FIGURE 1

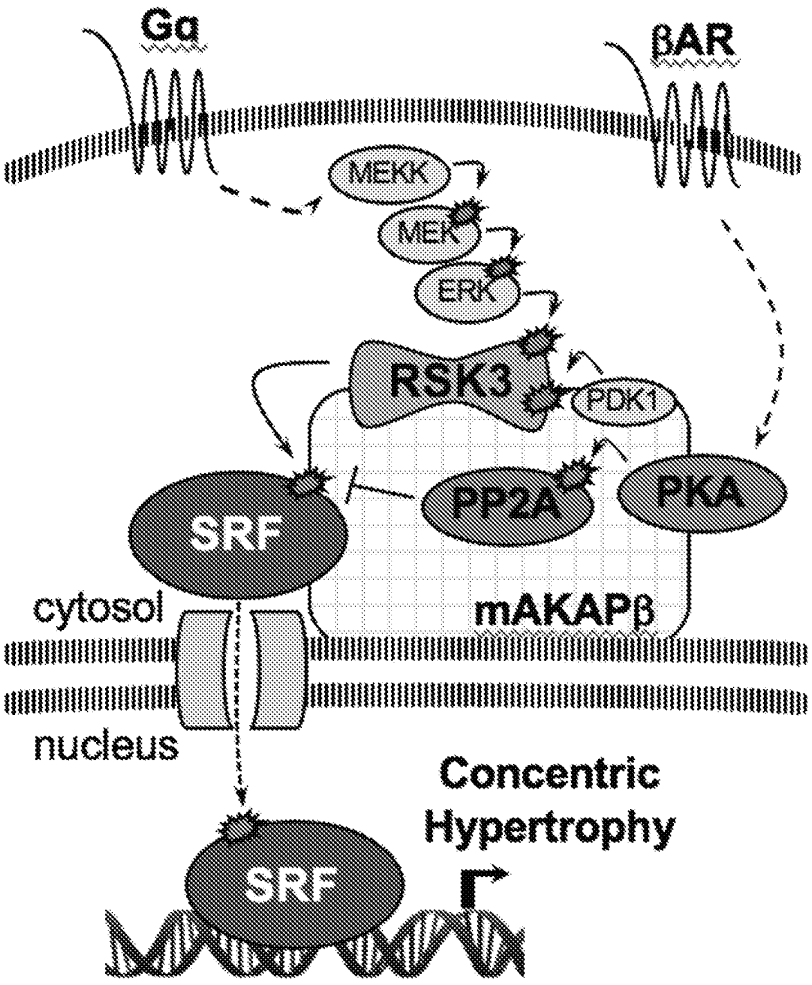

Gα
βAR
MEKK
MEK
ERK
RSK3
PDK1
SRF
PP2A
PKA
cytosol
mAKAPβ
nucleus
Concentric
Hypertrophy
SRF

FIGURE 2

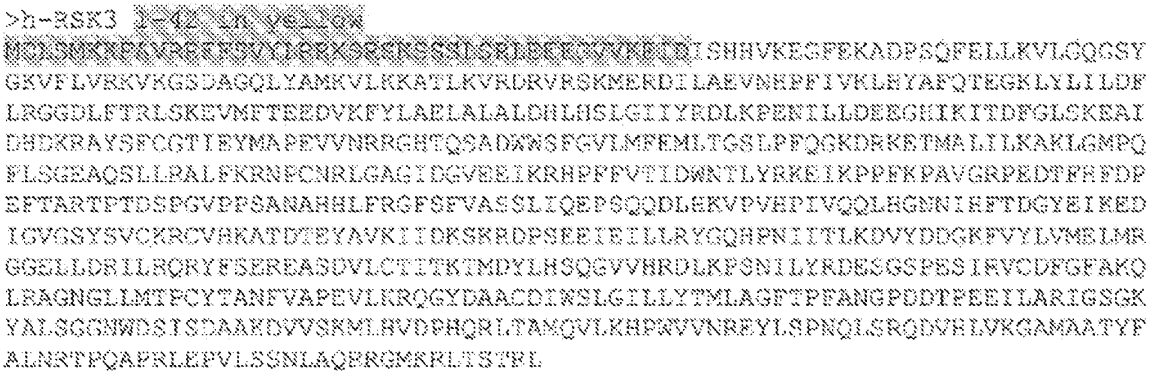


FIGURE 3

Figure 3. rat mAKAP sequence (PBD highlighted)

```
   1 MLTMSVTLSP LRSQGPDPMA TDASPMAINM TPTVEQEEGE GEEAVKAIDA
  51 EQQYGKPPPL HTAADWKIVL HLPEIETWLR MTSERVRDLT YSVQQDADSK
 101 HVDVHLVQLK DICEDISDHV EQIHALLETE FSLKLLSYSV NVIVDIHAVQ
 151 LLWHQLRVSV LVLRERILQG LQDANGNYTR QTDILQAFSE ETTEGRLDSL
 201 TEVDDSGQLT IKCSQDYLSL DCGITAFELS DYSPSEDLLG GLGDMTTSQA
 251 KTKSFDSWSY SEMEKEFPEL IRSVGLLTVA TEPVPSSCGE ANEDSSQASL
 301 SDDHKGEHGE DGAPVPGQQL DSTVGMSSLD GTLANAAEHP SETAKQDSTS
 351 SPQLGAKKTQ PGPCEITTPK RSIRDCFNYN EDSPTQPTLP KRGLFLKETQ
 401 KNERKGSDRK GQVVDLKPEL SRSTPSLVDP PDRSKLCLVL QSSYPSSPSA
 451 ASQSYECLHK VGLGNLENIV RSHIKEISSS LGRLTDCHKE KLRLKKPHKT
 501 LAEVSLCRIP KQGGGSGKRS ESTGSSAGPS MVSPGAPKAT MRPETDSAST
 551 ASGGLCHQRN RSGQLPVQSK ASSSPPCSHS SESSLGSDSI KSPVPLLSKN
 601 KSQKSSPPAP CHATQNGQVV EAWYGSDEYL ALPSHLKQTE VLALKLESLT
 651 KLLPQKPRGE TIQDIDDWEL SEMNSDSEIY PTYHIKKKHT RLGTVSPSSS
 701 SDIASSLGES IESGPLSDIL SDEDLCLPLS SVKKFTDEKS ERPSSSEKNE
 751 SHSATRSALI QKLMHDIQHQ ENYEAIWERI EGFVNKLDEF IQWLNEAMET
 801 TENWTPPKAE TDSLRLYLET HLSFKLNVDS HCALKEAVEE EGHQLLELVV
 851 SHKAGLKDTL RMIASQWKEL QRQIKRQHSW ILRALDTIKA EILATDVSVE
 901 DEEGTGSPKA EVQLCHLETQ RDAVEQMSLK LYSEQYTSGS KRKEEFANMS
 951 KAHAEGSNGL LDFDSEYQEL WDWLIDMESL VMDSHDLMMS EEQQQHLYKR
1001 YSVEMSIRHL KKSELLSKVE ALKKGGLSLP DDILEKVDSI NEKWELLGKT
1051 LREKIQDTIA GHSGSGPRDL LSPESGSLVR QLEVRIKELK RWLRDTELFI
1101 FNSCLRQEKE GTSAEKQLQY FKSLCREIKQ RRRGVASILR LCQHLLDDRD
1151 TCNLNADHQP MQLIIVNLER RWEAIVMQAV QWQTRLQKKM GKESETLNVI
1201 DPGLMDLNGM SEDALEWDET DISNKLISVH EESNDLDQDP EPMLPAVKLE
1251 ETHHKDSGYE EEAGDCGGSP YTSNITAPSS PHIYQVYSLH NVELHEDSHT
1301 PFLKSSPKFT GTTQPTVLTK SLSKDSSFSS TKSLPDLLGG SGLVRPYSCH
1351 SGDLSQNSGS ESGIVSEGDN EMPTNSDMSL FSMVDGSPSN PETEHPDPQM
1401 GDAANVLEQK FKDNGESIKL SSVSRASVSP VGCVNGKAGD LNSVTKHTAD
1451 CLGEELQGKH DVFTFYDYSY LQGSKLKLPM IMKQPQSEKA HVEDPLLGGF
1501 YFDKKSCKAK HQASESQPDA PPHERILASA PHEMGRSAYK SSDIEKTFTG
1551 IQSARQLSLL SRSSSVESLS PGGDLFGLGI FKNGSDSLQR STSLESWLTS
1601 YKSNEDLFSC HSSGDISVSS GSVGELSKRT LDLLNRLENI QSPSEQKIKR
1651 SVSDMTLQSS SQKMPFAGQM SLDVASSINE DSPASLTELS SSDELSLCSE
1701 DIVLHKNKIP ESNASFRKRL NRSVADESDV NVSMIVNVSC TSACTDDEDD
1751 SDLLSSSTLT LTEEELCLKD EDDDSSIATD DEIYEESNLM SGLDYIKNEL
1801 QTWIRPKLSL TREKKRSGVT DEIKVNKDGG GNEKANPSDT LDIEALLNGS
1851 IRCLSENNGN GKTPPRTHGS GTKGENKKST YDVSKDPHVA DMENGNIEST
1901 PEREREKPQG LPEVSENLAS NVKTISESEL SEYEAVMDGS EDSSVARKEF
1951 CPPNDRHPPQ MGPKLQHPEN QSGDCKPVQN PCPGLLSEAG VGSRQDSNGL
2001 KSLPNDAPSG ARKPAGCCLL EQNETEESAS ISSNASCCNC KPDVFHQKDD
```

FIGURE 3 (cont.)

2051 EDCSVHDFVK EIIDMASTAL KSKSQPESEV AAPTSLTQIK EKVLEHSHRP
2101 IHLRKGDFYS YLSLSSHDSD CGEVTNYIDE KSSTPLPPDA VDSGLDDKED
2151 MDCFFEACVE DEPVNEEAGL PGALPNESAI EDGAEQKSEQ KTASSPVLSD
2201 KTDLVPLSGL SPQKGADDAK EGDDVSHTSQ GCAESTEPTT PSGKANAEGR
2251 SRMQGVSATP EENAASAKPK IQAFSLNAKQ PKGKVAMRYP SPQTLTCKEK
2301 LVNFHEDRHS NMHR

FIGURE 4

Sequence for myc-PBD:

1 meqkliseed lspgmltmsv tlsplrsqtp lppdavdsgl ddkedmdcff eacvedepvn

61 eeaglpgalp nesaiedgae qkseqktass pvlsdktdly plsglspqkg addakegddv

121 shtsqgcaes tepttpsgka paegrsrmqg vsatpeenaa sakpkiqafs lnakqpkgkv

181 amrypspqtl tckeklvnfh edrhsnmhr.

FIGURE 5

Figure 5. pscA-TnT-myc-rat mAKAP PBD

```
   1  ACTCAACCAA GTCATTCTGA GAATAGTGTA TGCGGCGACC GAGTTGCTCT
  51  TGCCCGGCGT CAATACGGGA TAATACCGCG CCACATAGCA GAACTTTAAA
 101  AGTGCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACTC TCAAGGATCT
 151  TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGTGC ACCCAACTGA
 201  TCTTCAGCAT CTTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAAACAGG
 251  AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACGG AAATGTTGAA
 301  TACTCATACT CTTCCTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT
 351  TGTCTCATGA GCGGATACAT ATTTGAATGT ATTTAGAAAA ATAAACAAAT
 401  AGGGGTTCCG CGCACATTTC CCCGAAAAGT GCCACCTGAC GTCTAAGAAA
 451  CCATTATTAT CATGACATTA ACCTATAAAA ATAGGCGTAT CACGAGGCCC
 501  TTTCGTCTCG CGCGTTTCGG TGATGACGGT GAAAACCTCT GACACATGCA
 551  GCTCCCGGAG ACGGTCACAG CTTGTCTGTA AGCGGATGCC GGGAGCAGAC
 601  AAGCCCGTCA GGGCGCGTCA GCGGGTGTTG GCGGGTGTCG GGGCTGGCTT
 651  AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC ATATGGACAT
 701  ATTGTCGTTA GAACGCGGCT ACAATTAATA CATAACCTTA TGTATCATAC
 751  ACATACGATT TAGGTGACAC TATAGAACTC GAGCCTGCGC GCTCGCTCGC
 801  TCACTGAGGC CGCCCGGGCA AAGCCCGGGC GTCGGGCGAC CTTTGGTCGC
 851  CCGGCCTCAG TGAGCGAGCG AGCGCGCAGA GAGGGAGTGG CCAACTCCAT
 901  CACTAGGGGT TCCTTGTAGT TAATGATTAA CCCGCCATGC TACTTATCTA
 951  CGTAGCCATG CTCTAGAGCA GTCTGGGCTT TCACAAGACA GCATCTGGGG
1001  CTGCGGCAGA GGGTCGGGTC CGAAGCGCTG CCTTATCAGC GTCCCCAGCC
1051  CTGGGAGGTG ACAGCTGGCT GGCTTGTGTC AGCCCCTCGG GCACTCACGT
1101  ATCTCCGTCC GACGGGTTTA AAATAGCAAA ACTCTGAGGC CACACAATAG
1151  CTTGGGCTTA TATGGGCTCC TGTGGGGGAA GGGGGAGCAC GGAGGGGGCC
1201  GGGGCCGCTG CTGCCAAAAT AGCAGCTCAC AAGTGTTGCA TTCCTCTCTG
1251  GGCGCCGGGC ACATTCCTGC TGGCTCTGCC CGCCCCGGGG TGGGCGCCGG
1301  GGGGACCTTA AAGCCTCTGC CCCCCAAGGA GCCCTTCCCA GACAGCCGCC
1351  GGCACCCACC GCTCCGTGGG ACCTAAGCTT GCTAGCGCTA CCGGTCGCCA
         M  E  Q   K  L  I   S  E  E  D   L  S  P   G  M  L
1401  CCATGGAGCA GAAACTCATC TCTGAAGAGG ATCTGAGCCC GGGGATGTTA
       T  M  S  V   T  L  S   P  L  R   S  Q  T  P   L  P  P ·
1451  ACCATGAGCG TGACACTTTC CCCACTGAGG TCACAGACTC CATTGCCACC
      · D  A  V   D  S  G  L   D  D  K   E  D  M   D  C  F  F ·
1501  GGACGCTGTG GACTCTGGCT TAGATGACAA GGAAGACATG GACTGCTTCT
      · E  A  C   V  E  D   E  P  V  N   E  E  A   G  L  P
1551  TTGAAGCTTG TGTTGAGGAT GAGCCTGTCA ATGAGGAAGC TGGTCTCCCC
       G  A  L  P   N  E  S   A  I  E   D  G  A  E   Q  K  S ·
1601  GGTGCCCTTC CCAATGAATC AGCCATCGAG GATGGAGCAG AGCAAAAGTC
      · E  Q  K   T  A  S  S   P  V  L   S  D  K   T  D  L  V ·
1651  AGAACAAAAG ACAGCCAGCT CTCCTGTGCT CAGTGACAAG ACAGACCTGG
      · P  L  S   G  L  S   P  Q  K  G   A  D  D   A  K  E
```

