag    840

atctgcttca ttggattcca ggtggctgat ctgtttccca atccgcagag tctctacttt    900

atcgcctttg tgggctcgct gctcatcgca ctgttcatct actcgaagtg cggcgaaaat    960

atcaagagtg ccagcctgga tttcggaaac gggctgtacg agaccaactg gaccgacttc   1020

tcgccaccca ctaaaagagc cctcctcatt gccgccatgc gcgcccagcg accttgccag   1080

atgaagggct actttttcga ggccagcatg gccaccttct cgacgattgt tcgctctgcc   1140

gtgtcgtaca tcatgatgtt gcgctccttt aatgcc                             1176
```

```
<210> SEQ ID NO 100
<211> LENGTH: 392
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster  DOR95

<400> SEQUENCE: 100

Met Ser Asp Lys Val Lys Gly Lys Lys Gln Glu Glu Lys Asp Gln Ser
1               5                   10                  15

Leu Arg Val Gln Ile Leu Val Tyr Arg Cys Met Gly Ile Asp Leu Trp
            20                  25                  30

Ser Pro Thr Met Ala Asn Asp Arg Pro Trp Leu Thr Phe Val Thr Met
        35                  40                  45

Gly Pro Leu Phe Leu Phe Met Val Pro Met Phe Leu Ala Ala His Glu
    50                  55                  60

Tyr Ile Thr Gln Val Ser Leu Leu Ser Asp Thr Leu Gly Ser Thr Phe
65                  70                  75                  80

Ala Ser Met Leu Thr Leu Val Lys Phe Leu Leu Phe Cys Tyr His Arg
                85                  90                  95

Lys Glu Phe Val Gly Leu Ile Tyr His Ile Arg Ala Ile Leu Ala Lys
            100                 105                 110

Glu Ile Glu Val Trp Pro Asp Ala Arg Glu Ile Ile Glu Val Glu Asn
        115                 120                 125

Gln Ser Asp Gln Met Leu Ser Leu Thr Tyr Thr Arg Cys Phe Gly Leu
    130                 135                 140

Ala Gly Ile Phe Ala Ala Leu Lys Pro Phe Val Gly Ile Ile Leu Ser
145                 150                 155                 160

Ser Ile Arg Gly Asp Glu Ile His Leu Glu Leu Pro His Asn Gly Val
                165                 170                 175

Tyr Pro Tyr Asp Leu Gln Val Val Met Phe Tyr Val Pro Thr Tyr Leu
```

-continued

```
            180                 185                 190

Trp Asn Val Met Ala Ser Tyr Ser Ala Val Thr Met Ala Leu Cys Val
        195                 200                 205

Asp Ser Leu Leu Phe Phe Phe Thr Tyr Asn Val Cys Ala Ile Phe Lys
    210                 215                 220

Ile Ala Lys His Arg Met Ile His Leu Pro Ala Val Gly Gly Lys Glu
225                 230                 235                 240

Glu Leu Glu Gly Leu Val Gln Val Leu Leu Leu His Gln Lys Gly Leu
                245                 250                 255

Gln Ile Ala Asp His Ile Ala Asp Lys Tyr Arg Pro Leu Ile Phe Leu
            260                 265                 270

Gln Phe Phe Leu Ser Ala Leu Gln Ile Cys Phe Ile Gly Phe Gln Val
        275                 280                 285

Ala Asp Leu Phe Pro Asn Pro Gln Ser Leu Tyr Phe Ile Ala Phe Val
    290                 295                 300

Gly Ser Leu Leu Ile Ala Leu Phe Ile Tyr Ser Lys Cys Gly Glu Asn
305                 310                 315                 320

Ile Lys Ser Ala Ser Leu Asp Phe Gly Asn Gly Leu Tyr Glu Thr Asn
                325                 330                 335

Trp Thr Asp Phe Ser Pro Pro Thr Lys Arg Ala Leu Leu Ile Ala Ala
            340                 345                 350

Met Arg Ala Gln Arg Pro Cys Gln Met Lys Gly Tyr Phe Phe Glu Ala
        355                 360                 365

Ser Met Ala Thr Phe Ser Thr Ile Val Arg Ser Ala Val Ser Tyr Ile
    370                 375                 380

Met Met Leu Arg Ser Phe Asn Ala
385                 390


<210> SEQ ID NO 101
<211> LENGTH: 1170
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster  DOR99

