

ActRIIa ILGRSETQEC LFFNANWEKD RTNQTGVEPC YGDKDKRRHC FATWKNISGS
 ActRIIb GRGEAETREC IYYNANWELE RTNOSGLERC EGEQDKRLHC YASWRNSSGT

IEIVKQGCWL DDINCYDRTD CVEKKDSPEV YFCCCEGNMC NEKFSYFPFM
 IELVKKGCWL DDFNICYDROE CVATEENPQV YFCCCEGNFC NERFTHLPEA

EVTQPTSNPV TPKPP
 GGPEVTYEPPT PTAPT

FIGURA 1

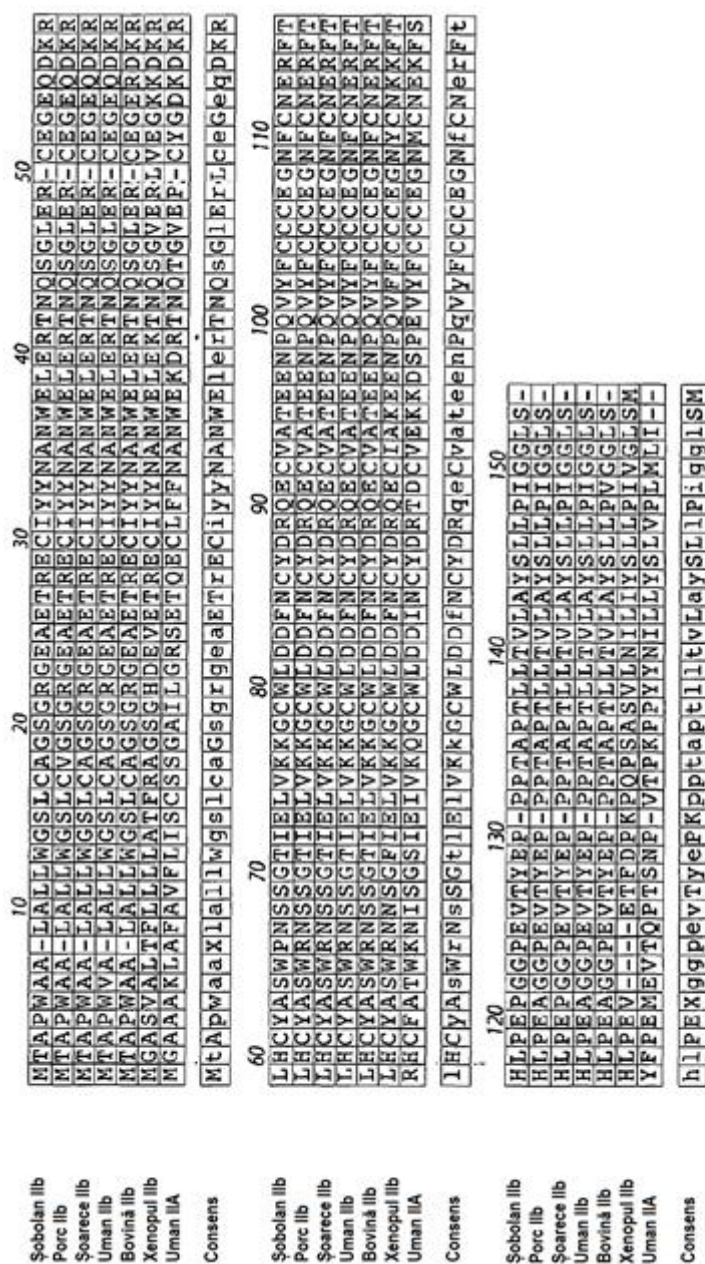


FIGURA 2

uman	•••••	10	•••••	20	•••••	30	•••••	40	•••••	50
oale	IL	ETQEC	•••••	•••••	•••••	•••••	•••••	•••••	•••••	•••••
cărtiță	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC
șoarece	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC
pui	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC
vacă	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC
bufniță	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC
liliac	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC	ILGRSETQEC
uman	•••••	60	•••••	70	•••••	80	•••••	90	•••••	100
oale	IEI	VKQGCWL	•••••	•••••	•••••	•••••	•••••	•••••	•••••	•••••
cărtiță	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL
șoarece	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL
pui	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL
vacă	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL
bufniță	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL
liliac	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL	IEI	VKQGCWL
uman	•••••	110	•••••	•••••	•••••	•••••	•••••	•••••	•••••	•••••
oale	EVT	QPTSNPV	•••••	•••••	•••••	•••••	•••••	•••••	•••••	•••••
cărtiță	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV
șoarece	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV
pui	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV
vacă	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV
bufniță	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV
liliac	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV	EVT	QPTSNPV

FIGURA 3

IgG1 -----THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 53
 IgG4 ---ESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSQEDPEVQF 57
 IgG2 -----VECPPCPAPPVAG-PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQF 51
 IgG3 EPKSCDTPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQF 60
 ** **** . * *****:*****;*:

IgG1 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 113
 IgG4 NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKT 117
 IgG2 NWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKT 111
 IgG3 KWIYVDGVEVHNAKTKPREEQYNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 :*****:***:*****:*****.***.****

IgG1 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 173
 IgG4 ISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 177
 IgG2 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 171
 IgG3 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 180
 :**:*****:*****.*****:***

IgG1 PVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 225
 PVLDSGGSFFLYSRLTVDKSRWQEGNVFCSCVMHEALHNHYTQKSLSLSLGK 229
 IgG4 PMLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 223
 IgG3 PMLDSGGSFFLYSKLTVDKSRWQQGNIFSCSCVMHEALHNRYTQKSLSLSPGK 232
 *:*****:*****:***:*****:***** **