FIGURE 5 (cont.)

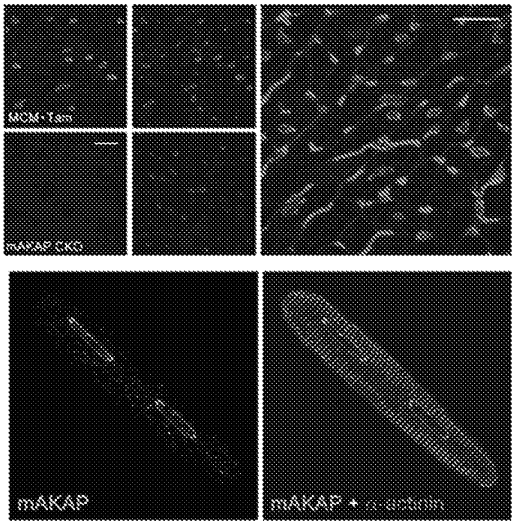
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1701  TGCCTCTTTC AGGACTTTCC CCTCAGAAGG GAGCTGATGA TGCAAAGGAA
        G   D   D   V   S   H   T   S   Q   G   C   A   E   S   T   E   P  ·
1751  GGAGATGATG TGTCTCACAC TTCCCAGGGC TGTGCAGAGA GCACAGAGCC
      ·  T   T   P   S   G   K   A   N   A   E   G   R   S   R   M   Q   G  ·
1801  TACCACCCCC TCAGGAAAGG CCAATGCAGA GGGGAGGTCA AGAATGCAAG
      ·  V   S   A   T   P   E   E   N   A   A   S   A   K   P   K   I
1851  GTGTATCAGC AACGCCAGAA GAAAACGCTG CTTCGGCCAA ACCGAAAATT
        Q   A   F   S   L   N   A   K   Q   P   K   G   K   V   A   M   R  ·
1901  CAAGCTTTCT CTTTGAATGC AAAACAGCCA AAAGGCAAGG TTGCCATGAG
      ·  Y   P   S   P   Q   T   L   T   C   K   E   K   L   V   N   F   H  ·
1951  GTATCCCAGC CCCCAAACTC TAACCTGTAA AGAGAAGCTC GTAAACTTTC
      ·  E   D   R   H   S   N   M   H   R
2001  ATGAAGATCG ACACAGTAAC ATGCATAGGT AGAGTGTAAT GCCCCCACGC
2051  ATGGAAATCA TCTCATTGAA AGATAGCCTG GCTGAAGCTC AGGGCTAGTT
2101  AAGTTTGATC CAGACATGAT AAGATACATT GATGAGTTTG GACAAACCAC
2151  AACTAGAATG CAGTGAAAAA AATGCTTTAT TTGTGAAATT TGTGATGCTA
2201  TTGCTTTATT TGTAACCATT ATAAGCTGCA ATAAACAAGT TAACAACAAC
2251  AATTGCATTC ATTTTATGTT TCAGGTTCAG GGGGAGGTGT GGGAGGTTTT
2301  TTAAAGCAAG TAAAACCTCT ACAAATGTGG TATGGCTGAT TACCACTCCC
2351  TCTCTGCGCG CTCGCTCGCT CACTGAGGCC GGGCGACCAA AGGTCGCCCG
2401  ACGCCCGGGC TTTGCCCGGG CGGCCTCAGT GAGCGAGCGA GCGCGCCAGC
2451  TGAAGCTATC AGATCTGCCG GTCTCCCTAT AGTGAGTCGT ATTAATTTCG
2501  ATAAGCCAGG TTAACCTGCA TTAATGAATC GGCCAACGCG CGGGGAGAGG
2551  CGGTTTGCGT ATTGGGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC
2601  GCTCGGTCGT TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA
2651  ATACGGTTAT CCACAGAATC AGGGGATAAC GCAGGAAAGA ACATGTGAGC
2701  AAAAGGCCAG CAAAAGGCCA GGAACCGTAA AAAGGCCGCG TTGCTGGCGT
2751  TTTTCCATAG GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA
2801  AGTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC
2851  CCCTGGAAGC TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG
2901  GATACCTGTC CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCATAGC
2951  TCACGCTGTA GGTATCTCAG TTCGGTGTAG GTCGTTCGCT CCAAGCTGGG
3001  CTGTGTGCAC GAACCCCCCG TTCAGCCCGA CCGCTGCGCC TTATCCGGTA
3051  ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA
3101  GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC
3151  AGAGTTCTTG AAGTGGTGGC CTAACTACGG CTACACTAGA AGAACAGTAT
3201  TTGGTATCTG CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT
3251  AGCTCTTGAT CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT
3301  TTGCAAGCAG CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT
3351  TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA
3401  GGGATTTTGG TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT
3451  AAATTAAAAA TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT
3501  GGTCTGACAG TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC
3551  TGTCTATTTC GTTCATCCAT AGTTGCCTGA CTCCCCGTCG TGTAGATAAC
3601  TACGATACGG GAGGGCTTAC CATCTGGCCC CAGTGCTGCA ATGATACCGC
```

FIGURE 5 (cont.)