<400> SEQUENCE: 101

atggaggagt ttctgcgtcc gcagatgttc caggaggtgg ctcagatggt gcatttccag     60

tggcggagaa atccggtgga caacagcatg gtgaacgcat ccatggtccc cttctgcttg    120

tcggcgtttc ttaatgtcct gtttttcggc tgcaatggtt gggacatcat aggacatttt    180

tggctgggac atcctgccaa ccagaatccg cccgtgctta gcatcaccat ttacttctcg    240

atcaggggat tgatgctata cctgaaacga aaggaaatcg ttgagtttgt taacgacttg    300

gatcgggagt gtccgcggga cttggtcagc cagttggaca tgcaaatgga tgagacgtac    360

cgaaactttt ggcagcgcta tcgcttcatc cgtatctact cccatttggg tggtccgatg    420

ttctgcgttg tgccattagc tctattcctc ctgacccacg agggtaaaga tactcctgtt    480

gcccagcacg agcagctcct tggaggatgg ctgccatgcg gtgtgcgaaa ggacccaaat    540

ttctaccttt tagtctggtc cttcgacctg atgtgcacca cttgcggcgt ctcctttttc    600

gttaccttcg acaacctatt caatgtgatg cagggacatt tggtcatgca tttgggccat    660

cttgctcgcc agttttcggc catcgatcct cgacagagtt tgaccgatga gaagcgattc    720

tttgtggatc ttaggttatt agttcagagg cagcagcttc ttaatggatt gtgcagaaaa    780

tacaacgaca tctttaaagt ggccttcctg gtgagcaatt ttgtaggcgc cggttccctc    840
```

-continued

```
tgcttctacc tctttatgct ctcggagaca tcagatgtcc ttatcatcgc ccagtatata    900

ttacccactt tggtcctggt gggcttcaca tttgagattt gtctacgggg aacccaactg    960

gaaaaggcgt cggagggact ggaatcgtcg ttgcgaagcc aggaatggta tttgggaagt   1020

aggcggtacc ggaagttcta tttgctctgg acgcaatatt gccagcgaac acagcaactg   1080

ggcgcctttg ggctaatcca agtcaatatg gtgcacttca ctgaaataat gcagctggcc   1140

tatagactct tcacttttct caaatctcat                                    1170


&lt;210&gt; SEQ ID NO 102
&lt;211&gt; LENGTH: 390
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Drosophila Melanogaster   DOR99

&lt;400&gt; SEQUENCE: 102

Met Glu Glu Phe Leu Arg Pro Gln Met Phe Gln Glu Val Ala Gln Met
1               5                   10                  15

Val His Phe Gln Trp Arg Arg Asn Pro Val Asp Asn Ser Met Val Asn
            20                  25                  30

Ala Ser Met Val Pro Phe Cys Leu Ser Ala Phe Leu Asn Val Leu Phe
        35                  40                  45

Phe Gly Cys Asn Gly Trp Asp Ile Ile Gly His Phe Trp Leu Gly His
    50                  55                  60

Pro Ala Asn Gln Asn Pro Pro Val Leu Ser Ile Thr Ile Tyr Phe Ser
65                  70                  75                  80

Ile Arg Gly Leu Met Leu Tyr Leu Lys Arg Lys Glu Ile Val Glu Phe
                85                  90                  95

Val Asn Asp Leu Asp Arg Glu Cys Pro Arg Asp Leu Val Ser Gln Leu
            100                 105                 110

Asp Met Gln Met Asp Glu Thr Tyr Arg Asn Phe Trp Gln Arg Tyr Arg
        115                 120                 125

Phe Ile Arg Ile Tyr Ser His Leu Gly Gly Pro Met Phe Cys Val Val
    130                 135                 140

Pro Leu Ala Leu Phe Leu Leu Thr His Glu Gly Lys Asp Thr Pro Val
145                 150                 155                 160

Ala Gln His Glu Gln Leu Leu Gly Gly Trp Leu Pro Cys Gly Val Arg
                165                 170                 175

Lys Asp Pro Asn Phe Tyr Leu Leu Val Trp Ser Phe Asp Leu Met Cys
            180                 185                 190

Thr Thr Cys Gly Val Ser Phe Phe Val Thr Phe Asp Asn Leu Phe Asn
        195                 200                 205

Val Met Gln Gly His Leu Val Met His Leu Gly His Leu Ala Arg Gln
    210                 215                 220

Phe Ser Ala Ile Asp Pro Arg Gln Ser Leu Thr Asp Glu Lys Arg Phe
225                 230                 235                 240

Phe Val Asp Leu Arg Leu Leu Val Gln Arg Gln Gln Leu Leu Asn Gly
                245                 250                 255

Leu Cys Arg Lys Tyr Asn Asp Ile Phe Lys Val Ala Phe Leu Val Ser
            260                 265                 270

Asn Phe Val Gly Ala Gly Ser Leu Cys Phe Tyr Leu Phe Met Leu Ser
        275                 280                 285

Glu Thr Ser Asp Val Leu Ile Ile Ala Gln Tyr Ile Leu Pro Thr Leu
```

-continued

```
    290                 295                 300

Val Leu Val Gly Phe Thr Phe Glu Ile Cys Leu Arg Gly Thr Gln Leu
305                 310                 315                 320

Glu Lys Ala Ser Glu Gly Leu Glu Ser Ser Leu Arg Ser Gln Glu Trp
                325                 330                 335

Tyr Leu Gly Ser Arg Arg Tyr Arg Lys Phe Tyr Leu Leu Trp Thr Gln
            340                 345                 350

Tyr Cys Gln Arg Thr Gln Gln Leu Gly Ala Phe Gly Leu Ile Gln Val
        355                 360                 365

Asn Met Val His Phe Thr Glu Ile Met Gln Leu Ala Tyr Arg Leu Phe
    370                 375                 380