FIGURA 4

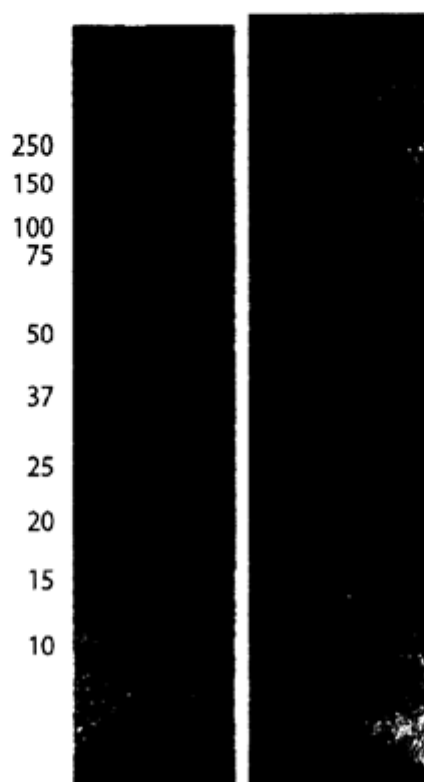
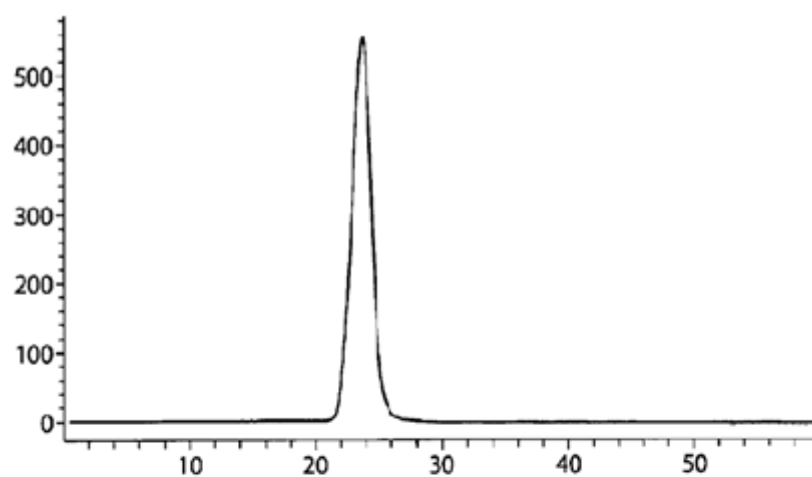
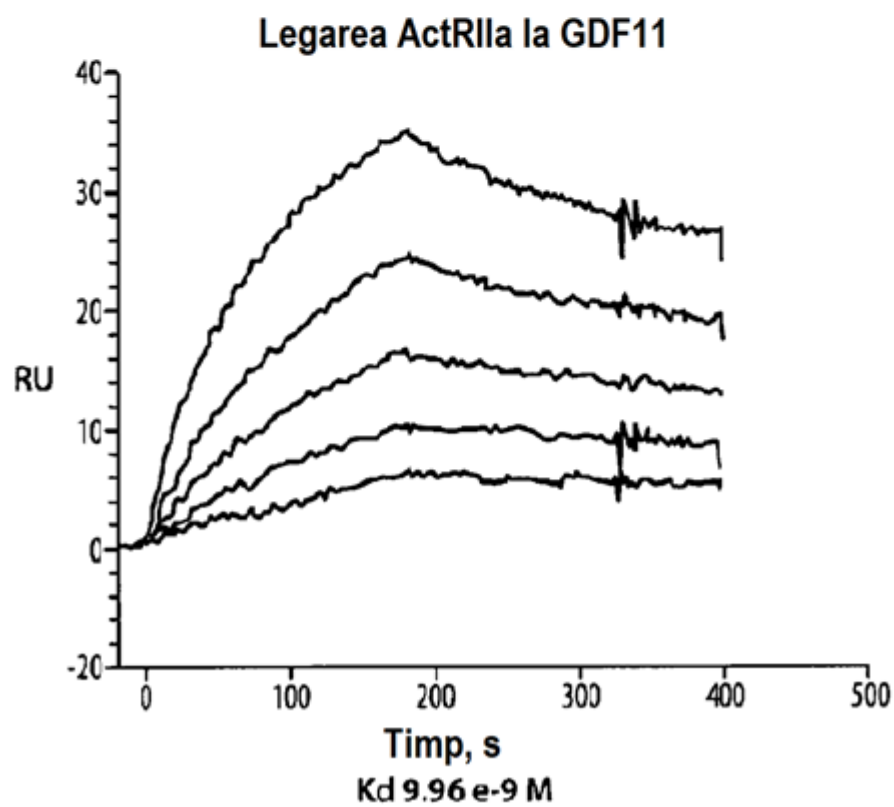
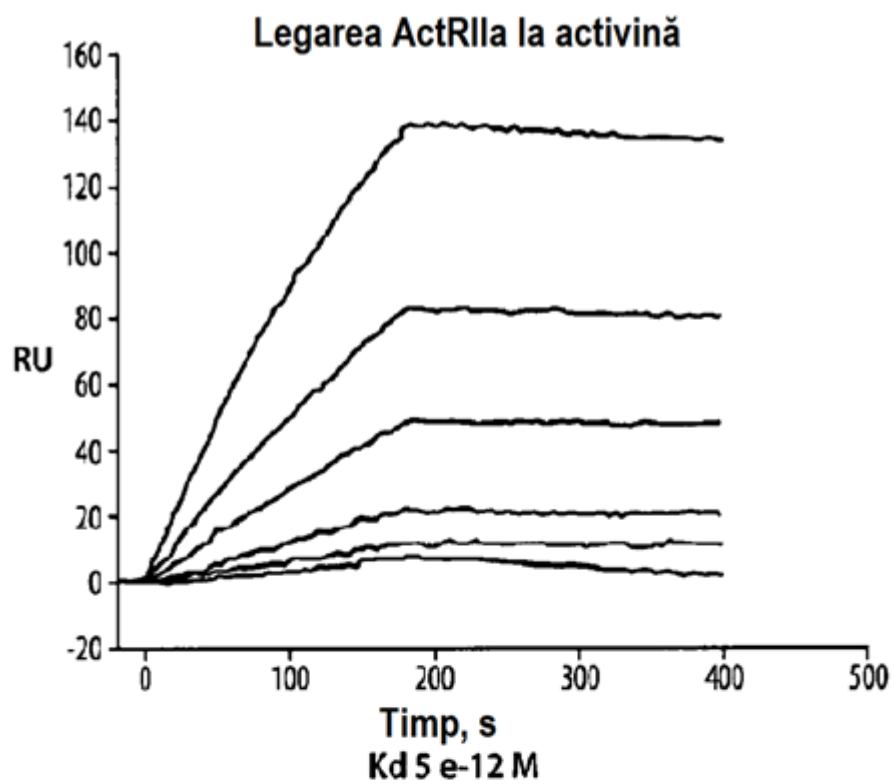


FIGURA 5

**FIGURA 6**

1 MDANKRGLCC VLLLCGAVFV SPGAA⁵TREC IYYNANWELE RTNQSGLERC
 51 EGEQDKRLHC YASWRNSSG7 IELVKKGCWL DDFNCYDROE CVATEENPCV
 101 YFCCCEGNFC NERFTHLPEA GGPEVTYEPF PTGGGTHTCP PCPAPELLGG
 151 PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA
 201 KTKPREEQYN STYRVVSVL7 VLHQDNLNGK EYKCKVSNKA LPAPIEKTI
 251 KAKQPREPQ VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP
 301 ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT
 351 QKSLSLSPGK (SEQ ID NO: 69)

FIGURA 7

1 ATGGATGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC
 TACCTACGTT ACTTCTCTCC CGAGACGACA CACGACGACG ACACACCTCG
 51 AGTCTTCGTT TCGCCCGGCG ^{A E T R E C I Y Y} CCGCTGAGAC ACGGGAGTGC ATCTACTACA
 TCAGAAACAA AGCGGGCCGC GCGGACTCTG TGCCCTCAGC TAGATGATGT
 101 N A N W E L E R T N Q S G L E R C
 ACGCCAACTG GGAGCTGGAG CGCACCAACC AGAGCGGCCT GGAGCGCTGC
 TGCGGTGAC CCTCCACCTC GCGTGGTTGG TCTCGCCGGA CCTCGCGACG
 151 E G E Q D K R L H C Y A S W R N S
 GAAGGCGAGC AGGACAAGCG GCTGCACTGC TACGCCTCCT GGCGCAACAG
 CTCCCGCTCG TCCTGTTCCG CGACGTGACG ATGCGGAGGA CCGCGTTGTC
 201 S G T I E L V K K G C W L D D F
 CTCTGCGACC ATCGAGCTCG TGAAGAAGGG CTGCTGGCTA GATGACTTCA
 GAGACCGTGG TAGCTCGAGC ACTTCTTCCC GACGACCGAT CTACTGAAGT
 251 N C Y D R Q E C V A T E E N P Q V
 ACTGCTACGA TAGGCAGGAG TGTGTGGCCA CTGAGGAGAA CCCCCAGGTG
 TGACGATGCT ATCCGTCTCT ACACACCGGT GACTCCTCTT GGGGGTCCAC
 301 Y F C C C E G N F C N E R F T H L
 TACTTCTGCT GCTGTGAAGG CAACTTCTGC AACGAGCGCT TCACTCATTT
 ATGAAGACGA CGACACTTCC GTTGAAGACG TTGCTCGCGA AGTGAGTAAA
 351 P E A G G P E V T Y E P P P T
 GCCAGGGGCT GGGGGGCCGG AAGTCACGTA CGAGCCACCC CCGACAGGTG
 CGGTCTCCGA CCCCCGGGCC TTCAGTGCAT GCTCGGTGGG GGCTGTCCAC
 401 GTGGAACCTCA CACATGCCCA CCGTGCCAG CACCTGAACCT CCTGGGGGGA
 CACCTTGAGT GTGTACGGGT GGCACGGGTC GTGGACTTGA GGACCCCCCT
 451 CCGTCAGTCT TCCTCTTCCC CCAAAACCC AAGGACACCC TCATGATCTC
 GGCAGTCAGA AGGAGAAGGG GGGTTTTGGG TTCCTGTGGG AGTACTAGAG
 501 CCGGACCCCT GAGGTACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC
 GGCTGGGGA CTCCAGTGTA CGCACCACCA CCTGCCTCTG GTGCTTCTGG
 551 CTGAGGTCAA GTTCAACTGG TACGTGGACG GCGTGGAGGT GCATAATGCC
 GACTCCAGTT CAAGTTGACC ATGCACCTGC CGCACCTCCA CGTATTACGG
 AAGACAAAGC CGCGGGAGGA GCAGTACAAC AGCACGTACC GTGTGGTCA
 TTCTGTTTCG GCGCCCTCCT CTCATGTTG TCGTGATGG CACACCAGTC
 651 CGTCTCACC GTCCTGCACC ACGACTGGCT GAATGGCAAG GAGTACAAGT
 GCAGGAGTGG CAGGACGTGG TCCTGACCGA CTTACCGTTC CTCATGTTCA
 701 GCAAGGTCTC CAACAAAGCC CCCCCAGCCC CCATCGAGAA AACCATCTCC
 CGTCCAGAG GTTGTTCGG GAGGGTCGGG GGTAGCTCTT TTGGTAGAGG
 751 AAAGCCAAAG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCCATC
 TTTCGGTTTC CCGTCGGGGC TCTGGGTGTC CACAIGTGGG ACGGGGGTAG