```
3651  GAGACCCACG CTCACCGGCT CCAGATTTAT CAGCAATAAA CCAGCCAGCC
3701  GGAAGGGCCG AGCGCAGAAG TGGTCCTGCA ACTTTATCCG CCTCCATCCA
3751  GTCTATTAAT TGTTGCCGGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA
3801  GTTTGCGCAA CGTTGTTGCC ATTGCTACAG GCATCGTGGT GTCACGCTCG
3851  TCGTTTGGTA TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT
3901  TACATGATCC CCCATGTTGT GCAAAAAAGC GGTTAGCTCC TTCGGTCCTC
3951  CGATCGTTGT CAGAAGTAAG TTGGCCGCAG TGTTATCACT CATGGTTATG
4001  GCAGCACTGC ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC
4051  TGTGACTGGT GAGT
```

FIGURE 6

A


MOM-Tom
mAKAP CKO
mAKAP
mAKAP + α-actinin

B

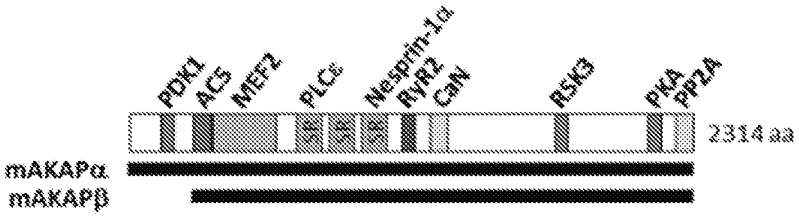

PDK1
AC5
MEF2
PLCε
Nesprin-1α
RyR2
CaN
RSK3
PKA
PP2A
2314 aa
mAKAPα
mAKAPβ

FIGURE 7

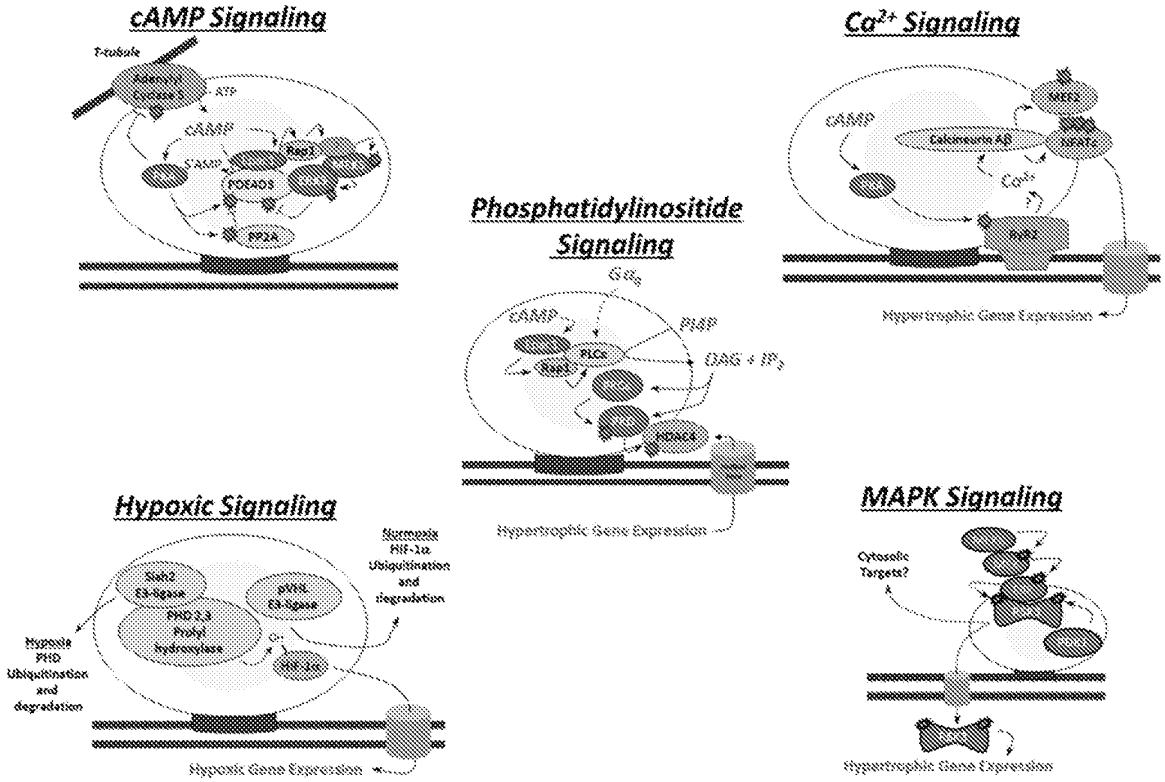

cAMP Signaling
T-tubule
ATP
cAMP
Ras2
FOXAO3
PP2A
Phosphatidylinositide Signaling
cAMP
PIP2
PLCε
Ras2
DAG + IP3
HDAC4
Hypertrophic Gene Expression
Ca2+ Signaling
cAMP
Calcineurin AB
Hypertrophic Gene Expression
Hypoxic Signaling
Normoxia HIF-1α Ubiquitination and degradation
Siah2 E3-ligase
pVHL E3-ligase
PHD 1,2 Prolyl hydroxylase
HIF-1α
Hypoxia PHD Ubiquitination and degradation
Hypoxic Gene Expression
MAPK Signaling
Cytosolic Targets?
Hypertrophic Gene Expression

FIGURE 8

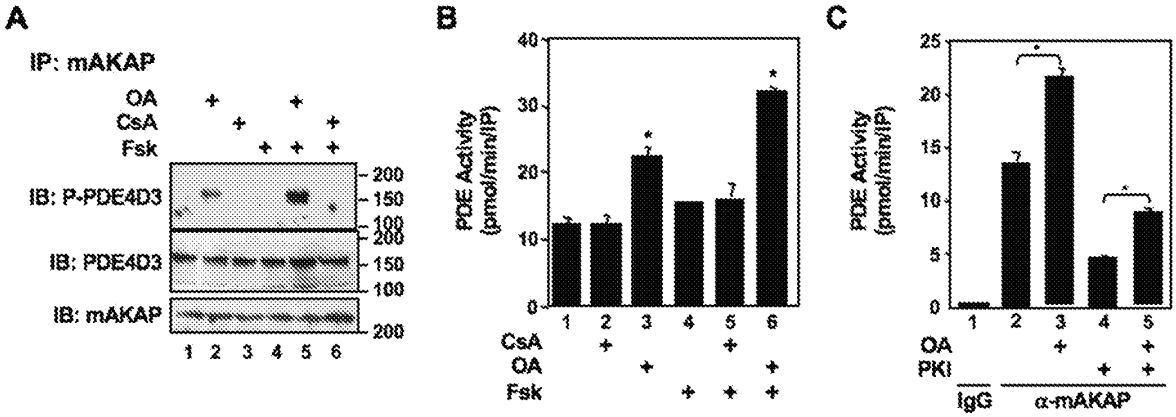

A
IP: mAKAP
OA
CsA
Fsk
IB: P-PDE4D3
IB: PDE4D3
IB: mAKAP
200
150
100
200
150
100
200
1 2 3 4 5 6
B
PDE Activity (pmol/min/IP)
40
30
20
10
0
1 2 3 4 5 6
CsA
OA
Fsk
C
PDE Activity (pmol/min/IP)
25
20
15
10
5
0
1 2 3 4 5
OA
PKI
IgG
α-mAKAP

FIGURE 9

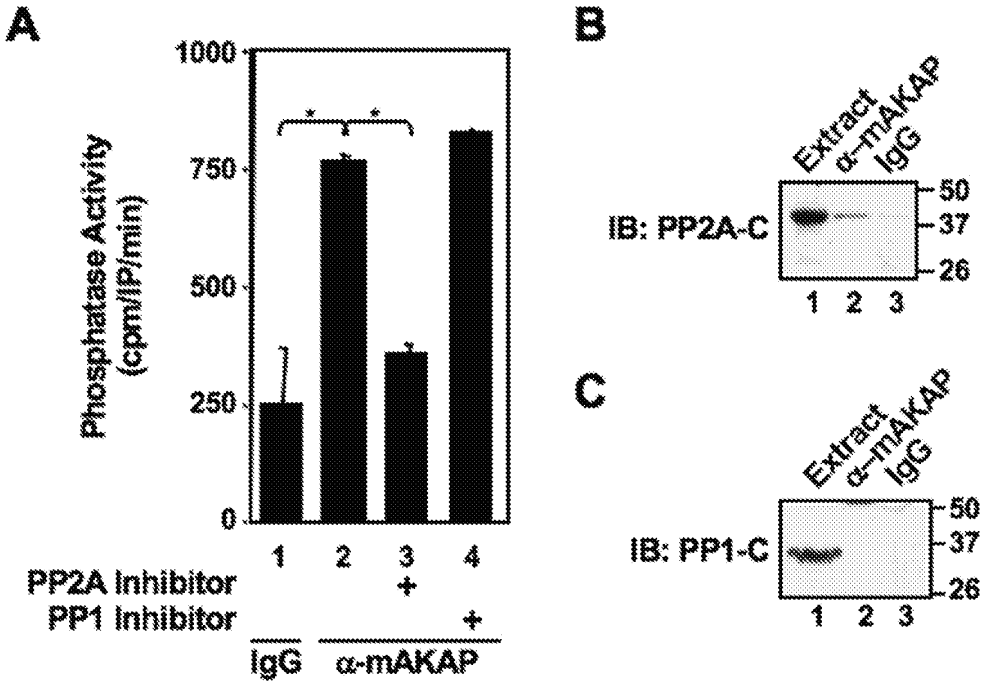

A
Phosphatase Activity (cpm/IP/min)
1000
750
500
250
0
1 2 3 4
PP2A Inhibitor + +
PP1 Inhibitor +
IgG α-mAKAP
B
Extract α-mAKAP IgG
IB: PP2A-C
50
37
26
1 2 3
C
Extract α-mAKAP IgG
IB: PP1-C
50
37
26
1 2 3

FIGURE 10

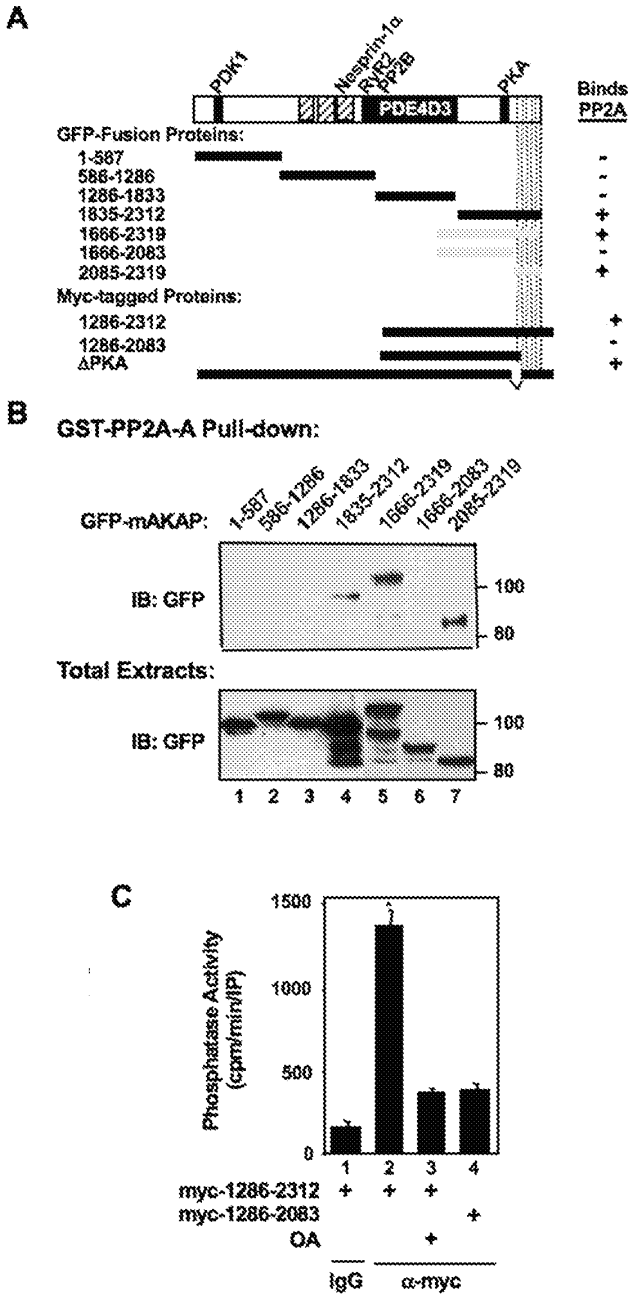

A
PDK1
Nesprin-1α
RyR2
PP2B
PKA
PDE4D3
Binds PP2A
GFP-Fusion Proteins:
1-587
586-1286
1286-1833
1835-2312
1666-2319
1666-2083
2085-2319
Myc-tagged Proteins:
1286-2312
1286-2083
ΔPKA
B
GST-PP2A-A Pull-down:
GFP-mAKAP:
1-587
586-1286
1286-1833
1835-2312
1666-2319
1666-2083
2085-2319
IB: GFP
100
80
Total Extracts:
IB: GFP
100
80
1 2 3 4 5 6 7
C
Phosphatase Activity (cpm/min/IP)
1500
1000
500
0
1 2 3 4
myc-1286-2312
myc-1286-2083
OA
IgG
α-myc

FIGURE 11

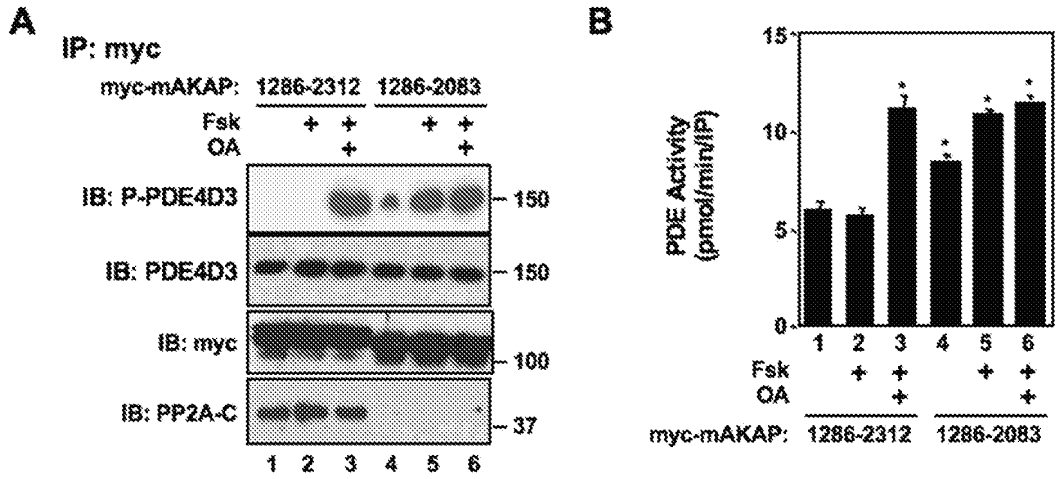

A
IP: myc
myc-mAKAP: 1286-2312 1286-2083
Fsk + + + +
OA + +
IB: P-PDE4D3
IB: PDE4D3
IB: myc
IB: PP2A-C
150
150
100
37
1 2 3 4 5 6
B
PDE Activity (pmol/min/IP)
15
10
5
0
1 2 3 4 5 6
Fsk + + + +
OA + +
myc-mAKAP: 1286-2312 1286-2083

FIGURE 12

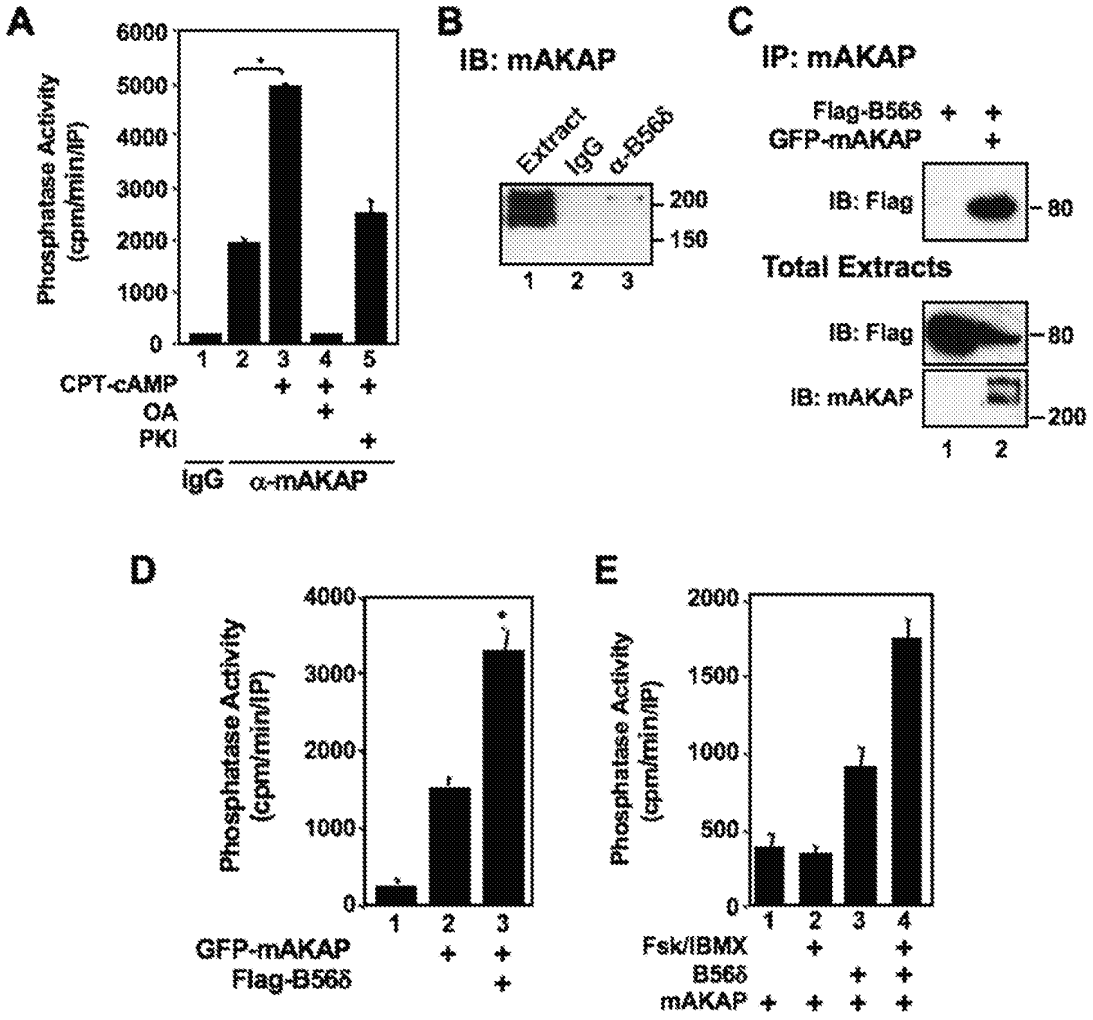

A
Phosphatase Activity (cpm/min/IP)
6000
5000
4000
3000
2000
1000
0
1 2 3 4 5
CPT-cAMP + + +
OA + +
PKI +
IgG α-mAKAP
B
IB: mAKAP
Extract
IgG
α-B56δ
200
150
1 2 3
C
IP: mAKAP
Flag-B56δ + +
GFP-mAKAP +
IB: Flag
80
Total Extracts
IB: Flag
80
IB: mAKAP
200
1 2
D
Phosphatase Activity (cpm/min/IP)
4000
3000
2000
1000
0
1 2 3
GFP-mAKAP + +
Flag-B56δ +
E
Phosphatase Activity (cpm/min/IP)
2000
1500
1000
500
0
1 2 3 4
Fsk/IBMX + +
B56δ + +
mAKAP + + + +

FIGURE 13

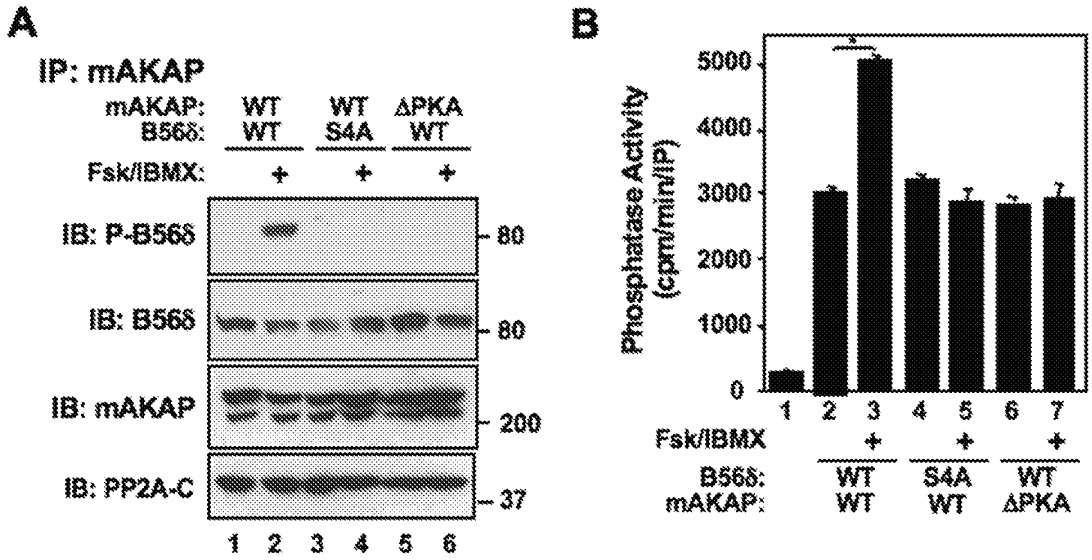

A
IP: mAKAP
mAKAP: WT WT ΔPKA
B56δ: WT S4A WT
Fsk/IBMX: + + +
IB: P-B56δ
IB: B56δ
IB: mAKAP
IB: PP2A-C
80
80
200
37
1 2 3 4 5 6
B
Phosphatase Activity (cpm/min/IP)
5000
4000
3000
2000
1000
0
1 2 3 4 5 6 7
Fsk/IBMX + + +
B56δ: WT S4A WT
mAKAP: WT WT ΔPKA

FIGURE 14

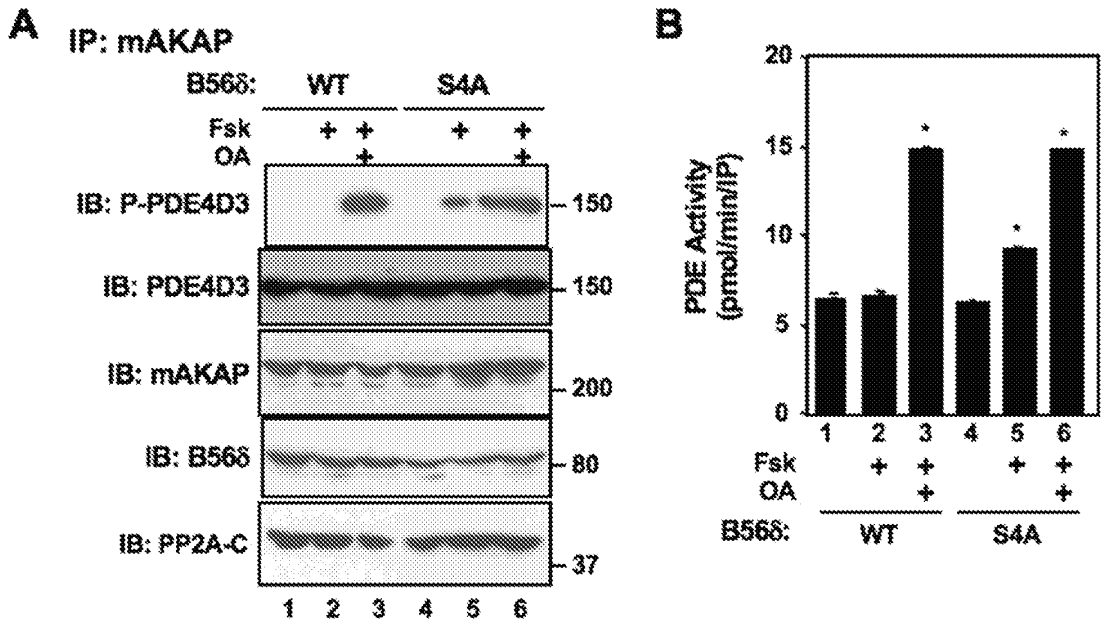

A
IP: mAKAP
B56δ: WT S4A
Fsk
OA
IB: P-PDE4D3
IB: PDE4D3
IB: mAKAP
IB: B56δ
IB: PP2A-C
150
150
200
80
37
1 2 3 4 5 6
B
PDE Activity (pmol/min/IP)
20
15
10
5
0
1 2 3 4 5 6
Fsk
OA
B56δ: WT S4A

FIGURE 15

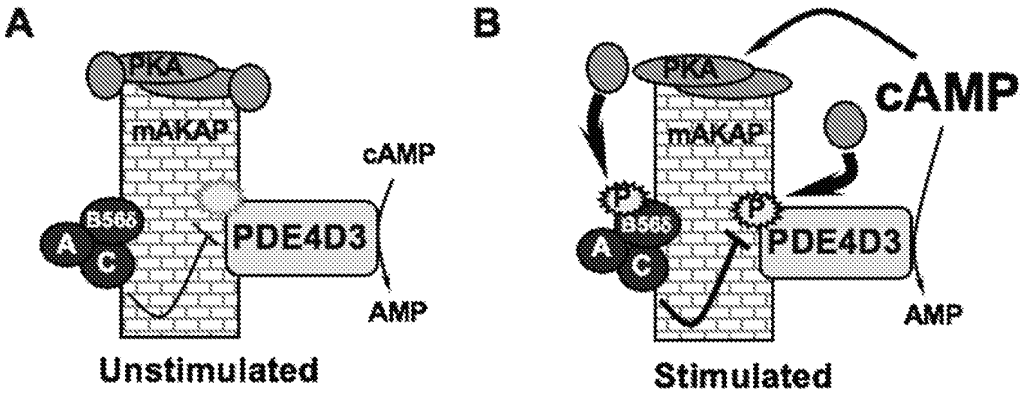

A
PKA
mAKAP
cAMP
B56δ
A
C
PDE4D3
AMP
Unstimulated
B
PKA
cAMP
mAKAP
P
P
B56δ
A
C
PDE4D3
AMP
Stimulated

FIGURE 16

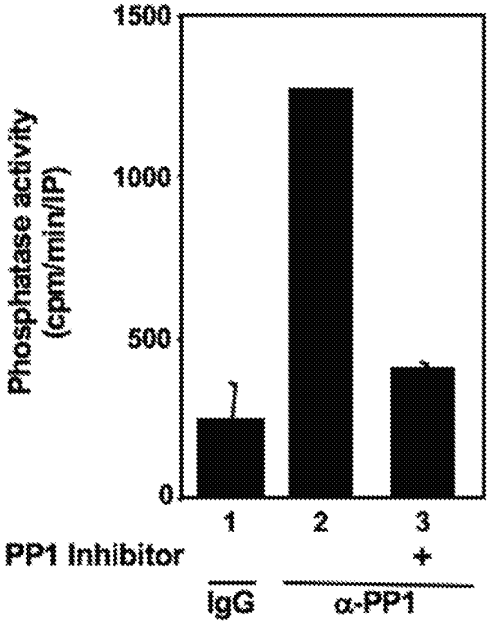