Thr Phe Leu Lys Ser His
385                 390


<210> SEQ ID NO 103
<211> LENGTH: 1917
<212> TYPE: DNA
<213> ORGANISM: Drosophila Melanogaster   DORA45

<400> SEQUENCE: 103

ggcacgagct ggttccggaa agcctcatat ctcgtatctt aaagtatccc ggttaagcct     60

taaagagtga aatgattgcc tagacgattg ctgcattact ggcactcaat taacccaagt    120

gtaccagaca acaattacat ttgtattttt aaagttcaat agcaaggatg acaacctcga    180

tgcagccgag caagtacacg ggcctggtcg ccgacctgat gcccaacatc cgggcgatga    240

agtactccgg cctgttcatg cacaacttca cgggcggcag tgccttcatg aagaaggtgt    300

actcctccgt gcacctggtg ttcctcctca tgcagttcac cttcatcctg gtcaacatgg    360

ccctgaacgc cgaggaggtc aacgagctgt cgggcaacac gatcacgacc ctcttcttca    420

cccactgcat cacgaagttt atctacctgg ctgttaacca gaagaatttc tacagaacat    480

tgaatatatg gaaccaggtg aacacgcatc ccttgttcgc cgagtcggat gctcgttacc    540

attcgatcgc actggcgaag atgaggaagc tgttctttct ggtgatgctg accacagtcg    600

cctcggccac cgcctggacc acgatcacct tctttggcga cagcgtaaaa atggtggtgg    660

accatgagac gaactccagc atcccggtgg agataccccg gctgccgatt aagtccttct    720

acccgtggaa cgccagccac ggcatgttct acatgatcag ctttgccttt cagatctact    780

acgtgctctt ctcgatgatc cactccaatc tatgcgacgt gatgttctgc tcttggctga    840

tattcgcctg cgagcagctg cagcacttga agggcatcat gaagccgctg atggagctgt    900

ccgcctcgct ggacacctac aggcccaact cggcggccct cttcaggtcc ctgtcggcca    960

actccaagtc ggagctaatt cataatgaag aaaaggatcc cggcaccgac atggacatgt   1020

cgggcatcta cagctcgaaa gcggattggg gcgctcagtt tcgagcaccc tcgacactgc   1080

agtcctttgg cgggaacggg ggcggaggca acgggttggt gaacggcgct aatcccaacg   1140

ggctgaccaa aaagcaggag atgatggtgc gcagtgccat caagtactgg gtcgagcggc   1200

acaagcacgt ggtgcgactg gtggctgcca tcggcgatac ttacggagcc gccctcctcc   1260

tccacatgct gacctcgacc atcaagctga ccctgctggc ataccaggcc accaaaatca   1320

acggagtgaa tgtctacgcc ttcacagtcg tcggatacct aggatacgcg ctggcccagg   1380

tgttccactt ttgcatcttt ggcaatcgtc tgattgaaga gagttcatcc gtcatggagg   1440
```

-continued

```
ccgcctactc gtgccactgg tacgatggct ccgaggaggc caagaccttc gtccagatcg   1500

tgtgccagca gtgccagaag gcgatgagca tatcgggagc gaaattcttc accgtctccc   1560

tggatttgtt tgcttcggtt ctgggtgccg tcgtcaccta ctttatggtg ctggtgcagc   1620

tcaagtaagt tgctgcgaag ctgatggatt tttgtaccag aaaagcgaat gccaagaagc   1680

cacctaccgc cccttgcccc ctccgcactg tgcaaccagc aatatcacag agcaattata   1740

acgcaaatta tatattttat acctgcgacg agcgagcctc gtggggcata atggagacat   1800

tctggggcac atagaagcct gcaaatactt atcgattttg tacacgcgta gagcttttaa   1860

tgtaaactca agatgcaaac taaataaatg tgtagtgaaa aaaaaaaaaa aaaaaaa      1917
```

<210> SEQ ID NO 104
<211> LENGTH: 486
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster   DORA45

<400> SEQUENCE: 104

```
Met Thr Thr Ser Met Gln Pro Ser Lys Tyr Thr Gly Leu Val Ala Asp
1               5                   10                  15

Leu Met Pro Asn Ile Arg Ala Met Lys Tyr Ser Gly Leu Phe Met His
            20                  25                  30

Asn Phe Thr Gly Gly Ser Ala Phe Met Lys Lys Val Tyr Ser Ser Val
        35                  40                  45

His Leu Val Phe Leu Leu Met Gln Phe Thr Phe Ile Leu Val Asn Met
    50                  55                  60

Ala Leu Asn Ala Glu Glu Val Asn Glu Leu Ser Gly Asn Thr Ile Thr
65                  70                  75                  80

Thr Leu Phe Phe Thr His Cys Ile Thr Lys Phe Ile Tyr Leu Ala Val
                85                  90                  95

Asn Gln Lys Asn Phe Tyr Arg Thr Leu Asn Ile Trp Asn Gln Val Asn
            100                 105                 110