FIGURA 8A

```

801  CCGGGAGGAG ATGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG
      GGCCCTCCTC TACTGGTTCT TGGTCCAGTC GGA CTGGACG GACCAGTTTC

851  GCTTCTATCC CAGCGACATC GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG
      CGAAGATAGG GTCGCTGTAG CGGCACCTCA CCCCTCGTT ACCCGTCGGC

901  GAGAACTACT ACAAGACCAC GCCTCCCGTG CTGCACTCCG ACGGCTCCTT
      CTCTTGTTGA TGTCTGGTG CGGAGGGCAC GACCTGAGGC TGCCGAGCAA

951  CTTCTCTAT AGCAAGCTCA CCGTGGACAA GAGCAGGTGG CAGCAGGGGA
      GAAGGAGATA TCGTTCGAGT GGCACCTGTT CTCGTCCACC GTCGTCCCT

1001 ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCIGCACAA CCACTACACG
      TGCAGAAGAG TACGAGGCAC TACGTACTCC GAGACGTGTT GGTGATGTGC

1051 CAGAAGAGCC TCTCCCTGTC CCCGGGTAAA TGA (SEQ ID NO: 70)
      GTCTTCTCGG AGAGGGACAG GGGCCCATTT ACT (SEQ ID NO: 71)

```

FIGURA 8B

```

1  ATGGATGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC
   TACCTACGTT ACTTCTCTCC CGAGACGACA CACGACGACG ACACACCTCG

                               A E T R E C I Y Y
51  AGTCTTCGTT TCGCCCGGCG CCGCCGAAAC CCGCGAATGT ATTTATTACA
   TCAGAAAGCAA AGCGGGCCGC GCGCGCTTTG GCGCGTTACA TAAATAATGT

N A N W E L E R T N Q S G L E R C
101  ATGCTAATTG GGAATCTGAA CCGACGAACC AATCCGGGCT CGAACGGTGT
   TACGAITAAC CCTTGAGCTT GCCTGCTTGG TTAGGCCCGA GCTTGCCACA

E G E O D K R L H C Y A S W R N S
151  GAGGGGGAAC AGGATAAAGC CCTCCATTGC TATGCGTGGT GGAGGAACTC
   CTCCCCCTTG TCCTATTTCG GGAGGTAACG ATACGCAGCA CCTCCTTGAG

S G T I E L V K K G C W L D D F
201  CTCCGGGACG ATTGAACTGG TCAGAAAGG GTGCTGGCTG GACGATTTCA
   GAGGCCCTGC TAACTTGACC AGTTCCTTCC CACGACCGAC CTGTAAAGT

N C Y D R Q E C V A T E E N P Q V
251  ATTGTTATGA CCGCCAGGAA TGTGTCGCGA CCGAAGAGAA TCCGACGGTC
   TAACATACTT GCGCGTCTTT ACACAGCGCT GGTCTCTCTT AGGCGTCCAG

Y F C C C E G N F C N E R F T H L
301  TATTTCGTGT GTTGCGAGGG GAATTTCTGT AATGAACGGT TTACCCACCT
   ATAAAGACAA CAACGCTCCC CTAAAGACA TTACTTGCCA AATGGGTGGA

P E A G G P E V T Y E P P P T
351  CCCCAGAGCC GCGGGGCTCG AGGTGACCTA TGAACCCCGG CCGACGGGTG
   GGGGCTTCGG CCGCCCGGGC TCCACTGGAT ACTTGGGGGC GGGTGGCCAC

401  GTGGAACCTA CACATGCCCA CCGTGCCCGC CACCTGAACCT CCTGGGGGGA
   CACCTTGAGT GTGTACGGGT GGCACGGGTC GTGGACTTGA GGACCCCCCT

451  CCGTCAGTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC
   GGCAGTCAGA AGGAGAAGGG GGGTTTTGGG TTCCTGTGGG AGTACTAGAG

501  CCGGACCCCT GAGGTACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC
   GGCCCGGGGA CTCCAGTGTA CGCACCACCA CCTGCACTCG GTGCTTCTGG

551  CTGAGGTCAA GTTCAACTGG TACGTGGACG GCGTGGAGGT GCATAATGCC
   GACTCCAGTT CAAGTTGACC ATGCACCTGC CGCACCTCCA CGTATTACGG

... AAGACAAAGC CGCGGGAGGA GCAGTACAAC AGCACGTACC GTGTGGTCAG
   TTCTGTTTCG GCGCCCTCCT CGTCATGTTG TCGTGCATGG CACACCAGTC

651  CGTCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG GAGTACAAGT
   GCAGGAGTGG CAGGACGTGG TCCTGACCGA CTTACCGTTC CTCATGTTCA

701  GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC
   CGTTCCAGAG GTTGTTCGGG GAGGGTCGGG GGTAGCTCTT TTGGTAGAGG

751  AAAGCCAAGG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCCATC
   TTTCGGTTTC CCGTCGGGGC TCTTGGTGTC CACATGTGGG ACGGGGGTAG

```

FIGURA 9A

801 CCGGGAGGAG ATGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG
 GGCCCTCCTC TACTGGTTCT TGGTCCAGTC GGA CTGACG GACCAGTTTC
 851 GCTTCTATCC CAGCGACATC GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG
 CGAAGATAGG GTCGCTGTAG CGGCACCTCA CCCTCTCGTT ACCCGTCGGC
 901 GAGAACPACT ACAAGACCAC GCCTCCCGTG CTGGACTCCG ACGGCTCCTT
 CTCTTGTGA TGTCTCTGGTG CGGAGGGCAC GACCTGAGGC TGCCGAGGAA
 951 CTTCTCTAT AGCAAGCTCA CCGTGGACAA GAGCAGGTGG CAGCAGGGGA
 GAAGGAGATA TCGTTCGAGT GGCACCTGTT CTCGTCCACC GTCGTCCCCT
 1001 ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG
 TGCAGAAGAG TACGAGGCAC TACGTACTCC GAGACGTGTT GGTGATGTGC
 1051 CAGAAGAGCC TCTCCCTGTC CCCGGGTAAA TGA (SEQ ID NO: 72)
 GTCTTCTCGG AGAGGGACAG GGGCCCATTT ACT (SEQ ID NO: 73)

FIGURA 9B

1 MDAMKRG LCC VLLLCGAVFV SPGASGRGEA ETRECIYYNA NWELERTNQS
 51 GLERCEGEQD KRLHCYASWR NSSGTIELVK KGCWDDDFNC YDRQECVATE
 101 ENPQVYFCCC EGNFCNERFT HLPEAGGPEV TYEPPFTAPT GGGTHTCPPC
 151 PAPELLGGPS VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV
 201 DGVEVHNAKT KPREEQYNST YRVVSVLTVL HQDWLNGKEY KCKVSNKALP
 251 APIEKTISKA KGQPREPQVY TLPPSREEMT KNQVSLTCLV KGFYPSDIAV
 301 EWESNGQPEN NYKTTTPVLD SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH
 351 EALHNHYTQK SLSLSPGK (SEQ ID NO: 74)