1500
1000
500
0
Phosphatase activity
(cpm/min/IP)
1
2
3
PP1 Inhibitor
+
IgG
α-PP1

FIGURE 17

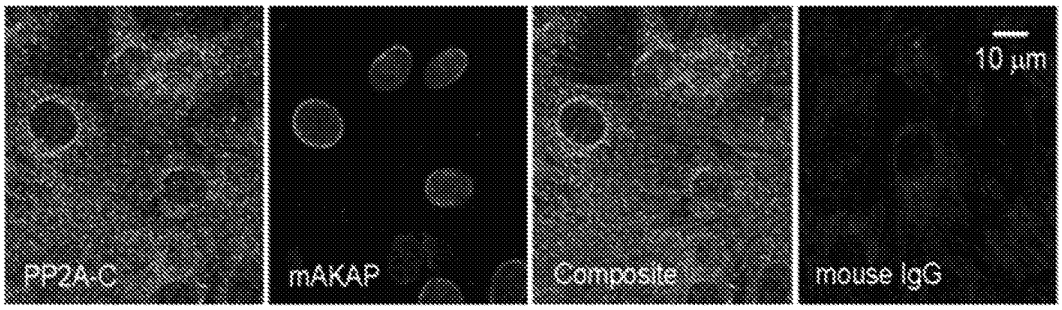


FIGURE 18

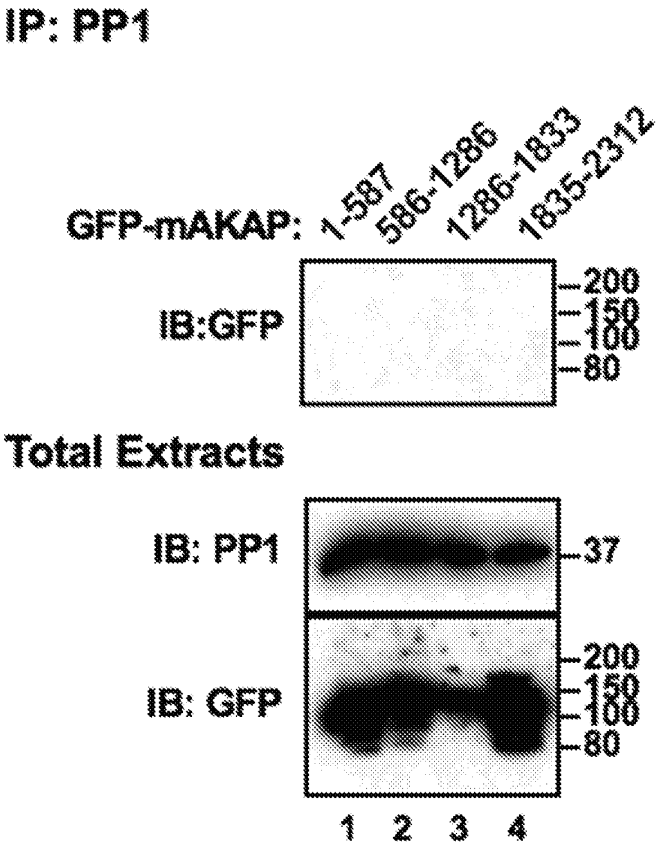

IP: PP1
GFP-mAKAP:
1-587
586-1286
1286-1833
1835-2312
IB:GFP
200
150
100
80
Total Extracts
IB: PP1
37
IB: GFP
200
150
100
80
1 2 3 4

FIGURE 19

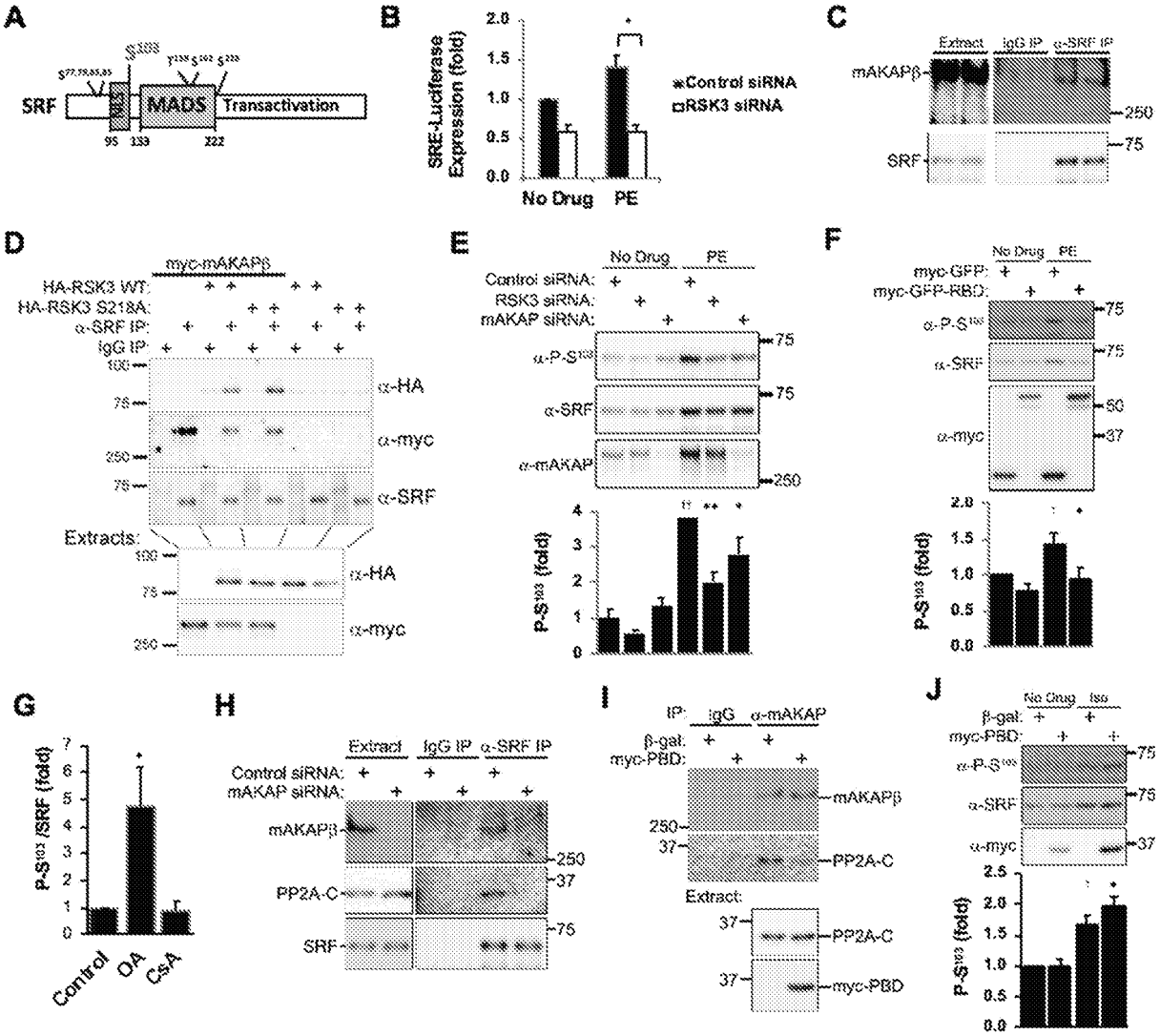

A
SRF
MADS
Transactivation
95
133
222
B
SRE-Luciferase Expression (fold)
Control siRNA
RSK3 siRNA
No Drug
PE
C
Extract
IgG IP
α-SRF IP
mAKAPβ
SRF
250
75
D
myc-mAKAPβ
HA-RSK3 WT:
HA-RSK3 S218A:
α-SRF IP:
IgG IP:
α-HA
α-myc
α-SRF
Extracts:
E
No Drug
PE
Control siRNA:
RSK3 siRNA:
mAKAP siRNA:
α-mAKAP
F
myc-GFP:
myc-GFP-RBD:
α-SRF
α-myc
G
Control
OA
CsA
H
Control siRNA:
mAKAP siRNA:
mAKAPβ
PP2A-C
SRF
I
IP:
IgG
α-mAKAP
β-gal:
myc-PBD:
Extract:
J
Iso

FIGURE 20

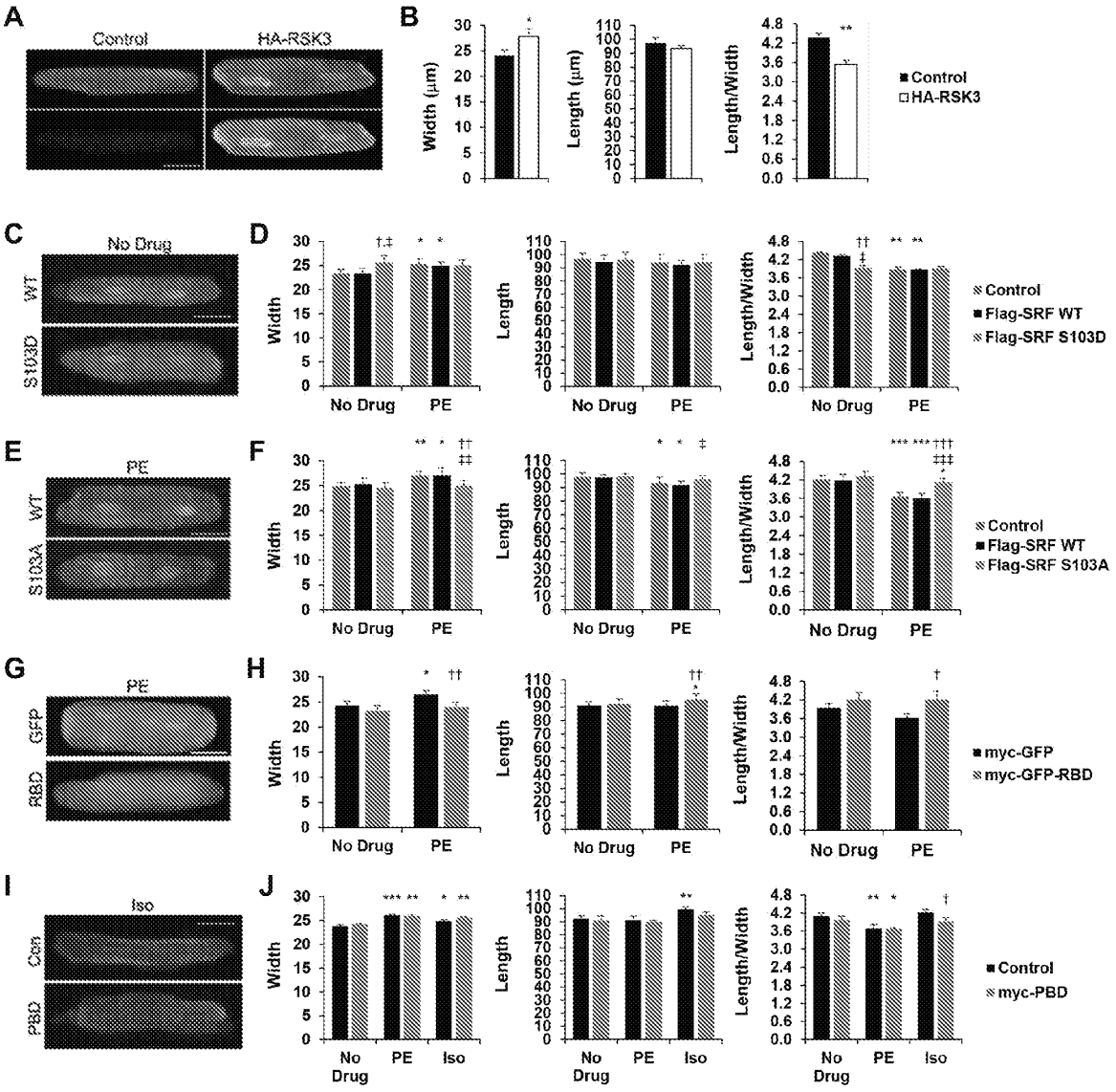

A
Control
HA-RSK3
B
Width (μm)
Length (μm)
Length/Width
Control
HA-RSK3
C
No Drug
WT
S103D
D
Width
Length
Length/Width
No Drug
PE
Control
Flag-SRF WT
Flag-SRF S103D
E
PE
WT
S103A
F
Width
Length
Length/Width
No Drug
PE
Control
Flag-SRF WT
Flag-SRF S103A
G
PE
GFP
RBD
H
Width
Length
Length/Width
No Drug
PE
myc-GFP
myc-GFP-RBD
I
Iso
Con
PBD
J
Width
Length
Length/Width
No Drug
PE
Iso
Control
myc-PBD

FIGURE 21

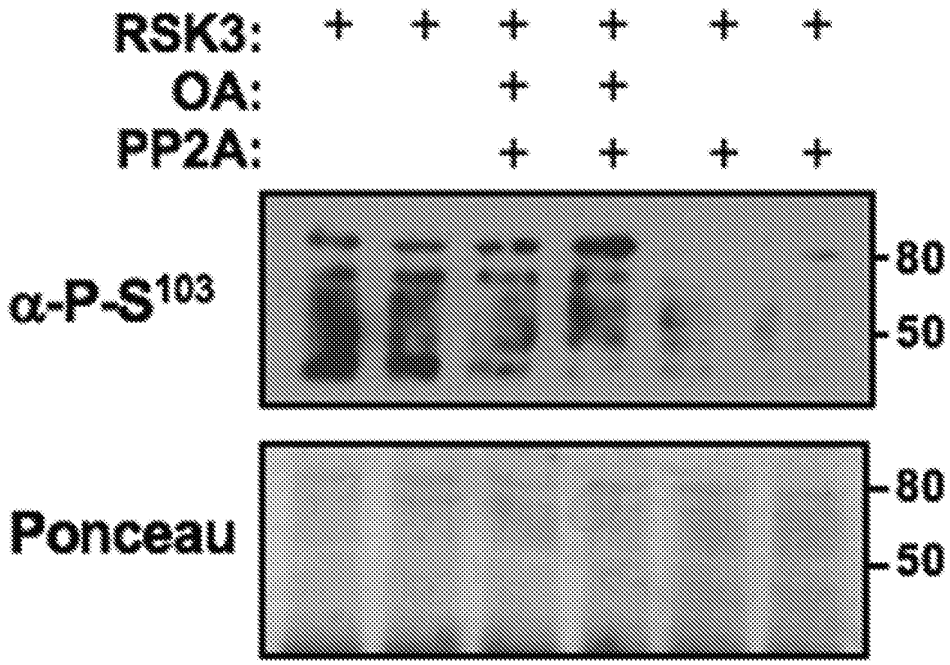


FIGURE 22

A


ITR
cTnT
myc-PBD
SV40 polyA
ITRΔ

B

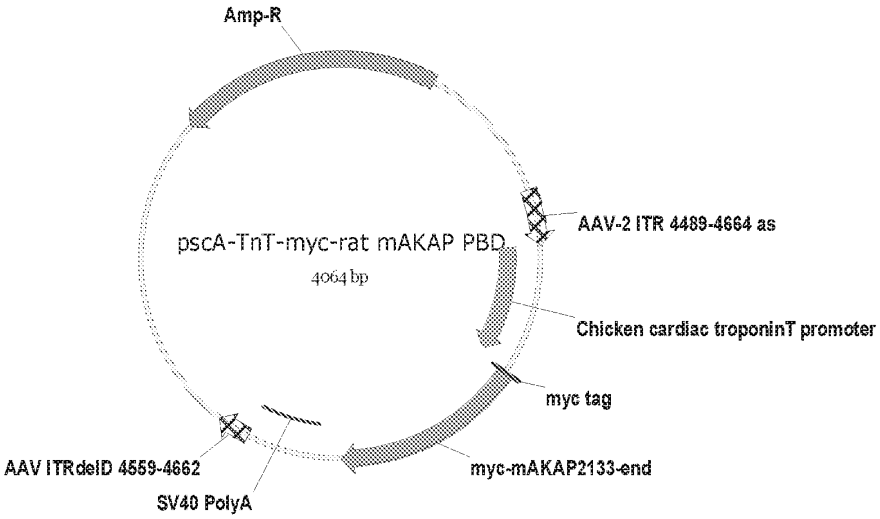

Amp-R
pscA-TnT-myc-rat mAKAP PBD
4064 bp
AAV-2 ITR 4489-4664 as
Chicken cardiac troponinT promoter
myc tag
myc-mAKAP2133-end
AAV ITRdelD 4559-4662
SV40 PolyA

FIGURE 23

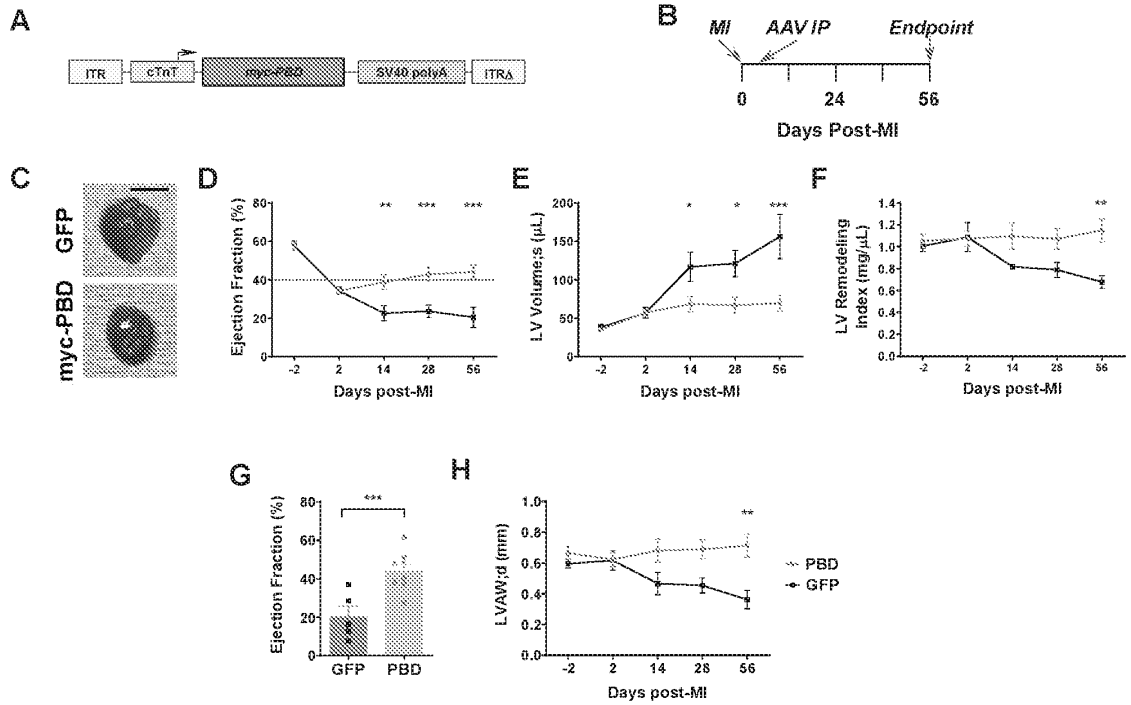

A
ITR
cTnT
myc-PBD
SV40 polyA
ITRΔ
B
MI
AAV IP
Endpoint
0
24
56
Days Post-MI
C
GFP
myc-PBD
D
Ejection Fraction (%)
Days post-MI
E
LV Volume;s (µL)
Days post-MI
F
LV Remodeling index (mg/µL)
Days post-MI
G
Ejection Fraction (%)
GFP
PBD
H
LVAW;d (mm)
Days post-MI
PBD
GFP

FIGURE 24