Thr His Pro Leu Phe Ala Glu Ser Asp Ala Arg Tyr His Ser Ile Ala
        115                 120                 125

Leu Ala Lys Met Arg Lys Leu Phe Phe Leu Val Met Leu Thr Thr Val
    130                 135                 140

Ala Ser Ala Thr Ala Trp Thr Thr Ile Thr Phe Phe Gly Asp Ser Val
145                 150                 155                 160

Lys Met Val Val Asp His Glu Thr Asn Ser Ser Ile Pro Val Glu Ile
                165                 170                 175

Pro Arg Leu Pro Ile Lys Ser Phe Tyr Pro Trp Asn Ala Ser His Gly
            180                 185                 190

Met Phe Tyr Met Ile Ser Phe Ala Phe Gln Ile Tyr Tyr Val Leu Phe
        195                 200                 205

Ser Met Ile His Ser Asn Leu Cys Asp Val Met Phe Cys Ser Trp Leu
    210                 215                 220

Ile Phe Ala Cys Glu Gln Leu Gln His Leu Lys Gly Ile Met Lys Pro
225                 230                 235                 240

Leu Met Glu Leu Ser Ala Ser Leu Asp Thr Tyr Arg Pro Asn Ser Ala
                245                 250                 255

Ala Leu Phe Arg Ser Leu Ser Ala Asn Ser Lys Ser Glu Leu Ile His
            260                 265                 270

Asn Glu Glu Lys Asp Pro Gly Thr Asp Met Asp Met Ser Gly Ile Tyr
```

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```
        275                 280                 285

Ser Ser Lys Ala Asp Trp Gly Ala Gln Phe Arg Ala Pro Ser Thr Leu
    290                 295                 300

Gln Ser Phe Gly Gly Asn Gly Gly Gly Gly Asn Gly Leu Val Asn Gly
305                 310                 315                 320

Ala Asn Pro Asn Gly Leu Thr Lys Lys Gln Glu Met Met Val Arg Ser
                325                 330                 335

Ala Ile Lys Tyr Trp Val Glu Arg His Lys His Val Val Arg Leu Val
            340                 345                 350

Ala Ala Ile Gly Asp Thr Tyr Gly Ala Ala Leu Leu Leu His Met Leu
        355                 360                 365

Thr Ser Thr Ile Lys Leu Thr Leu Leu Ala Tyr Gln Ala Thr Lys Ile
    370                 375                 380

Asn Gly Val Asn Val Tyr Ala Phe Thr Val Val Gly Tyr Leu Gly Tyr
385                 390                 395                 400

Ala Leu Ala Gln Val Phe His Phe Cys Ile Phe Gly Asn Arg Leu Ile
                405                 410                 415

Glu Glu Ser Ser Ser Val Met Glu Ala Ala Tyr Ser Cys His Trp Tyr
            420                 425                 430

Asp Gly Ser Glu Glu Ala Lys Thr Phe Val Gln Ile Val Cys Gln Gln
        435                 440                 445

Cys Gln Lys Ala Met Ser Ile Ser Gly Ala Lys Phe Phe Thr Val Ser
    450                 455                 460

Leu Asp Leu Phe Ala Ser Val Leu Gly Ala Val Val Thr Tyr Phe Met
465                 470                 475                 480

Val Leu Val Gln Leu Lys
                485
```

<210> SEQ ID NO 105
<211> LENGTH: 1317
<212> TYPE: DNA
<213> ORGANISM: Drosophila melanogaster DOR44

<400> SEQUENCE: 105

```
atgaagagca cattcaagga agaaaggatt aaggacgact ccaagcgtcg cgacctgttt      60

gtattcgtga ggcaaaccat gtgtatagcg gccatgtatc ccttcggtta ctacgtgaat     120

ggatctggag tcctggccgt tctggtgcga ttctgtgact tgacctacga gctctttaac     180

tacttcgttt cggtacacat agctggcctg tacatctgca ccatctacat caactatggg     240

caaggcgatt tggacttctt cgtgaactgt ttgatacaaa ccattattta tctgtggaca     300

atagcgatga aactctactt tcggaggttc agacctggtt tgttgaatac cattctgtcc     360

aacatcaatg atgagtacga gacacgttcg gctgtgggat tcagtttcgt cacaatggcg     420

ggatcctatc ggatgtccaa gctatggatc aaaacctatg tgtattgctg ctacataggc     480

accattttct ggctggctct tcccattgcc taccgggata ggagtcttcc tcttgcctgc     540

tggtatccct ttgactatac acaacccggt gtctatgagg tagtgttcct tctccaggcg     600

atgggacaga tccaagtggc cgcatccttt gcctcctcca gtggcctgca tatggtgctt     660

tgtgtgctga tatcagggca gtacgatgtc ctcttttgca gtctcaagaa tgtattagcc     720

agcagctatg tccttatggg agccaatatg acggaactga atcaattgca ggctgagcaa     780

tctgcggccg atgtcgagcc aggtcagtat gcttactccg tggaggagga gacacctttg     840
```