FIGURA 10

```

1  ATGGATGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC
   TACCTACGTT ACTTCTCTCC CGAGACGACA CACGACGACG ACACACCTCG

51  AGTCTTCGTT TCGCCCGGCG CCTCTGGGCG TGGGGAGGCT GAGACACGGG
   TCAGAAGCAA AGCGGGCCGC GGAGACCCGC ACCCCTCCGA CTCTGTGCCC

101 AGTGCA7CTA CTACAACGCC AACTGGGAGC TGGAGCGCAC CAACCAGAGC
   TCACGTAGAT GATGTTGCGG TTGACCCCTG ACCTCGCGTG GTTGTCTCTG

151 GGCCTGGAGC GCTGCGAAGG CGAGCAGGAC AAGCGGCTGC ACTGCTACGC
   CCGGACCTCG CGACGCTTCC GCTCGTCTTG TTCGCCGACG TGACGATGCG

201 CTCCTGGGCG AACAGCTCTG GCACCATCGA GCTCGTGAAG AAGGGCTGCT
   GAGGACCGCG TTGTCGAGAC CGTGGTAGCT CGAGCACTTC TTCCCGACGA

251 GGGATGATGA CTTCAACTGC TACGATAGGC AGGAGTGTGT CGCCACTCAG
   CCCTACTACT GAAGTTGACG ATGCTATCCG TCCTCACACA CCGGTGACTC

301 GAGAACCCCC AGGTGTACTT CTGCTGCTGT GAAGGCAACT TCTGCAACGA
   CTCTTGGGGG TCCACATGAA GACGACGACA CTTCGGTTGA AGACGTGCT

351 GCGCTTCACT CATTTGCCAG AGGCTGGGGG CCCGGAAGTC ACGTACGAGC
   CGCGAAGTGA GTAAACGGTC TCCGACCCCC GGGCCTTCAG TGCATGCTCG

401 CACCCCGGAC AGCCCCCACC GGTGGTGGAA CTCACACATG CCCACCGTGC
   GTGGGGGCTG TCGGGGTGG CCACCACCTT GAGTG7GTAC GGGTGGCAGG

451 CCAGCACCTG AACTCCTGGG CGGACCGTCA GTCTTCTCTT TCCCCCAAA
   GGTGCTGGAC TTGAGGACCC CCTTGGCAGT CAGAAGGAGA AGGGGGGTTT

501 ACCCAAGGAC ACCCTCATGA ICTCCCGGAC CCCTGAGGTC ACATGCGTGG
   TGGCTTCCTG TGGGAGTACT AGAGGGGCTG GGGACTCCAG TGTACGCACC

551 TGGTGGACGT GAGCCACCAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG
   ACCACCTGCA CTCGGTGCTT CTGGGACTCC AGTTCAAAGT GACCATGCAC

601 GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA
   CTGCCGCACC TCCACGTATT ACGGTTCTGT TTCGGCGCCC TCCTCGTCAT

   CAACAGCAAG TACCGTGTGG TCAGCGTCCT CACCGTCTTG CACCAGGACT
   GTTGTCGTGC ATGGCACACC ACTCGCAGGA GTGGCAGGAC GTGTCCTGA

701 GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA
   CCGACTTACC GTTCCTCATG TTCACGTTCC AGAGGTTGTT TCGGGAGGGT

751 GCCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAACC
   CGGGGGTAGC TCTTTTGGA GAGGTTTCGG TTTCCCCTCG GGGCTCTTGG

```

FIGURA 11A

801 ACAGGTGTAC ACCCTGCCCC CATCCCGGGA GGAGATGACC AAGAACCAGG
 TGTCCACATG TGGGACGGGG GTAGGGCCCT CCTCTACTGG TTCTTGGTCC

851 TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT ATCCCAGCGA CATCGCCGTG
 AGTCGGACTG GACGGACCAG TTTCCGAAGA TAGGCTCGCT GTAGCGGCAC

901 GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA CCACGCCCTCC
 CTCACCCTCT CGTTACCCGT CGGCCTCTTG TTGATGTTCT GGTGCGGAGG

951 CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTATAGCAAG CTCACCGTGG
 GCACGACCTG AGGCTGCCGA GGAAGAAGGA GATATCGTTC GAGTGGCACC

1001 ACAAGAGCAG GTGGCAGCAG GGGAACGTCT TCTCATGCTC CGTGATGCAT
 TGTTCCTCGTC CACCGTCGTC CCCTTGCAGA AGAGTACGAG GCACTACGTA

1051 GAGGCTCTGC ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCCCCGGG
 CTCCGAGACG TGTTGGTGAT GTGCGTCTTC TCGGAGAGGG ACAGGGGCCC

1051 TAAATGA (SEQ ID NO: 75)
 ATTTACT (SEQ ID NO: 76)

FIGURA 11B

1 MDAMKRGLCC VLLLCGAVFV SPGAAETREC IYYNANWELE RTNQSGLERC

51 EGEQDKRLHC YASWRNSSGT IELVKKGCWDDDFNCYDRQE CVATEENPOV

101 YFCCCEGNFC NERFTHLPEA GGPEVTYEPP PTGGGTHTCP PCPAPELLGG

151 PSVFLFPPKP KDTLMIS RTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA

201 KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS

251 KAKGQPREPQ VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP

301 ENNYKTTTPV LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALENHYT

351 QKSLSLSPGK (SEQ ID NO: 77)

FIGURA 12

1 ETRECIYYNA NWELERTNQS GLERCEGEQD KRLHCYASWR NSSGTIELVK

51 KGCWDDDFNC YDRQECVATE ENPQVYFCCC EGNFCNERFT HLPEAGGPEV

101 TYEPPPTIGGG THTCPPCPAP ELLGGPSVFL FPPKFKDTLM ISRTPRVTCV

151 VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD

201 WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTL PPSREEMTKNQ

251 VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSKLTV

301 DKSRWQQGNV FSCSVMEAL HNHYTQKSLS LSPGK (SEQ ID NO: 78)

FIGURA 13

1 ETRECIYYNA NWELERTNQS GLERCEGEQD KRLHCYASWR NSSGTIELVK
 51 KGCWDDDFNC YDRQECVATE ENPQVIFCCC EGNFCNERFT
 101 HLPEAGGPEV TYEPPPT (SEQ ID NO: 79)

FIGURA 14

1 ATGGATCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC
TACCTACGTT ACTTCTCTCC CGAGACGACA CACGACGACG ACACACCTCG
 E T R E C I Y Y
 51 AGTCTTCGTT TCGCCCGGCG CCGCTGAGAC ACGGGAGTGC ATCTACTACA
TCAGAAGCAA AGCGGGCCGC GCGGACTCTG TGCCCTCAGC TAGATGATGT
 N A N W E L E R T N Q S G L E R C
 101 ACGCCAACTG GGAGCTGGAG CGCACCAACC AGAGCGGCCT GGAGCGCTGC
TGCGGTTGAC CCTCGACCTC GCGTGGTTGG TCTCGCCGGA CCTCGCGACG
 E G E Q D K R L H C Y A S W R N S
 151 GAAGGCGAGC AGGACAAGCG GCTGCACTGC TACGCCTCCT GGCGCAACAG
CTTCCGCTCG TCCTGTTTCG CGACGTGACG ATGCGGAGGA CCGCGTTGTC
 S G T I E L V K K G C W D D D F
 201 CTCTGGCACC ATCGAGCTCG TGAAGAAGGG CTGCTGGGAC GATGACTTCA
GAGACCCTGG TAGCTCGAGC ACTTCTTCCC GACGACCTCG CTACTGAAGT
 N C Y D R Q E C V A T E E N P Q V
 251 ACTGCTACGA TAGGCAGGAG TGTGTGGCCA CTGAGGAGAA CCCCCAGGTG
TGACGATGCT ATCCGTCCTC ACACACCGGT GACTCCTCTT GGGGGTCCAC
 Y F C C C E G N F C N E R F T H L
 301 TACTTCTGCT GCTGTGAAGG CAACTTCTGC AACGAGCGCT TCATCTATTI
ATGAAGACGA CGACACTTCC GTTGAAGACG TTGCTCGCGA AGTGAGTAAA
 P E A G G P E V T Y E P P P T
 351 GCCAGAGGCT GGGGGCCCCG AAGTCACGTA CGAGCCACCC CCGACAGGTG
CGGTCTCCGA CCCCCGGGCC TTCAGTGCAT GCTCGGTGGG GGCTGTCCAC
 401 GTGGA ACTCA CACATGCCCA CCGTGCC CAG CACCTGAACT CCTGGGGGGA
 CACCTTGAGT GTGTACGGGT GGCACGGGTC GTGGACTTGA GGACCCCCCT
 451 CCGTCAGTCT TCCTCTTCCC CCAAAAACCC AAGGACACCC TCATGATCTC
 GGCAGTCAGA AGGAGAAGGG GGGTTTTGGG TTCCTGTGGG AGTACTAGAG
 --- CCGGACCCCT GAGGTCACAT GCGTGGTGGT GGACGIGAGC CACGAAGACC
 GGCTTGGGGA CTCAGTGTA CGCACCACCA CCTGCACTCG GTGCTTCTGG
 551 CTGAGGTCAA GTTCAACTGG TACGTGGACG GCGTGGAGGT GCATAATGCC
 GACTCCAGTT CAAGTTGACC CTGCACCTGC CGCACCTCCA CGTATTACGG