```
LOCUS       hRSK3         5817 bp     DNA     linear   PRI 22-JAN-2009
DEFINITION  Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2
(RPS6KA2), transcript variant 1, mRNA.
BASE COUNT     1285 a      1585 c      1591 g      1356 t
ORIGIN
        1 gcggagaagg aggcggaggg agcgattgtg gccccggccg cggtggccgg cgcggcctgc
       61 cctttgtgac cgcagctcgc gccccacgcc ccgcgcccat ggccgccgtg ccgggctccc
      121 tggccacgcg tgcccgcccg cggacctgag cccccgcgcc tgggatgccgg ggatgccgcg
      181 ccccgggccc tgcggcgtgt ccgggctggg cgcggggcga tggacctgag catgaagaag
      241 ttcgccgtgc gcaggttctt ctctgtgtac ctgcgcaagga agtccgcgtc caagagctcc
      301 agcctgagcc ggctcgagga agaaggcgtc gtgaaggaga tagacatcag ccatcatgtg
      361 aaggagggct ttgagaaggc agatccttcc cagtttgagc tgctgaaggt tttaggacac
      421 ggatcctatg gaaaggtgtt cctggtgagg aagggtgaag ggtccgacgc tgggcagctc
      481 tacgccatga aggtcttaaa gaaagccacc ctaaaagttc gggaccgagt gagatcgaag
      541 atggagagag acatcttggc agaagtgaat cacccccttc ttgtgaagct tcattatgcc
      601 tttcagacgg aaggaaagct ctacctgatc ctggacttcc tgcggggagg ggacctcttc
      661 acccggctct ccaaagaggt catgttcacg gaggaggatg tcaagttcta cctggctgag
      721 ctggccttgg ctttagaccc tctccacagc ctggggatca tctacagaga tctgaagcct
      781 gagaacatcc tcctggatga agagggccac attaagatca cagattttgg cctgagtaag
      841 gaggccattg accacgacaa gagagcgtac tccttctgcg ggacgatcga gtacatggcg
      901 cccgaggtgg tgaacggcgg aggacacagg cagagtgccg actggtggtc ctttggcgtg
      961 ctcatgttcg agatgctcac ggggtcccct ccgttccagg ggaaggacag gaaggagacc
     1021 atggctatca tcctcaaagc caagctgggg atgccgcagt tcctcagtgg ggaggcacag
     1081 agtttgctgc gagctctctt caaacggaac cctgcaacc ggctgggtgc tggcattgac
     1141 ggagtggagg aaattaagcg ccatccattc tttgtgacca tagactggaa cacgctgtac
     1201 cggaaggaga tcaagccacc gttcaaacca gcagtgggca ggcctgagga cacccttccac
     1261 tttgacccag agttcacagc gcggacgccc acagactctc ctggcgtccc ccgagtgca
     1321 aacgctcatc accgtttag aggattcagc tttgtggcct caagcctgat ccaggagccc
     1381 tcacagcaag atctgcacaa agtcccagtt cacccaatcg tgcagcagtt acacgggaac
     1441 aacatccact tcaccgatgg ctacgagatc aaggaggaca tcgggtggg ctcctactca
     1501 gtgtgcaagc gatgtgtgca taaagccaca gacaccgagt atgccgtgaa gatcattgat
     1561 aagagcaaga gagaccctc ggaagagatt gagatcctcc tgcggtacgg ccagcaccc
     1621 aacatcatca ccctcaagga tgtctatgat gatggcaagt ttgtgtacct ggtaatggag
     1681 ctgatgcgtg gtggggagct cctggaccgc atcctccggc agagatactt ctcggagcgc
     1741 gaagccagtg acgtcctgtg caccatcacc aagaccatgg actacctcca ttcccagggg
     1801 gttgttcatc gagacctgaa gccgagtaac atcctgtaca gggatgagtc ggggagccca
     1861 gaatccatcc gagtctgcga cttcggcttt gccaagcagc tgcgcgcggg gaacgggctg
     1921 ctcatgacac cctgctacac ggccaatttc gtggcccctg aggtcctgaa gcgtcaaggc
     1981 tatgatgcgg cgtgtgacat ctggagtttg gggatcctgt tgtacaccat gctggcagga
     2041 tttaccccct ttgcaaatgg gccagacgat acccctgagg agattctggc gcggatcggc
     2101 agtgggaagt atgccctttc tggggaaac tgggactcga tatctgacgc agctaaagac
     2161 gtcgtgtcca agatgctcca cgtggaccct catcagcgcc tgacggcgat gcaagtgctc
     2221 aaacaccccg gggtggtcaa cagagagtac ctgtccccaa accagctcag ccgacaggac
     2281 gtgcacctgg tgaagggcgc gatggccgcc acctactttg ctctaaacag aacacctcag
     2341 gcccgcggc tggagccgt gctgtcatcc aacctggctc agcgcagagg catgaagaga
     2401 ctcacgtcca cgcggctgta gcgggtggga ccctggcccc agcgtcccct gccagcatcc
     2461 tcgtgggctc acagacccog gcctcggagc ccgtctggca cccagagtga ccacaagtcc
     2521 agcagggagg cggcgcccgc cctcgccgtg tccgtgtttt cttttcagc cccggagagg
     2581 gtcctgacct ggggggcttct ccaagcctca ctgcgccagc ctccccgccc gctctctttt
     2641 ctcccaagcg aaaccaaatg cgccccttca cctgcgtgc ccgtgcgagg ccgggggctt
     2701 ctttcagagc ccgcgggtcc tctcatacat ggcttctgtt tctgccgaga gatctgtttt
     2761 ccaattatga agccggtcgg tttggtcaga ctcccgacac ccacgtccca ggtacccggt
```

FIGURE 24 (cont.)

2821 gggaaagtgg cagtgcgagg gcgcagccat tggtggttgc agggccccag agggctgggg
2881 tgacctggca tcccgggggt ccccacgggc tggatgacgg ggttggcact gtggcgtcca
2941 ggaggagatg cctggttctg cccaaaataa tccaaagagc cgtttcctcc tcgccccttca
3001 gttttgcct gaggtgctgg gtagcccatc ctttcctctg tcccagattc aaatgaggag
3061 taagagccca gacgagagga aggcaggctg gatctttgcc ttgagagctc cgtgtcacca
3121 ggatggaagg gggtgcctct cggaggagcc tgtgtccacc tccagtctcg gctttccccg
3181 gggggccaag cgcactgggc tgccgtctgt ccccagctcc cgtggccaca cagctatctg
3241 gaggctttgc agggagtcgt gggttctcgc acctgctcag ccctgtgtcg gcttcctgtg
3301 tgctcaccta aagctgtggt tttgctgtgt tcacttcgat ttttctggtc tgtggagaaa
3361 ctgtgaattg gagaaatgga gctctgtggc ttcccaccca aaccttctca gtccagctgg
3421 aggctggagg gagacacagg ccccacccag cagactgagg ggcagaggca caggtgggag
3481 ggcagcggag atcagcgtgg acaggagcga tgcactttgt agatgctgtg gctttgtgtt
3541 gcgttttgtg tctctgttgc acagatctgt ttttcacac tgatccgtat tcccctgggt
3601 gtgcacacag ggcgggtgtg gggcatttag gccatgcngt gctctacttc attgagtaaa
3661 atcgagtgag aggttccggg cagcaggatc gacgcccagt ccagccggca gagggaacac
3721 acgggtcctt cattgtcctg taagggtgtt gaagatgctc cctggcggcc cccaagcaga
3781 ctagatggga ggaggcgccg ctcagcccct caccctgcat cactgaagag cggcgcctct
3841 gcagcaagca gggcttcagg aggtgcccgc tggccacagc caggttttcc ctaagaagat
3901 gttatttttgt tgggttttgt tcccccccca tctcgattct cgtacccaac taaaaaaaaa
3961 aaaataaaga aaaaatgtgc tgcgttctga aaaataactc cttagcttgg tctgattgtt
4021 ttcagacctt aaaatataaa cttgtttcac aagctttaat ccatgtggat ttttttttte
4081 ttagagaacc acaaaacata aaaggagcaa gtcggactga atacctgttt ccatagtgcc
4141 cacagggtat tcctcacatt ttctccatag aagatgcttt ttcccaaggc tagaacgact
4201 tccaccatga tgaatttgct ttttaggtct taatttattc acttcttttt agaaacttag
4261 gaagaagtgg ataatcctga ggtcacacaa tctgtcctcc cagaaatgaa caaaagtcat
4321 caccttttct gcttgctaca caggcaacga ttccccccatc agctgcccgg acccttggc
4381 ctggcttggt gtgcaggcct gtctgtttgc ttaaagtcag tgggttctgg tgcagggagt
4441 gagaagtggg ggaagtgaaa gggaaagcat ccgtgagaaa gcggccacgg ttttccctcc
4501 ttgtgtgccc atggggcacc agctcatggt ctttttcagt catcccagtt tgtacagact
4561 tagcttctga actctaagaa tgccaaaggg accgacgaga ctcccccatca cagcgagctc
4621 tgtccttaca tgtattttgat gtgcatcagc ggaggagaac actggcttgg ccctgctccg
4681 ctgagtgtct gtgaaatacc tctactttcc ctcccatatc cagaacaaaa tgatacttga
4741 catccttcca caaaagtcag cctaaagaag ttatggtatc atatgttaaa ctaagctttc
4801 aaaaacctta gtgaaatagc aagtgactgc tttcaagcag cagtcgacat gtaaatgaag
4861 gtgttcttag aattcgcatt ttgccagctc agcgcacctc cacaacgaat gaaatgctcc
4921 gtatgatttg cacaaatgac atagacctcc ccaaaagtta actggctctc cttcctcaca
4981 cagttcatca taacccaacc ccccaccccc gggtcatgaa aatcacagaa cttataaaca
5041 cattgaaccc tagatctcag gcttcctgac ctaccgccag tggccccttg ctggccaccc
5101 tatagggtcc tccttccctg gcagcccccc atgtgggaga aataccbgat tctcccaatc
5161 tgcagtggga gagctttgct gaattccatc ccaaagtcaa acatgggcaa gaggtgagga
5221 tttcactttt accctcaagt ccgatttgtc tgtgatttta aactaactgt gtatgtattg
5281 atgtttggaa gattgtttga attttaaagt gataatagta cttaatgtta tccagtattg
5341 ttcattaaat ggtgttatcc taaagctgca cttgggattt ttacctaacg ctttactgat
5401 tctctcaagc acatggcaaa gtttgatttg cactccgttc atttctgaca cgttttgctg
5461 cctcctacct ttctaagcgt catgcaaatt cgagaatgga gaaggacgct gccggtccct
5521 gagcggtgtg gagagggcgg aaggtggact ccagcgcagc ttgaggggct gaggacggag
5581 gctgcagcat ctgtgtcgtt ctactgagca cgcttctctg cctcgctcct gactcagcac
5641 tttgttcact ggctcagcag ttatgtttac acatcatttt tatgttcctg ctttgtaatt
5701 catgtttgag atgggtggcc actgtacaga tatttattac gctttccaga ctttctgcat
5761 agatttttt gaataaacat ggttttatga agtgtaatct ttttctagcc taacaat

FIGURE 25

Figure 25. rat mAKAPα mRNA with open reading frame translated:

```
   1 GCATCATGCA GCAGGTCAAA CAAGGCATCT CCTAGTATTG CATCCTCCAG ATGTGCTGTA AACATCAAAA
                                                                 M   L   T   M   S  ·
  71 GGAGACGCTG GGAGCAGGAG ATGCTGTTTT GGAAAGAAGT AAGGCTTAGA TTTCTCCATG TTAACCATGA
     ·   V   T   L   S   P   L   R   S   Q   G   P   D   P   M   A   T   D   A   S   P   M   A   I  ·
 141 GCGTGACACT TTCCCCACTG AGGTCACAGG GCCCAGATCC CATGGCGACG GATGCTTCAC CCATGGCCAT
     ·   N   M   T   P   T   V   E   Q   E   E   G   E   G   E   E   A   V   K   A   I   D   A   E
 211 CAACATGACA CCCACTGTGG AGCAGGAGGA AGGAGAGGGA GAGGAAGCCG TGAAGGCCAT AGACGCTGAG
      Q   Q   Y   G   K   P   P   P   L   H   T   A   A   D   W   K   I   V   L   H   L   P   E   I  ·
 281 CAGCAGTATG GAAAGCCACC TCCGCTCCAC ACAGCAGCCG ACTGGAAGAT TGTCCTGCAC TTACCTGAGA
     ·   E   T   W   L   R   M   T   S   E   R   V   R   D   L   T   Y   S   V   Q   Q   D   A   D  ·
 351 TTGAGACCTG GCTCCGGATG ACCTCAGAGA GGGTCCGTGA CCTGACCTAC TCAGTCCAGC AGGATGCAGA
     ·   S   K   H   V   D   V   H   L   V   Q   L   K   D   I   C   E   D   I   S   D   H   V   E
 421 CAGCAAGCAT GTGGATGTGC ATCTAGTTCA GCTGAAGGAC ATTTGTGAGG ATATTTCTGA CCATGTGGAG
      Q   I   H   A   L   L   E   T   E   F   S   L   K   L   L   S   Y   S   V   N   V   I   V   D  ·
 491 CAGATCCATG CCCTCCTTGA GACGGAGTTT TCCCTAAAGC TGCTGTCCTA CTCGGTCAAC GTCATCGTAG
     ·   I   H   A   V   Q   L   L   W   H   Q   L   R   V   S   V   L   V   L   R   E   R   I   L  ·
 561 ACATCCACGC AGTACAGCTG CTCTGGCACC AGCTCCGCGT ATCCGTGCTG GTCCTCCGGG AGCGCATCCT
     ·   Q   G   L   Q   D   A   N   G   N   Y   T   R   Q   T   D   I   L   Q   A   F   S   E   E
 631 ACAAGGTCTG CAGGACGCCA ATGGCAACTA CACCAGGCAG ACTGACATTC TGCAAGCGTT CTCTGAAGAA
      T   T   E   G   R   L   D   S   L   T   E   V   D   D   S   G   Q   L   T   I   K   C   S   Q  ·
 701 ACAACGGAGG GCCGGCTTGA TTCCCTTACA GAAGTGGACG ACTCAGGGCA GTTAACTATC AAATGTTCAC
     ·   D   Y   L   S   L   D   C   G   I   T   A   F   E   L   S   D   Y   S   P   S   E   D   L  ·
 771 AGGATTACTT GTCTCTGGAT TGTGGCATTA CCGCATTTGA ACTCTCCGAC TACAGTCCAA GTGAGGATCT
     ·   L   G   G   L   G   D   M   T   T   S   Q   A   K   T   K   S   F   D   S   W   S   Y   S
 841 GCTTGGTGGC CTGGGCGACA TGACCACCAG CCAGGCCAAA ACTAAATCTT TTGACTCTTG GAGCTACAGT
      E   M   E   K   E   F   P   E   L   I   R   S   V   G   L   L   T   V   A   T   E   P   V   P  ·
 911 GAGATGGAGA AAGAGTTCCC TGAGCTTATC CGAAGCGTTG GGCTGCTTAC AGTGGCCACC GAGCCTGTCC
     ·   S   S   C   G   E   A   N   E   D   S   S   Q   A   S   L   S   D   D   H   K   G   E   H  ·
 981 CTTCCAGCTG TGGAGAAGCC AATGAGGATT CATCTCAAGC GTCCCTTTCA GATGATCACA AAGGTGAACA
     ·   G   E   D   G   A   P   V   P   G   Q   Q   L   D   S   T   V   G   M   S   S   L   D   G
1051 CGGGGAAGAC GGTGCTCCCG TACCTGGACA GCAGCTGGAC TCAACGGTGG GAATGTCTTC CTTAGACGGC
      T   L   A   N   A   A   E   H   P   S   E   T   A   K   Q   D   S   T   S   S   P   Q   L   G  ·
1121 ACGCTGGCAA ATGCTGCCGA ACACCCTTCG GAGACAGCAA AACAAGACTC TACTTCCTCC CCACAGCTTG
     ·   A   K   K   T   Q   P   G   P   C   E   I   T   T   P   K   R   S   I   R   D   C   F   N  ·
1191 GTGCGAAGAA AACCCAGCCT GGTCCTTGTG AAATTACGAC TCCCAAGAGA TCCATCCGCG ATTGCTTTAA
     ·   Y   N   E   D   S   P   T   Q   P   T   L   P   K   R   G   L   F   L   K   E   T   Q   K
1261 TTATAACGAG GACTCCCCCA CACAGCCCAC ATTACCCAAA AGAGGGCTTT TTCTAAAAGA AACTCAAAAG
      N   E   R   K   G   S   D   R   K   G   Q   V   V   D   L   K   P   E   L   S   R   S   T   P  ·
1331 AATGAGCGCA AAGGCAGTGA CAGGAAGGGG CAGGTGGTTG ATTTAAAGCC TGAACTGAGC AGAAGCACCC
     ·   S   L   V   D   P   P   D   R   S   K   L   C   L   V   L   Q   S   S   Y   P   S   S   P  ·
1401 CTTCCCTGGT GGACCCCCCT GACAGATCGA AGCTCTGCCT AGTGTTGCAG TCCTCCTACC CCAGCAGCCC
     ·   S   A   A   S   Q   S   Y   E   C   L   H   K   V   G   L   G   N   L   E   N   I   V   R
1471 TTCTGCTGCC AGCCAGTCCT ATGAATGTTT GCACAAGGTG GGGCTCGGCA ATCTTGAAAA CATAGTCAGA
      S   H   I   K   E   I   S   S   S   L   G   R   L   T   D   C   H   K   E   K   L   R   L   K  ·
1541 AGTCACATTA AAGAAATTTC TTCCAGTCTG GGAAGGCTTA CTGACTGCCA TAAAGAGAAA TTGCGACTGA
     ·   K   P   H   K   T   L   A   E   V   S   L   C   R   I   P   K   Q   G   G   G   S   G   K  ·
1611 AAAAGCCACA CAAGACCTTG GCCGAAGTGT CTCTGTGCAG AATCCCTAAA CAGGGAGGCG GTTCAGGAAA
     ·   R   S   E   S   T   G   S   S   A   G   P   S   M   V   S   P   G   A   P   K   A   T   M
1681 GCGATCTGAG AGCACCGGGA GCTCAGCAGG GCCCAGCATG GTATCACCTG GAGCTCCCAA AGCCACGATG
      R   P   E   T   D   S   A   S   T   A   S   G   G   L   C   H   Q   R   N   R   S   G   Q   L  ·
1751 AGACCAGAAA CAGATTCTGC GTCTACAGCC TCAGGTGGCC TGTGCCACCA GAGAAATCGC AGTGGACAAT
     ·   P   V   Q   S   K   A   S   S   S   P   P   C   S   H   S   S   E   S   S   L   G   S   D  ·
1821 TGCCAGTGCA GTCGAAGGCC TCCAGTTCAC CCCCTTGCAG TCACAGCAGT GAATCTTCTC TTGGCTCAGA
     ·   S   I   K   S   P   V   P   L   L   S   K   N   K   S   Q   K   S   S   P   P   A   P   C
1891 TAGCATCAAA TCCCCGGTTC CTCTTCTTTC AAAAAACAAA AGCCAAAAAA GCTCCCCACC TGCTCCATGT
      H   A   T   Q   N   G   Q   V   V   E   A   W   Y   G   S   D   E   Y   L   A   L   P   S   H  ·
1961 CACGCCACAC AGAACGGTCA GGTGGTGGAG GCCTGGTACG GCTCTGATGA GTACCTAGCG CTGCCCTCTC
     ·   L   K   Q   T   E   V   L   A   L   K   L   E   S   L   T   K   L   L   P   Q   K   P   R  ·
```

FIGURE 25 (cont.)