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```
caagaacttc taaaagttgg gagctcaatg gacttctcct ccgcattcag gctgtctttt    900

gtgcggtgca ttcagcacca tcgatacata gtggcggcac tgaagaaaat tgagagtttc    960

tacagtccca tatggttcgt gaagattggc gaagtcacct ttcttatgtg cctggtagcc   1020

ttcgtctcca cgaagagcac cgcggccaac tcattcatgc gaatggtctc cttgggccag   1080

tacctgctct tagttctcta cgagctgttc atcatctgct acttcgcgga catcgttttt   1140

cagaacagcc agcggtgcgg tgaagccctc tggcgaagtc cttggcagcg acatttgaag   1200

gatgttcgca gtgattacat gttctttatg ctgaattccc gcaggcagtt ccaacttacg   1260

gccggaaaaa taagcaatct aaacgtggat cgtttcagag gggtgggtat ccttact      1317


<210> SEQ ID NO 106
<211> LENGTH: 439
<212> TYPE: PRT
<213> ORGANISM: Drosophila melanogaster  DOR44

<400> SEQUENCE: 106

Met Lys Ser Thr Phe Lys Glu Glu Arg Ile Lys Asp Asp Ser Lys Arg
1               5                   10                  15

Arg Asp Leu Phe Val Phe Val Arg Gln Thr Met Cys Ile Ala Ala Met
            20                  25                  30

Tyr Pro Phe Gly Tyr Tyr Val Asn Gly Ser Gly Val Leu Ala Val Leu
        35                  40                  45

Val Arg Phe Cys Asp Leu Thr Tyr Glu Leu Phe Asn Tyr Phe Val Ser
    50                  55                  60

Val His Ile Ala Gly Leu Tyr Ile Cys Thr Ile Tyr Ile Asn Tyr Gly
65                  70                  75                  80

Gln Gly Asp Leu Asp Phe Phe Val Asn Cys Leu Ile Gln Thr Ile Ile
                85                  90                  95

Tyr Leu Trp Thr Ile Ala Met Lys Leu Tyr Phe Arg Arg Phe Arg Pro
            100                 105                 110

Gly Leu Leu Asn Thr Ile Leu Ser Asn Ile Asn Asp Glu Tyr Glu Thr
        115                 120                 125

Arg Ser Ala Val Gly Phe Ser Phe Val Thr Met Ala Gly Ser Tyr Arg
    130                 135                 140

Met Ser Lys Leu Trp Ile Lys Thr Tyr Val Tyr Cys Cys Tyr Ile Gly
145                 150                 155                 160

Thr Ile Phe Trp Leu Ala Leu Pro Ile Ala Tyr Arg Asp Arg Ser Leu
                165                 170                 175

Pro Leu Ala Cys Trp Tyr Pro Phe Asp Tyr Thr Gln Pro Gly Val Tyr
            180                 185                 190

Glu Val Val Phe Leu Leu Gln Ala Met Gly Gln Ile Gln Val Ala Ala
        195                 200                 205

Ser Phe Ala Ser Ser Ser Gly Leu His Met Val Leu Cys Val Leu Ile
    210                 215                 220

Ser Gly Gln Tyr Asp Val Leu Phe Cys Ser Leu Lys Asn Val Leu Ala
225                 230                 235                 240

Ser Ser Tyr Val Leu Met Gly Ala Asn Met Thr Glu Leu Asn Gln Leu
                245                 250                 255

Gln Ala Glu Gln Ser Ala Ala Asp Val Glu Pro Gly Gln Tyr Ala Tyr
            260                 265                 270
```

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```
Ser Val Glu Glu Glu Thr Pro Leu Gln Glu Leu Leu Lys Val Gly Ser
        275                 280                 285

Ser Met Asp Phe Ser Ser Ala Phe Arg Leu Ser Phe Val Arg Cys Ile
    290                 295                 300

Gln His His Arg Tyr Ile Val Ala Ala Leu Lys Lys Ile Glu Ser Phe
305                 310                 315                 320

Tyr Ser Pro Ile Trp Phe Val Lys Ile Gly Glu Val Thr Phe Leu Met
                325                 330                 335

Cys Leu Val Ala Phe Val Ser Thr Lys Ser Thr Ala Ala Asn Ser Phe
            340                 345                 350

Met Arg Met Val Ser Leu Gly Gln Tyr Leu Leu Leu Val Leu Tyr Glu
        355                 360                 365

Leu Phe Ile Ile Cys Tyr Phe Ala Asp Ile Val Phe Gln Asn Ser Gln
    370                 375                 380

Arg Cys Gly Glu Ala Leu Trp Arg Ser Pro Trp Gln Arg His Leu Lys
385                 390                 395                 400

Asp Val Arg Ser Asp Tyr Met Phe Phe Met Leu Asn Ser Arg Arg Gln
                405                 410                 415

Phe Gln Leu Thr Ala Gly Lys Ile Ser Asn Leu Asn Val Asp Arg Phe
            420                 425                 430

Arg Gly Val Gly Ile Leu Thr
        435
```