FIGURA 15A

```

601  AAGACAAAGC CGCGGGAGGA GCAGTACAAC AGCACGTACC GTGTGGTCAG
      TCTGTTTTCG GCGCCCTCCT CGTCATGTTG TCGTGCATGG CACACCAGTC

651  CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG GAGTACAAGT
      GCAGCAGTGG CAGGACGTGG TCCTGACCGA CTTACCGTTC CTCATGTTCA

701  GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC
      CGTTCAGAG GTTGTTTCGG GAGGGTCGGG GGTAGCTCTT TTGGTAGAGG

751  AAAGCCAAAG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCCATC
      TTCCGTTTC CCGTCGGGGC TCTTGGTGTC CACATGTGGG ACGGGGGTAG

801  CCGGGAGGAG ATGACCAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG
      GGCCCTCCTC TACTGGTTCT TGGTCCAGTC GGACTGGACG GACCAGTTTC

851  GCTICTATCC CAGCGACATC GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG
      CGAAGATAGG GTCGCTGTAG CGGCACCTCA CCCCTCGTT ACCCGTCGGC

901  GAGAACAAC AACAAGACCAC GCCTCCCGTG CTGGACTCCG ACGGCTCCTT
      CTCITGTTGA TGTTCTGGTG CGGAGGGCAC GACCTGAGGC TGCCGAGGAA

951  CTTCCTCTAT AGCAAGCTCA CCGTGGACAA GAGCAGGTGG CAGCAGGGGA
      GAAGGAGATA TCGTTCGAGT GGCACCTGTT CTCGTCCACC GTCGTCCCTT

1001 ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCIGCACAA CCACTACACG
      TGCAGAAGAG TACGAGGCAC TACGTACTCC GAGACGTGTT GGTGATGIGC

1051 CAGAAGAGCC TCTCCCTGTC CCCGGGTAAA TGA (SEQ ID NO: 80)
      GTCTTCTCGG AGAGGGACAG GGGCCCATTT ACT (SEQ ID NO: 81)

```

FIGURA 15B

```

1  ATGGAIGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC
   TACCTACGTT ACTTCTCTCC CGAGACGACA CACGACCACG ACACACCTCG
                                     E T R E C I Y Y
51  AGTCTTCGTT TCGCCCGGCG CCGCCGAAAC CCGCGAATGT ATTTATTACA
   TCAGAAGCAA AGCGGGCCGC GCGGCTTTG GCGGCTTACA TAAATAATGT
                                     N A N W E L E R T N Q S G L E R C
101  ATGCTTAATTG GGAATCTGAA CCGACGAACC AATCCGGCT CGAACGGTGT
   TACGATTAAAC CCTTGAGCTT GCCTGCTTGG TTAGGCCCGA GCTTGCCACA
                                     E G E Q D K R L H C Y A S W R N S
151  GAGGGGGAAC AGGATAAACG CCTCCATGTC TATGCGTGT GAGGGAACCT
   CTCCCCCTTG TCCTATTGTC GGAGGTAACG ATACGACGCA CCTCCTTGAG
                                     S G T I E L V K K G C N D D D F
201  CTCGGGACG ATTGAACTGG TCAAGAAAGG GTGCTGGAC GACGATTCA
   GAGGCCCTGC TAACTTGACC AGTTCTTTCC CACGACCTCG CTGCTAAAGT
                                     N C Y D R Q E C V A T E E N P Q V
251  ATGCTTATGA CCGCCAGGAA TGTGTGCGGA CCGAAGAGAA TCCGCAGGTG
   TAACAATACT GCGGTCCTT ACACAGCGCT GGCTTCCTT AGGCGTCCAG
                                     Y F C C C E G N F C N E R F T H L
301  TATTTCTGTT GTTGGAGGG GAATTTCTGT AATGACCGGT TTACCCACCT
   ATAAAGACAA CAACGCTCCC CTTAAAGACA TTAATTGCA AATGGGTGGA
                                     P E A G G P E V T Y E P P P T
351  CCCCAGAGCG GCGGGGCCG AGGTACCTA TGAACCCCG CCCACCGGTG
   GGGGCTTCGG CCGCCCGGC TCACTGGAT ACTGSGGGC GGGTGGCCAC
401  GTGGAAC TCA CACATGCCCA CCGTGCCAG CACCTGACT CCTGGGGGGA
   CACCTGAGT GTGTACGGGT GGCACGGTC GTGGACTTGA GGACCCCCCT
451  CCGTCAGTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC
   GGCAGTCAGA AGGAGAAGGG GGGTTTGGG TTCCTGTGG AGTACTAGAG
501  CCGGACCCCT GAGGTCACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC
   GGCCTGGGGA CTCAGTGTA CGCACCACCA CCTGCACTCG GTGCTTCTGG
551  CTGAGGICAA GTTCAACTGG TACGTGGACC GCGTGGAGGT GCATAATGCC
   GACTCCAGTT CAAGTTGACC ATGCACCTGC CGCACCTCCA CGTATTACGG
601  AAGACAAAGC CGCGGGAGGA GCAGTACAAC AGCACGTACC GTGTGGTCAG
   TTCTGTTTCG GCGCCCTCCT CGTCATGTTG TCGTGCATGG CACACCAGTC
651  CGTCCTCACC GTCTGCACC AGGACTGGCT GAATGGCAAG GAGTACAAGT
   GCAGGAGTGG CAGGACGTGG TCCTGACCGA CTTACCGTTC CTCATGTTCA

```

FIGURA 16A

```

701   GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCAICGAGAA AACCATCTCC
      CGTTCCAGAG GTTGTTCGG GAGGGTCGGG GGTAGCTCTT TTGGTAGAGG

751   AAAGCCAAAG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCCATC
      TTTCGGTTTC CCGTCGGGGC TCTTGGTGTC CACATGTGGG ACGGGGGTAG

801   CCGGGAGGAG ATGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG
      GGCCCTCCTC TACTGGTTCT TGGTCCAGTC GGACTGGACG GACCAGTTTC

851   GCTTCTATCC CAGCGACATC GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG
      CGAAGATAGG GTCGCTGTAG CGGCACCTCA CCTCTCGTT ACCCGTCGGC

901   GAGAACAACT ACAAGACCAC GCCTCCCGTG CTGGAATCCG ACGGCTCCTT
      CTCTTGTGTA TGTTCCTGGT GCGAGGGCAC GACCTGAGGC TCCCCAGCAA

951   CTTCTCTAT AGCAAGCTCA CCGTGGACAA GAGCAGGTGG CAGCAGGGGA
      GAAGGAGATA TCGTTCGAGT GGCACCTGTT CTCGTCCACC GTCGTCCCTT

1001  ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG
      TGCAGAAGAG TACGAGGCAC TACGTACTCC GAGACGTGTT GGTGATGTGC

1051  CAGAAGAGCC TCTCCCTGTC CCCGGGTAAA TGA (SEQ ID NO: 82)
      GTCTTCTCGG AGAGGGACAG GGGCCCATTT ACT (SEQ ID NO: 83)