<210> SEQ ID NO 107
<211> LENGTH: 363
<212> TYPE: PRT
<213> ORGANISM: DROSOPHILA MELANOGASTER DOR61

<400> SEQUENCE: 107

```
Met Gly His Lys Asp Asp Met Asp Ser Thr Asp Ser Thr Ala Leu Ser
1               5                   10                  15

Leu Lys His Ile Ser Ser Leu Ile Phe Val Ile Ser Ala Gln Tyr Pro
            20                  25                  30

Leu Ile Ser Tyr Val Ala Tyr Asn Arg Asn Asp Met Glu Lys Val Thr
        35                  40                  45

Ala Cys Leu Ser Val Val Phe Thr Asn Met Leu Thr Val Ile Lys Ile
    50                  55                  60

Ser Thr Phe Leu Ala Asn Arg Lys Asp Phe Trp Glu Met Ile His Arg
65                  70                  75                  80

Phe Arg Lys Met His Glu Gln Cys Lys Tyr Arg Glu Gly Leu Asp Tyr
                85                  90                  95

Val Ala Glu Ala Asn Lys Leu Ala Ser Phe Leu Gly Arg Ala Tyr Cys
            100                 105                 110

Val Ser Cys Gly Leu Thr Gly Leu Tyr Phe Met Leu Gly Pro Ile Val
        115                 120                 125

Lys Ile Gly Val Cys Arg Trp His Gly Thr Thr Cys Asp Lys Glu Leu
    130                 135                 140

Pro Met Pro Met Lys Phe Pro Phe Asn Asp Leu Glu Ser Pro Gly Tyr
145                 150                 155                 160

Glu Val Cys Phe Leu Tyr Thr Val Leu Val Thr Val Val Val Val Ala
                165                 170                 175

Tyr Ala Ser Ala Val Asp Gly Leu Phe Ile Ser Phe Ala Ile Asn Leu
            180                 185                 190
```

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```
Arg Ala His Phe Gln Thr Leu Gln Arg Gln Ile Glu Asn Trp Glu Phe
        195                 200                 205

Pro Ser Ser Glu Pro Asp Thr Gln Ile Arg Leu Lys Ser Ile Val Glu
    210                 215                 220

Tyr His Val Leu Leu Leu Ser Leu Ser Arg Lys Leu Arg Ser Ile Tyr
225                 230                 235                 240

Thr Pro Thr Val Met Gly Gln Phe Val Ile Thr Ser Leu Gln Val Gly
                245                 250                 255

Val Ile Ile Tyr Gln Leu Val Thr Asn Met Asp Ser Val Met Asp Leu
            260                 265                 270

Leu Leu Tyr Ala Ser Phe Phe Gly Ser Ile Met Leu Gln Leu Phe Ile
        275                 280                 285

Tyr Cys Tyr Gly Gly Glu Ile Ile Lys Ala Glu Ser Leu Gln Val Asp
    290                 295                 300

Thr Ala Val Arg Leu Ser Asn Trp His Leu Ala Ser Pro Lys Thr Arg
305                 310                 315                 320

Thr Ser Leu Ser Leu Ile Ile Leu Gln Ser Gln Lys Glu Val Leu Ile
                325                 330                 335

Arg Ala Gly Phe Phe Val Ala Ser Leu Ala Asn Phe Pro Tyr Arg Leu
            340                 345                 350

Ile Thr Leu Ile Lys Ser Ile Asp Ser Ile Cys
        355                 360


<210> SEQ ID NO 108
<211> LENGTH: 411
<212> TYPE: PRT
<213> ORGANISM: Drosophila Melanogaster DOR37
<220> FEATURE:
<221> NAME/KEY: UNSURE
<222> LOCATION: (243)..(243)
<223> OTHER INFORMATION: Unknown
<221> NAME/KEY: UNSURE
<222> LOCATION: (256)..(256)
<223> OTHER INFORMATION: Unknown

<400> SEQUENCE: 108

Lys Val Asp Ser Thr Arg Ala Leu Val Asn His Trp Arg Ile Phe Arg
1               5                   10                  15

Ile Met Gly Ile His Pro Pro Gly Lys Arg Thr Phe Trp Gly Arg His
            20                  25                  30

Tyr Thr Ala Tyr Ser Met Val Trp Asn Val Thr Phe His Ile Cys Ile
        35                  40                  45

Trp Val Ser Phe Ser Val Asn Leu Leu Gln Ser Asn Ser Leu Glu Thr
    50                  55                  60

Phe Cys Glu Ser Leu Cys Val Thr Met Pro His Thr Leu Tyr Met Leu
65                  70                  75                  80

Lys Leu Ile Asn Val Arg Arg Met Arg Gly Gln Met Ile Ser Ser His
                85                  90                  95

Trp Leu Leu Arg Leu Leu Asp Lys Arg Leu Gly Cys Asp Asp Glu Arg
            100                 105                 110

Gln Ile Ile Met Ala Gly Ile Glu Arg Ala Glu Phe Ile Phe Arg Thr
        115                 120                 125

Ile Phe Arg Gly Leu Ala Cys Thr Val Val Leu Gly Ile Ile Tyr Ile
    130                 135                 140
```

-continued

```
Ser Ala Ser Ser Glu Pro Thr Leu Met Tyr Pro Thr Trp Ile Pro Trp
145                 150                 155                 160

Asn Trp Arg Asp Ser Thr Ser Ala Tyr Leu Ala Thr Ala Met Leu His
                165                 170                 175

Thr Thr Ala Leu Met Ala Asn Ala Thr Leu Val Leu Asn Leu Ser Ser
            180                 185                 190

Tyr Pro Gly Thr Tyr Leu Ile Leu Val Ser Val His Thr Lys Ala Leu
        195                 200                 205

Ala Leu Arg Val Ser Lys Leu Gly Tyr Gly Ala Pro Leu Pro Ala Val
    210                 215                 220

Arg Met Gln Ala Ile Leu Val Gly Tyr Ile His Asp His Gln Ile Ile
225                 230                 235                 240

Leu Arg Xaa Val Ser Gly Asn Leu Ile Ser Gln Cys Lys Asn Phe Xaa
                245                 250                 255

Ser Ile Ser Gly Val Leu Thr Phe Ile Glu Arg Arg Met Tyr Thr His
            260                 265                 270

Phe Gly Val Pro Asn Ile Phe Ile Val Ile Glu Asp Tyr Tyr Ile Leu
        275                 280                 285

Phe Leu Asn Tyr Ser Leu Phe Lys Ser Leu Glu Arg Ser Leu Ser Met
    290                 295                 300

Thr Cys Phe Leu Gln Phe Phe Ser Thr Ala Cys Ala Gln Cys Thr Ile
305                 310                 315                 320

Cys Tyr Phe Leu Leu Phe Gly Asn Val Gly Ile Met Arg Phe Met Asn
                325                 330                 335

Met Leu Phe Leu Leu Val Ile Leu Thr Thr Glu Thr Leu Leu Leu Cys
            340                 345                 350

Tyr Thr Ala Glu Leu Pro Cys Lys Glu Gly Glu Ser Leu Leu Thr Ala
        355                 360                 365

Val Tyr Ser Cys Asn Trp Leu Ser Gln Ser Val Asn Phe Arg Arg Leu
    370                 375                 380

Leu Leu Leu Met Leu Ala Arg Cys Gln Ile Pro Met Ile Leu Val Ser
385                 390                 395                 400