```

FIGURA 16B

```

GAAAC CCGGAAATGT ATTAATACA ATGCTAAATG GGAATCGAA CGGACCAACC
AATCCGGCT CGAECGTGT GAGGGGAAAC AGGAATAACG CCTCCATGTC TATGCTCTGT
GGAGGAACTC CTCGGGACG ATGAACTGG TGAAGAAAGG GTGCTGGGAC GACGAATTCA
ATTGTTATGA CCGCCAGGAA TGTGTGGCA CCGAAGAGAA TCCGCAGGTC TATTTCTGTT
GTTGCGAGGG GAATTTCTGT AATGAACGCT TTACCCACCT CCCGAAGCC GCGGGCCCG
AGGTGAOCTA AGAACCCCCG CCACCC (SEQ ID NO: 84)

```

FIGURA 17

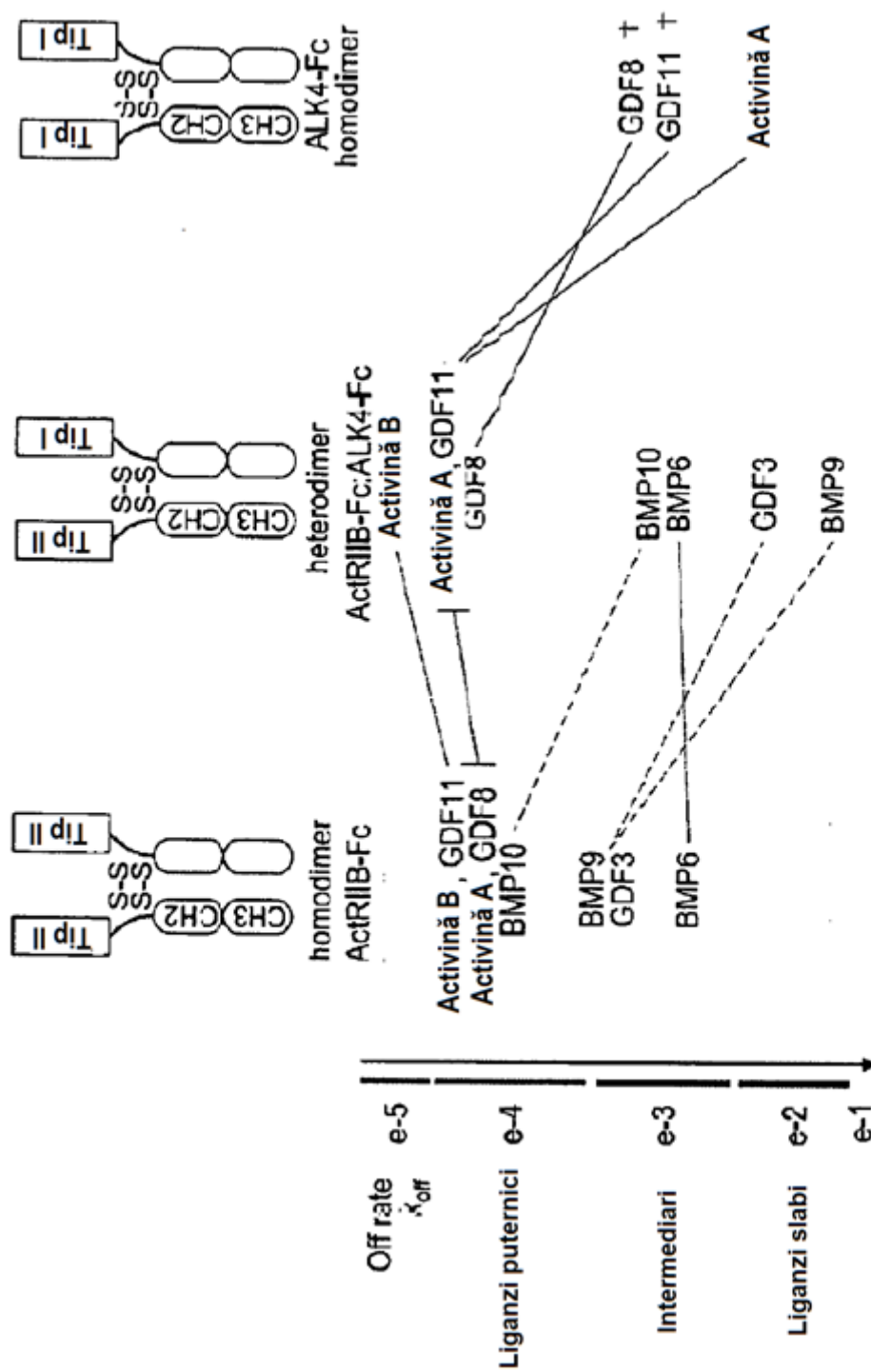
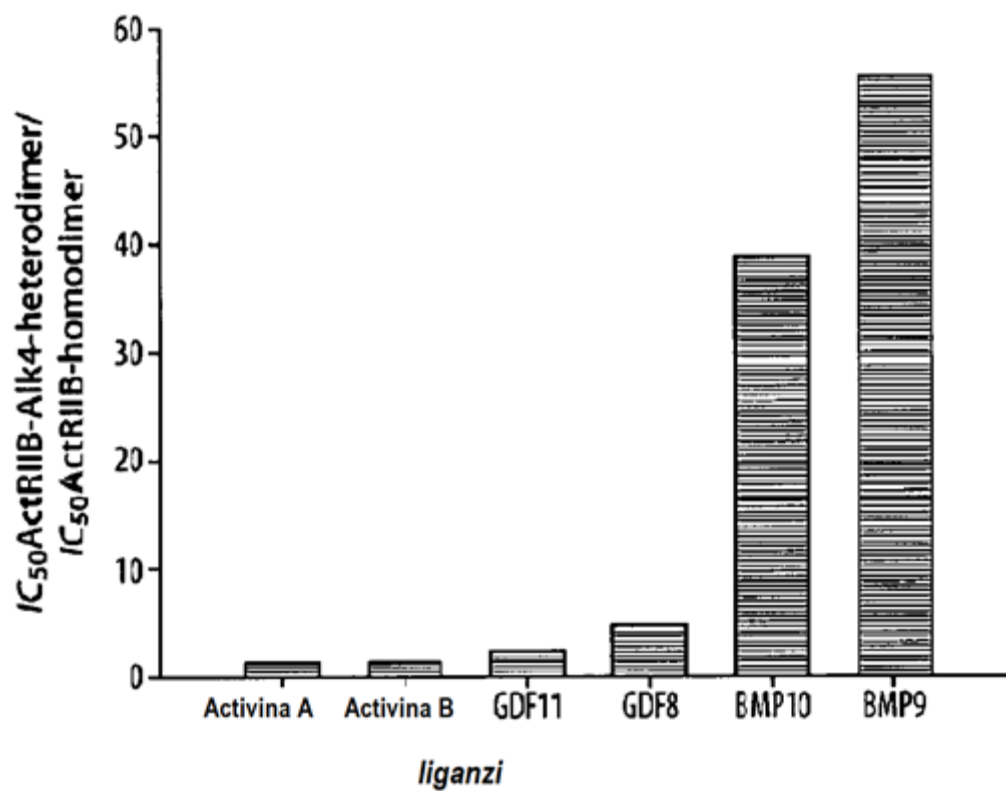
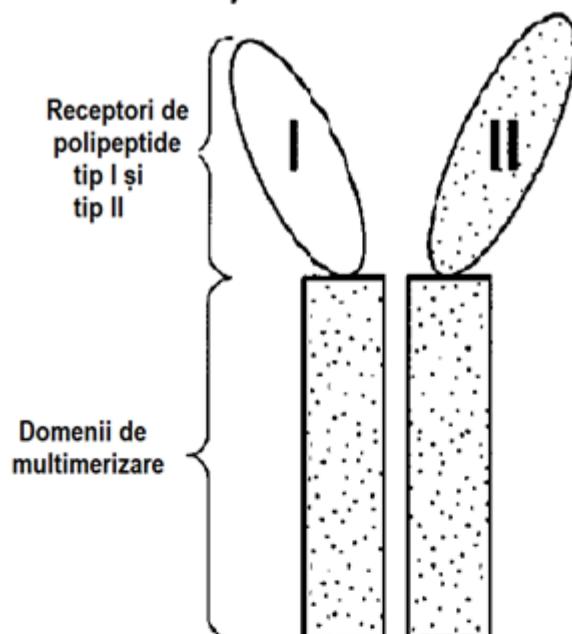
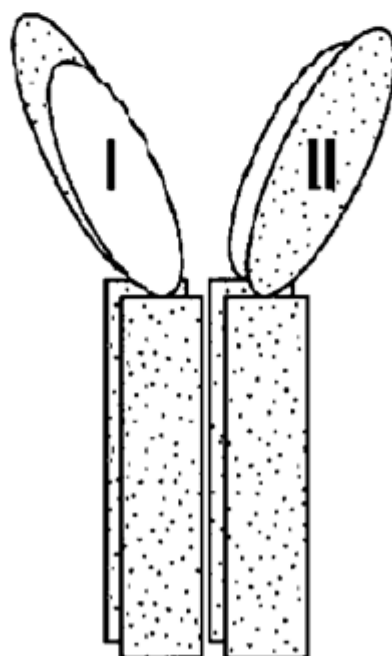


FIGURA 19

**FIGURA 20**

Complex Heterodimeric**FIGURA 21A*****Complex Heterotetrameric*****FIGURA 21B**

Complex proteic heterodimeric schematic

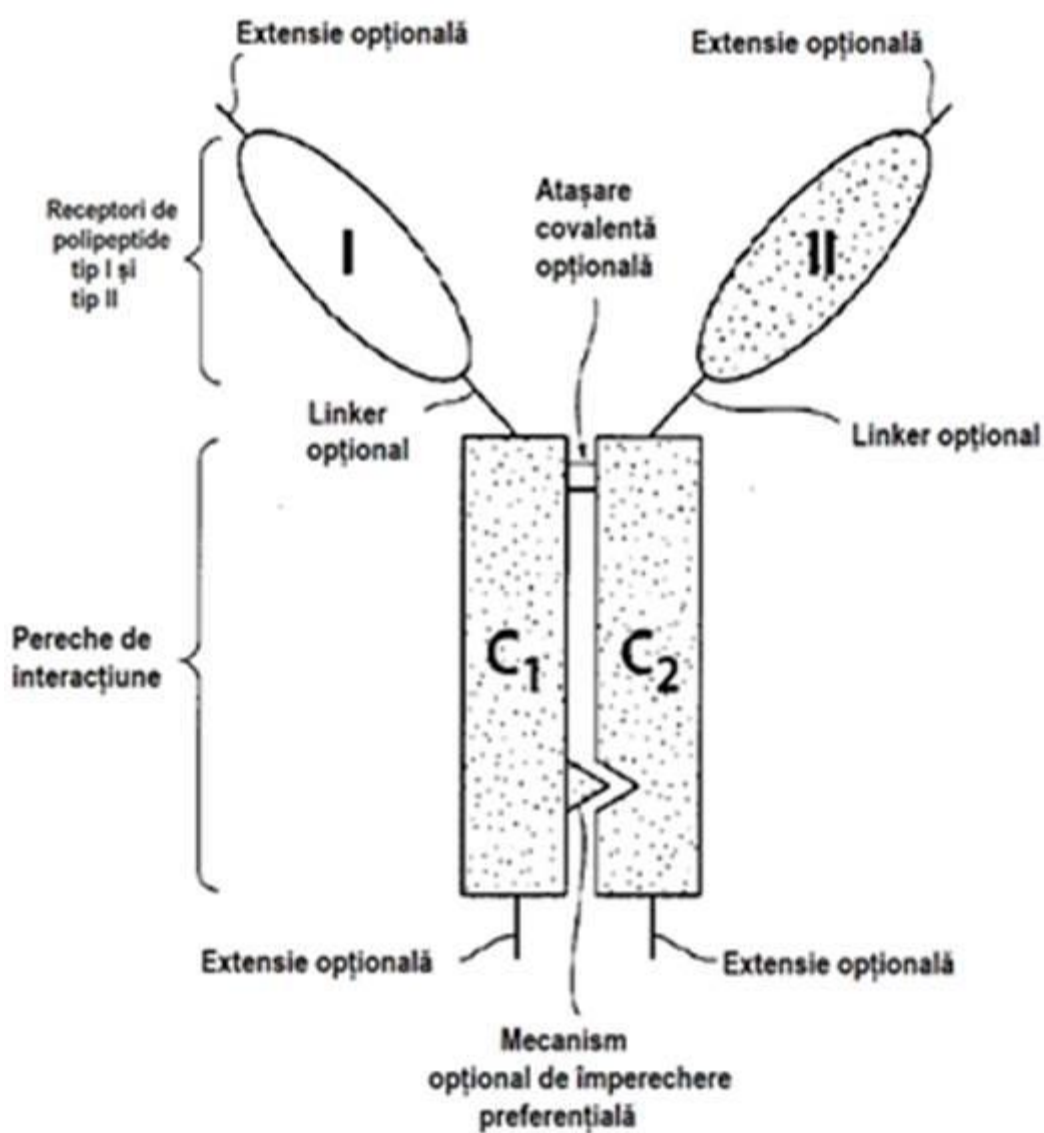


FIGURA 22