Gly Val Ile Val Pro Ile Ser Met Lys Thr Phe
                405                 410
```

What is claimed is:

1. An isolated nucleic acid molecule encoding an insect odorant receptor.

2. An isolated DNA, cDNA, genomic DNA, synthetic DNA or RNA of claim 1.

3. An isolated nucleic acid molecule of claim 1, wherein the nucleic acid molecule encodes a Drosophila odorant receptor.

4. The isolated nucleic acid molecule of claim 3 which comprise:

(a) one of the nucleic acid sequences as set forth in **FIG. 8**,

(b) a sequence being degenerated to a sequence of (a) as a result of the genetic code; or

(c) a sequence encoding one of the amino acid sequences as set forth in **FIG. 8**.

5. A nucleic acid molecule of at least 12 nucleotides capable of specifically hybridizing with the sequence of a nucleic acid molecule of claim 1.

6. A DNA, cDNA, genomic DNA, synthetic DNA or RNA of claim 5.

7. A vector which comprises the isolated nucleic acid molecule of claim 1, or **5**.

8. An isolated nucleic acid molecule of claim 7 operatively linked to a regulatory element.

9. A plasmid of claim 8.

10. A host vector system for the production of a polypeptide having the biological activity of an insect odorant receptor which comprises the vector of claim 7 and a suitable host.

11. A host vector system of claim 10, wherein the suitable host is a bacterial cell, yeast cell, insect cell, or animal cell.

12. A method of producing a polypeptide having the biological activity of an insect odorant receptor which comprising growing the host vector system of claim 11 under conditions permitting production of the polypeptide and recovering the polypeptide so produced.

13. A purified, insect odorant receptor.

14. A polypeptide encoded by the isolated nucleic acid molecule of claim 1.

15. An antibody capable of specifically binding to an insect odorant receptor.

16. An antibody capable of competitively inhibiting the binding of the antibody of claim 15.

17. A monoclonal antibody of claim 15 or **16**.

18. A method for identifying cDNA inserts encoding an insect odorant receptors comprising:

(a) generating a cDNA library which contains clones carrying cDNA inserts from antennal or maxillary palp sensory neurons;

(b) hybridizing nucleic acid molecules of the clones from the cDNA libraries generated in step (a) with probes prepared from the antenna or maxillary palp neurons and probes from heads lacking antenna or maxillary palp neurons or from virgin female body tissue;

(c) selecting clones which hybridized with probes from the antenna or maxillary palp neurons but not from head lacking antenna or maxillary palp neurons or virgin female body tissue; and

(d) isolating clones which carry the hybridized inserts, thereby identifying the inserts encoding odorant receptors.

19. A method of claim 18, after step (c), further comprising:

(a) amplifying the inserts from the selected clones by polymerase chain reaction;

(b) hybridizing the amplified inserts with probes from the antennal or maxillary palp neurons; and

(c) isolating the clones which carry the hybridized inserts, thereby identifying the inserts encoding the odorant receptors.

20. A method of claim 19, wherein the probes are cDNA probes.

21. The cDNA inserts identified by the method of claim 18 or **19**.

22. A method for identifying DNA inserts encoding an insect odorant receptors comprising:

(a) generating DNA libraries which contain clones carrying inserts from a sample which contains at least one antennal or maxillary palp neuron;

(b) contacting clones from the cDNA libraries generated in step (a) with nucleic acid molecule of claim 5 in appropriate conditions permitting the hybridization of the nucleic acid molecules of the clones and the nucleic acid molecule;

(c) selecting clones which hybridized with the nucleic acid molecule; and

(d) isolating the clones which carry the hybridized inserts, thereby identifying the inserts encoding the odorant receptors.

23. A method to identify DNA inserts encoding an insect odorant receptors comprising:

(a) generating DNA libraries which contain clones with inserts from a sample which contains at least one antenna or maxillary palp sensory neuron;

(b) contacting the clones from the DNA libraries generated in step (a) with appropriate polymerase chain reaction primers capable of specifically binding to nucleic acid molecules encoding odorant receptors in appropriate conditions permitting the amplification of the hybridized inserts by polymerase chain reaction;

(c) selecting the amplified inserts; and

(d) isolating the amplified inserts, thereby identifying the inserts encoding the odorant receptors.

24. A method to isolate DNA molecules encoding insect odorant receptors comprising:

(a) contacting a biological sample known to contain nucleic acids with appropriate polymerase chain reaction primers capable of specifically binding to nucleic acid molecules encoding insect odorant receptors in appropriate conditions permitting the amplification of the hybridized molecules by polymerase chain reaction;

(b) isolating the amplified molecules, thereby identifying the DNA molecules encoding the insect odorant receptors.

25. A method of transforming cells which comprises transfecting a host cell with a suitable vector of claim 7.

26. Transformed cells produced by the method of claim 25.

27. The transformed cells of claim 26, wherein the host cells are not usually expressing odorant receptors.

28. The transformed cells of claim 26, wherein the host cells are expressing odorant receptors.

29. A method of identifying a compound capable of specifically bind to an insect odorant receptor which comprises contacting a transfected cells or membrane fractions of the transfected cells of claim 26 with an appropriate amount of the compound under conditions permitting binding of the compound to such receptor, detecting the presence of any such compound Specifically bound to the receptor, and thereby determining whether the compound specifically binds to the receptor.

30. A method of identifying a compound capable of specifically bind to an insect odorant receptor which comprises contacting an appropriate amount of the purified odorant receptor of claim 13 with an appropriate amount of the compound under conditions permitting binding of the compound to such purified receptor, detecting the presence of any such compound specifically bound to the receptor, and thereby determining whether the compound specifically binds to the receptor.

31. A method of claim 30, wherein the purified receptor is embedded in a lipid bilayer.

32. A method of identifying a compound capable of activating the activity of an insect odorant receptor which comprises contacting the transfected cells or membrane fractions of the transfected cells of claim 26 with the compound under conditions permitting the activation of a functional odorant receptor response, the activation of the receptor indicating that the compound is capable of activating the activity of a odorant receptor.

33. A method of identifying a compound capable of activating the activity of an odorant receptor which comprises contacting a purified odorant receptor of claim 13 with the compound under conditions permitting the activation of a functional odorant receptor response, the activation of the receptor indicating that the compound is capable of activating the activity of a odorant receptor.

34. A method of claim 33, wherein the purified receptor is embedded in a lipid bilayer.

35. A method of identifying a compound capable of inhibiting the activity of a odorant receptor which comprises contacting the transfected cells or membrane fractions of the transfected cells of claim 26 with an appropriate amount of the compound under conditions permitting the inhibition of a functional odorant receptor response, the inhibition of the receptor response indicating that the compound is capable of inhibiting the activity of a odorant receptor.

36. A method of identifying a compound capable of inhibiting the activity of a odorant receptor which comprises contacting an appropriate amount of the purified odorant receptor of claim 13 with an appropriated amount of the compound under conditions permitting the inhibition of a functional odorant receptor response, the inhibition of the receptor response indicating that the compound is capable of activating the activity of a odorant receptor.

37. A method of claim 30, wherein the purified receptor is embedded in a lipid bilayer.

38. A method of claims **29**, **30**, **31**, **32**, **33**, **34**, **35**, **36**, or **37** wherein the compound is not previously known.

39. The compound identified by the method of claim 38.

40. A method of controlling pest populations which comprises identifying odorant ligands by the method of claims **29**, **30**, **31**, **32**, **33**, **34**, **35**, **36**, or **37** which are alarm odorant ligands and spraying the desired area with the identified odorant ligands.

41. A method of controlling a pest population which comprises identifying odorant ligands by the method of claims **29**, **30**, **31**, **32**, **33**, **34**, **35**, **36**, or **37** which interfere with the interaction between the odorant ligands and the odorant receptors which are associated with fertility.

* * * * *