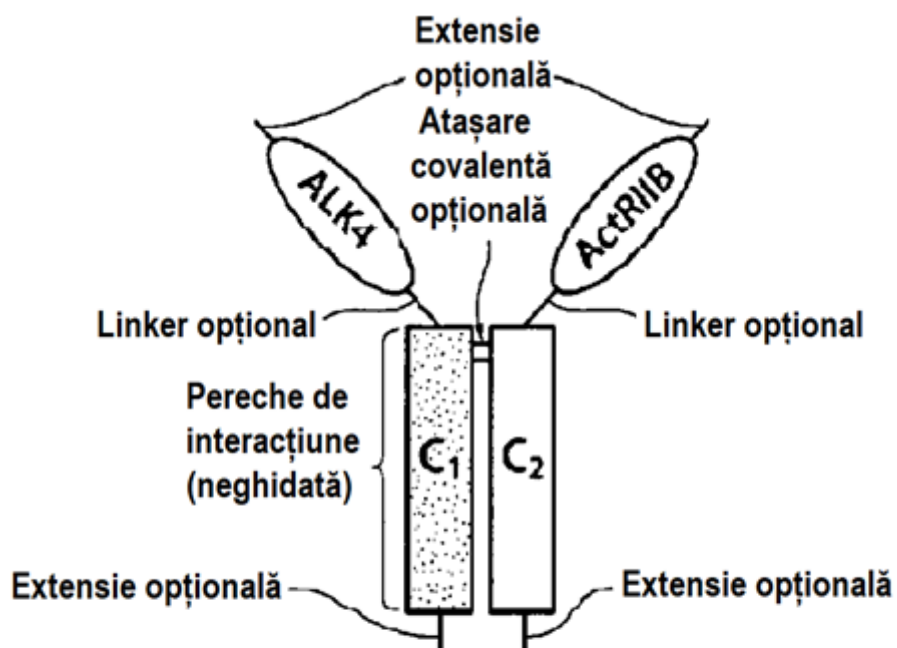


FIGURA 23A

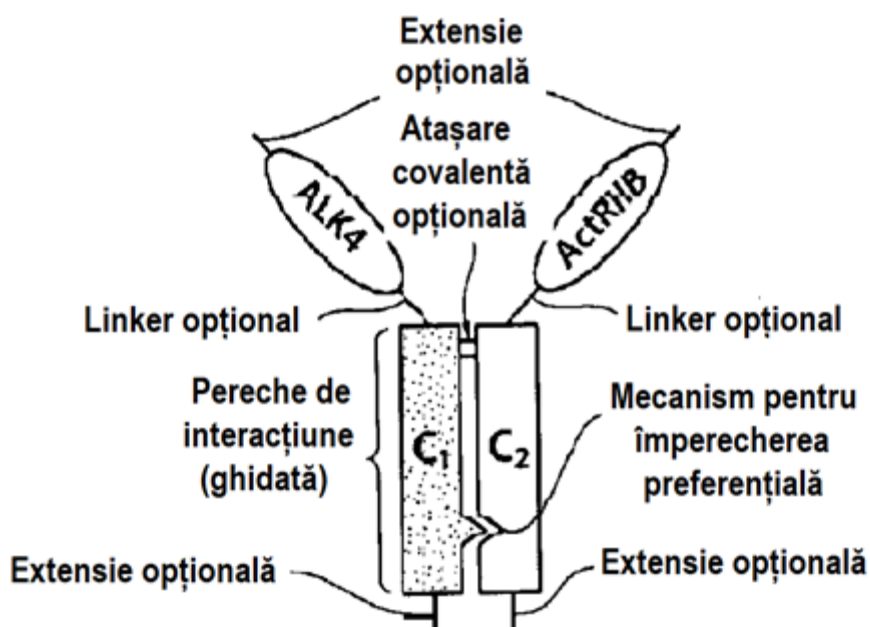


FIGURA 23B

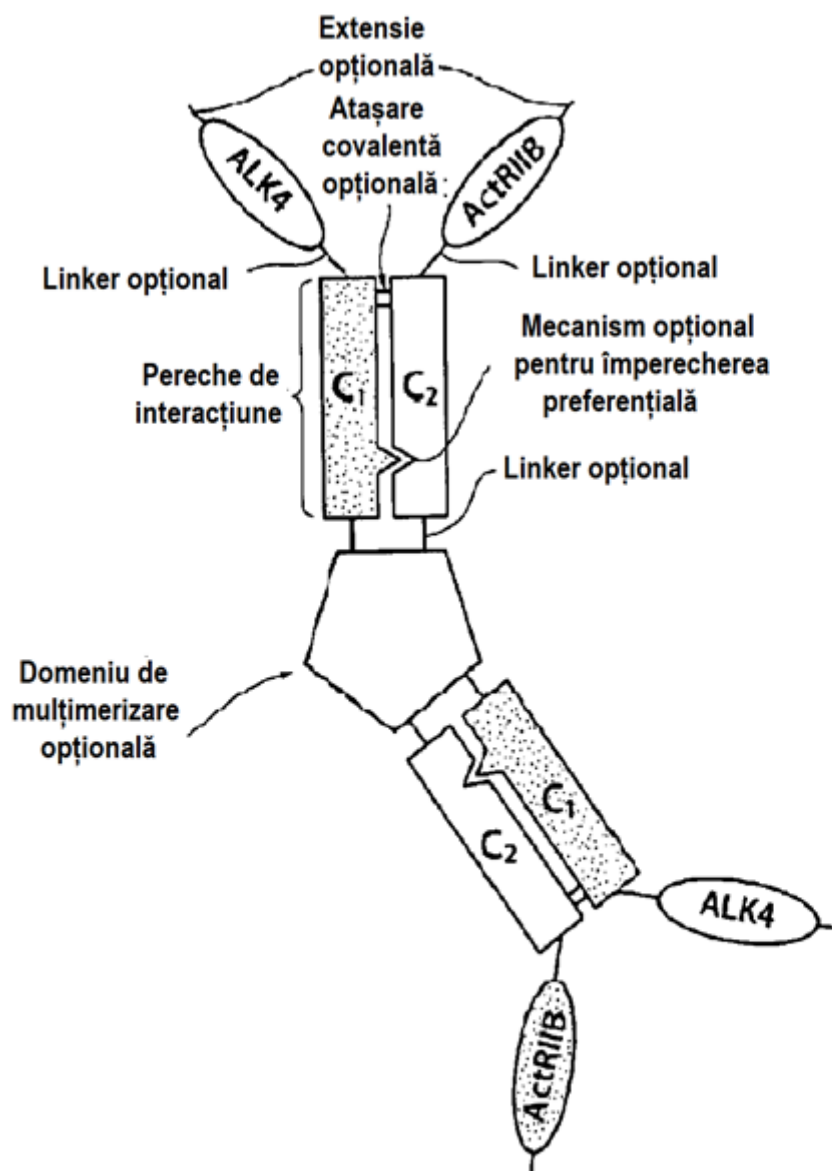


FIGURA 23C

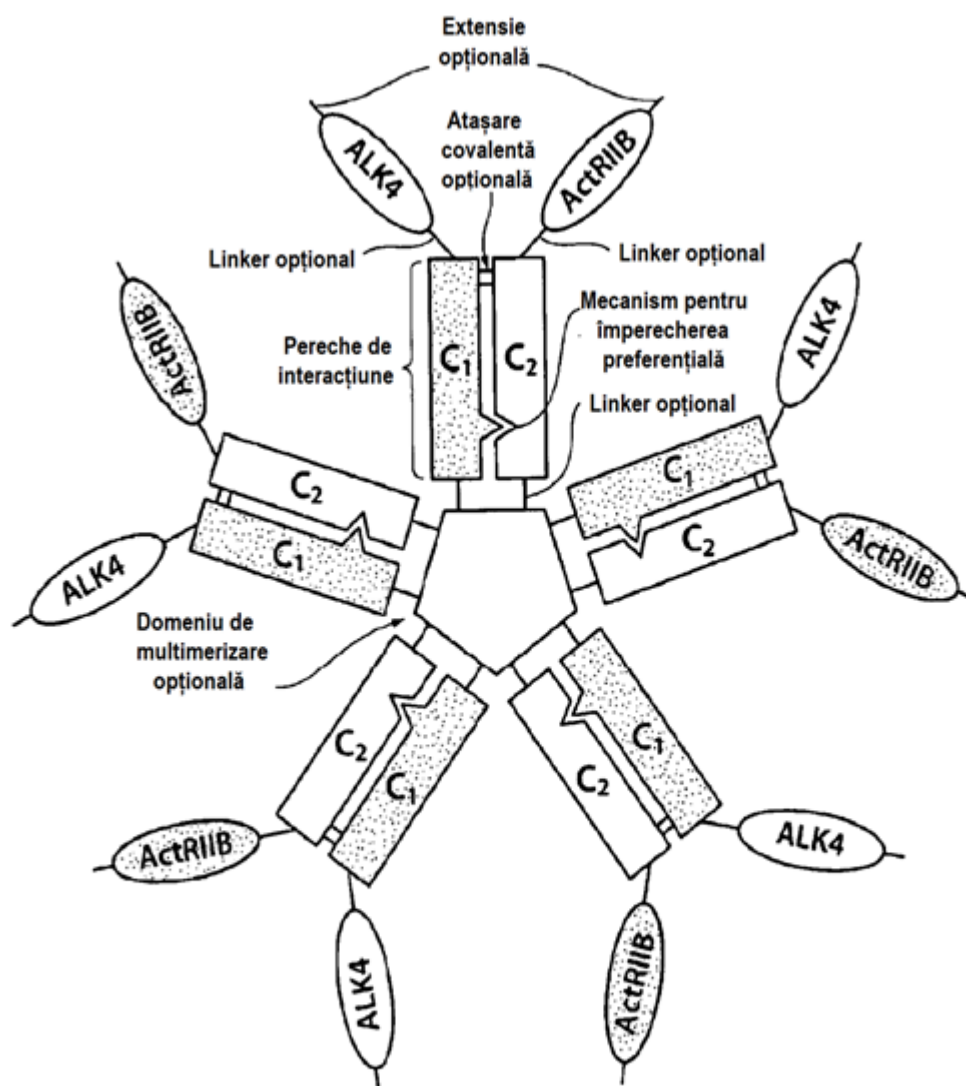


FIGURA 23D