```
2031 ACCTGAAGCA GACGGAGGTG TTAGCTCTCA AGCTGGAGAG CCTAACCAAG CTCCTACCCC AGAAACCCAG
     · G  E  T  I  Q  D  I  D  D  W  E  L  S  E  M  N  S  D  S  E  I  Y  P
2101 AGGAGAGACC ATCCAGGATA TTGATGACTG GGAACTGTCT GAAATGAATT CAGATTCCGA AATCTATCCA
      T  Y  H  I  K  K  K  H  T  R  L  G  T  V  S  P  S  S  S  S  D  I  A  S ·
2171 ACATACCACA TCAAGAAAAA ACACACGAGA CTGGGCACAG TGTCTCCAAG CTCATCCAGC GACATAGCCT
     · S  L  G  E  S  I  E  S  G  P  L  S  D  I  L  S  D  E  D  L  C  L  P ·
2241 CATCTCTCGG GGAGAGCATT GAATCCGGGC CCCTGAGTGA CATTCTTTCT GACGAGGACT TATGTCTGCC
     · L  S  S  V  K  K  F  T  D  E  K  S  E  R  P  S  S  S  E  K  N  E  S
2311 CCTCTCCAGC GTGAAAAAGT TCACTGACGA GAAATCAGAG AGACCTTCAT CCTCCGAGAA GAACGAGAGC
      H  S  A  T  R  S  A  L  I  Q  K  L  M  H  D  I  Q  H  Q  E  N  Y  E  A ·
2381 CATTCTGCAA CAAGATCAGC TTTGATTCAG AAACTAATGC ACGATATTCA GCACCAAGAG AACTATGAAG
     · I  W  E  R  I  E  G  F  V  N  K  L  D  E  F  I  Q  W  L  N  E  A  M ·
2451 CCATCTGGGA AAGAATTGAG GGGTTTGTGA ACAAGCTGGA TGAATTCATT CAGTGGCTAA ACGAAGCCAT
     · E  T  T  E  N  W  T  P  P  K  A  E  T  D  S  L  R  L  Y  L  E  T  H
2521 GGAGACCACC GAGAACTGGA CTCCTCCTAA AGCCGAGACC GACAGCCTCC GGCTGTACCT GGAGACACAC
      L  S  F  K  L  N  V  D  S  H  C  A  L  K  E  A  V  E  E  E  G  H  Q  L ·
2591 TTGAGTTTTA AGTTGAACGT AGACAGCCAC TGTGCCCTCA AGGAAGCCGT GGAGGAAGAA GGACACCAAC
     · L  E  L  V  V  S  H  K  A  G  L  K  D  T  L  R  M  I  A  S  Q  W  K ·
2661 TTCTTGAGCT CGTTGTATCT CACAAAGCAG GACTGAAGGA CACGCTGAGG ATGATTGCGA GTCAATGGAA
     · E  L  Q  R  Q  I  K  R  Q  H  S  W  I  L  R  A  L  D  T  I  K  A  E
2731 GGAGCTGCAG AGGCAAATCA AACGGCAACA CAGCTGGATT CTCAGAGCCC TGGACACCAT CAAAGCCGAG
      I  L  A  T  D  V  S  V  E  D  E  E  G  T  G  S  P  K  A  E  V  Q  L  C ·
2801 ATACTGGCTA CTGATGTGTC TGTGGAGGAC GAGGAGGGGA CGGGAAGCCC CAAGGCCGAG GTTCAGCTCT
     · H  L  E  T  Q  R  D  A  V  E  Q  M  S  L  K  L  Y  S  E  Q  Y  T  S ·
2871 GCCACCTGGA AACACAGAGA GACGCCGTGG AACAGATGTC CCTGAAGCTG TACAGCGAGC AGTACACCAG
     · G  S  K  R  K  E  E  F  A  N  M  S  K  A  H  A  E  G  S  N  G  L  L
2941 CGGGAGCAAG AGGAAGGAAG AGTTTGCCAA CATGTCGAAA GCGCACGCGG AGGGAAGCAA TGGGCTTCTG
      D  F  D  S  E  Y  Q  E  L  W  D  W  L  I  D  M  E  S  L  V  M  D  S  H ·
3011 GACTTTGATT CAGAATATCA GGAGCTCTGG GATTGGCTGA TTGACATGGA GTCCCTCGTG ATGGACAGCC
     · D  L  M  M  S  E  E  Q  Q  Q  H  L  Y  K  R  Y  S  V  E  M  S  I  R ·
3081 ACGACCTGAT GATGTCAGAG GAGCAGCAGC AGCATCTTTA CAAGAGGTAC AGTGTGGAAA TGTCCATCAG
     · H  L  K  K  S  E  L  L  S  K  V  E  A  L  K  K  G  G  L  S  L  P  D
3151 GCATCTGAAA AAGTCAGAGC TACTCAGCAA GGTTGAAGCT TTGAAGAAAG GTGGCCTTTC ACTACCAGAC
      D  I  L  E  K  V  D  S  I  N  E  K  W  E  L  L  G  K  T  L  R  E  K  I ·
3221 GATATCCTGG AAAAAGTGGA TTCAATTAAT GAAAAATGGG AGCTGCTTGG GAAAACCCTA AGAGAGAAGA
     · Q  D  T  I  A  G  H  S  G  S  G  P  R  D  L  L  S  P  E  S  G  S  L ·
3291 TACAGGACAC AATAGCGGGG CACAGTGGGT CGGGCCCACG TGACCTGCTA TCTCCTGAAA GCGGAAGCCT
     · V  R  Q  L  E  V  R  I  K  E  L  K  R  W  L  R  D  T  E  L  F  I  F
3361 GGTAAGGCAG CTGGAGGTCA GGATCAAAGA GCTGAAAAGG TGGCTAAGAG ATACAGAGCT TTTCATCTTC
      N  S  C  L  R  Q  E  K  E  G  T  S  A  E  K  Q  L  Q  Y  F  K  S  L  C ·
3431 AATTCCTGTC TGAGACAAGA GAAGGAAGGA ACAAGCGCCG AGAAACAGCT CCAATACTTT AAGTCGCTCT
     · R  E  I  K  Q  R  R  R  G  V  A  S  I  L  R  L  C  Q  H  L  L  D  D ·
3501 GTCGTGAGAT CAAGCAGCGG CGTCGAGGAG TGGCCTCCAT TCTGAGGTTG TGCCAGCACC TTCTGGATGA
     · R  D  T  C  N  L  N  A  D  H  Q  P  M  Q  L  I  I  V  N  L  E  R  R
3571 CCGGGACACG TGCAACCTGA ACGCAGATCA CCAGCCCATG CAGCTGATCA TTGTAAACCT CGAGAGGCGG
      W  E  A  I  V  M  Q  A  V  Q  W  Q  T  R  L  Q  K  K  M  G  K  E  S  E ·
3641 TGGGAGGCCA TCGTCATGCA AGCTGTCCAG TGGCAAACAC GGTTACAAAA GAAGATGGGG AAGGAATCCG
     · T  L  N  V  I  D  P  G  L  M  D  L  N  G  M  S  E  D  A  L  E  W  D ·
3711 AGACTTTGAA TGTGATTGAT CCTGGCTTGA TGGACCTGAA TGGAATGAGT GAGGATGCCC TGGAATGGGA
     · E  T  D  I  S  N  K  L  I  S  V  H  E  E  S  N  D  L  D  Q  D  P  E
3781 TGAAACAGAC ATAAGTAACA AACTCATTAG TGTGCATGAA GAATCAAACG ACCTTGATCA AGACCCAGAG
      P  M  L  P  A  V  K  L  E  E  T  H  H  K  D  S  G  Y  E  E  E  A  G  D ·
3851 CCTATGCTAC CCGCAGTGAA GCTTGAAGAG ACACACCACA AGGACTCTGG TTATGAAGAG GAGGCAGGTG
     · C  G  G  S  P  Y  T  S  N  I  T  A  P  S  S  P  H  I  Y  Q  V  Y  S ·
3921 ACTGTGGAGG GTCTCCGTAT ACCTCAAATA TCACTGCACC TTCCAGCCCA CACATTTACC AAGTGTACAG
     · L  H  N  V  E  L  H  E  D  S  H  T  P  F  L  K  S  S  P  K  F  T  G
3991 TCTTCACAAT GTGGAGCTCC ACGAGGACAG CCACACTCCA TTTCTGAAAA GCAGCCCTAA GTTCACAGGC
      T  T  Q  P  T  V  L  T  K  S  L  S  K  D  S  S  F  S  S  T  K  S  L  P ·
4061 ACAACACAGC CTACTGTTTT AACTAAGAGC CTCAGCAAGG ACTCTTCCTT TTCATCTACA AAATCGTTAC
     · D  L  L  G  G  S  G  L  V  R  P  Y  S  C  H  S  G  D  L  S  Q  N  S ·
```

FIGURE 25 (cont.)

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4131 CAGACCTTCT AGGGGGTTCC GGTTTGGTGA GGCCTTACTC GTGTCACAGT GGAGACTTGA GCCAGAATTC
     · G  S  E  S  G  I  V  S  E  G  D  N  E  M  P  T  N  S  D  M  S  L  F
4201 AGGCAGTGAG AGTGGAATTG TCAGCGAAGG AGACAACGAG ATGCCGACCA ACTCTGACAT GAGCTTGTTC
      S  M  V  D  G  S  P  S  N  P  E  T  E  H  P  D  P  Q  M  G  D  A  A  N ·
4271 AGTATGGTAG ACGGGTCCCC AAGTAACCCT GAAACGGAGC ATCCGGACCC ACAAATGGGA GATGCAGCCA
     · V  L  E  Q  K  F  K  D  N  G  E  S  I  K  L  S  S  V  S  R  A  S  V ·
4341 ATGTGCTAGA GCAAAAGTTT AAAGACAACG GGGAAAGCAT TAAGCTTTCA AGTGTCTCTC GGGCATCCGT
     · S  P  V  G  C  V  N  G  K  A  G  D  L  N  S  V  T  K  H  T  A  D  C
4411 CTCACCAGTG GGTTGTGTAA ATGGAAAAGC AGGGGATTTA AACAGTGTTA CCAAACACAC TGCTGATTGT
      L  G  E  E  L  Q  G  K  H  D  V  F  T  F  Y  D  Y  S  Y  L  Q  G  S  K ·
4481 TTGGGAGAAG AACTACAAGG AAAACATGAC GTGTTTACAT TTTATGATTA CTCGTACCTC CAAGGCTCAA
     · L  K  L  P  M  I  M  K  Q  P  Q  S  E  K  A  H  V  E  D  P  L  L  G ·
4551 AACTCAAATT ACCAATGATA ATGAAACAGC CACAGAGTGA AAAGGCACAC GTGGAGGATC CCCTTCTTGG
     · G  F  Y  F  D  K  K  S  C  K  A  K  H  Q  A  S  E  S  Q  P  D  A  P
4621 TGGTTTTTAT TTTGATAAAA AGTCCTGCAA AGCTAAACAT CAGGCTTCAG AGTCACAACC AGATGCGCCT
      P  H  E  R  I  L  A  S  A  P  H  E  M  G  R  S  A  Y  K  S  S  D  I  E ·
4691 CCCCACGAAA GGATTCTGGC AAGCGCGCCC CACGAGATGG GACGCAGCGC ATACAAAAGT AGCGACATAG
     · K  T  F  T  G  I  Q  S  A  R  Q  L  S  L  L  S  R  S  S  S  V  E  S ·
4761 AGAAGACATT CACGGGCATT CAGAGTGCCA GACAGCTCTC CCTTCTATCT CGTAGCTCAT CTGTAGAGTC
     · L  S  P  G  G  D  L  F  G  L  G  I  F  K  N  G  S  D  S  L  Q  R  S
4831 CCTTTCTCCA GGGGGTGATT TGTTTGGATT GGGAATCTTT AAAAATGGCA GTGACAGCCT CCAGCGGAGC
      T  S  L  E  S  W  L  T  S  Y  K  S  N  E  D  L  F  S  C  H  S  S  G  D ·
4901 ACTTCTTTAG AAAGTTGGTT GACATCCTAT AAGAGCAATG AGGATCTCTT TAGCTGTCAC AGCTCTGGGG
     · I  S  V  S  S  G  S  V  G  E  L  S  K  R  T  L  D  L  L  N  R  L  E ·
4971 ACATAAGTGT GAGCAGTGGC TCAGTTGGTG AGCTGAGTAA GAGGACGTTA GACCTTCTGA ATCGCCTGGA
     · N  I  Q  S  P  S  E  Q  K  I  K  R  S  V  S  D  M  T  L  Q  S  S  S
5041 GAATATACAG AGCCCCTCGG AGCAAAAGAT CAAGCGGAGT GTTTCTGACA TGACTCTACA AAGCAGTTCC
      Q  K  M  P  F  A  G  Q  M  S  L  D  V  A  S  S  I  N  E  D  S  P  A  S ·
5111 CAAAAGATGC CCTTCGCTGG CCAGATGTCA CTGGATGTCG CATCCTCCAT CAATGAAGAC TCTCCGGCAT
     · L  T  E  L  S  S  S  D  E  L  S  L  C  S  E  D  I  V  L  H  K  N  K ·
5181 CTCTTACAGA ACTGAGTAGT AGCGATGAGC TCTCTCTTTG CTCGGAGGAC ATTGTGTTAC ACAAAAACAA
     · I  P  E  S  N  A  S  F  R  K  R  L  N  R  S  V  A  D  E  S  D  V  N
5251 GATCCCAGAA TCCAACGCAT CATTCAGGAA GCGCCTGAAT CGCTCAGTGG CTGATGAGAG CGACGTCAAT
      V  S  M  I  V  N  V  S  C  T  S  A  C  T  D  D  E  D  D  S  D  L  L  S ·
5321 GTTAGCATGA TTGTCAATGT GTCCTGCACC TCTGCTTGCA CTGATGATGA AGATGACAGC GACCTCCTCT
     · S  S  T  L  T  L  T  E  E  E  L  C  L  K  D  E  D  D  D  S  S  I  A ·
5391 CCAGCTCCAC TCTCACCTTA ACTGAAGAAG AGCTGTGCCT CAAAGATGAG GATGACGACT CCAGTATTGC
     · T  D  D  E  I  Y  E  E  S  N  L  M  S  G  L  D  Y  I  K  N  E  L  Q
5461 AACAGATGAT GAAATTTATG AAGAGAGCAA CCTGATGTCT GGGCTGGACT ACATAAAGAA TGAACTGCAG
      T  W  I  R  P  K  L  S  L  T  R  E  K  K  R  S  G  V  T  D  E  I  K  V ·
5531 ACTTGGATAA GACCAAAACT TTCCTTGACG AGAGAAAAGA AACGGTCCGG TGTCACTGAT GAAATAAAGG
     · N  K  D  G  G  G  N  E  K  A  N  P  S  D  T  L  D  I  E  A  L  L  N ·
5601 TCAATAAAGA TGGGGGAGGC AATGAGAAGG CCAATCCCTC GGACACCCTG GACATCGAGG CCCTTCTCAA
     · G  S  I  R  C  L  S  E  N  N  G  N  G  K  T  P  P  R  T  H  G  S  G
5671 TGGCTCCATA AGATGTCTTT CCGAAAACAA CGGGAATGGT AAGACTCCGC CCAGAACTCA TGGCTCAGGA
      T  K  G  E  N  K  K  S  T  Y  D  V  S  K  D  P  H  V  A  D  M  E  N  G ·
5741 ACCAAAGGTG AAAATAAGAA AAGTACGTAT GACGTTAGTA AGGATCCGCA CGTGGCTGAC ATGGAAAATG
     · N  I  E  S  T  P  E  R  E  R  E  K  P  Q  G  L  P  E  V  S  E  N  L ·
5811 GCAATATTGA AAGTACCCCA GAAAGAGAAA GGGAGAAGCC ACAAGGGCTT CCAGAGGTGT CAGAGAACCT
     · A  S  N  V  K  T  I  S  E  S  E  L  S  E  Y  E  A  V  M  D  G  S  E
5881 TGCTTCAAAT GTGAAAACGA TTTCTGAATC TGAGCTCAGC GAGTATGAAG CAGTAATGGA TGGTTCTGAG
      D  S  S  V  A  R  K  E  F  C  P  P  N  D  R  H  P  P  Q  M  G  P  K  L ·
5951 GATTCAAGTG TTGCCAGAAA GGAATTTTGT CCCCCAAATG ACAGACATCC TCCACAGATG GGTCCCAAAC
     · Q  H  P  E  N  Q  S  G  D  C  K  P  V  Q  N  P  C  P  G  L  L  S  E ·
6021 TCCAGCATCC CGAAAATCAA AGTGGCGACT GCAAGCCAGT CCAGAACCCT TGCCCGGGGC TACTGTCGGA
     · A  G  V  G  S  R  Q  D  S  N  G  L  K  S  L  P  N  D  A  P  S  G  A
6091 AGCTGGCGTT GGAAGCAGGC AAGACAGCAA TGGACTAAAA TCTTTGCCTA ACGATGCACC AAGTGGGGCT
      R  K  P  A  G  C  C  L  L  E  Q  N  E  T  E  E  S  A  S  I  S  S  N  A ·
6161 AGAAAACCTG CCGGTTGCTG CCTGCTGGAG CAGAATGAGA CAGAGGAAAG TGCTTCTATC AGCAGCAACG
     · S  C  C  N  C  K  P  D  V  F  H  Q  K  D  D  E  D  C  S  V  H  D  F ·
```

FIGURE 25 (cont.)

```
6231 CTTCCTGTTG CAACTGCAAG CCAGATGTTT TCCATCAAAA AGATGATGAA GATTGTTCAG TACATGACTT
     · V  K  E  I  I  D  M  A  S  T  A  L  K  S  K  S  Q  P  E  S  E  V  A
6301 TGTTAAGGAA ATCATTGACA TGGCATCAAC AGCCCTAAAA AGTAAGTCAC AGCCTGAAAG TGAGGTGGCC
      A  P  T  S  L  T  Q  I  K  E  K  V  L  E  H  S  H  R  P  I  H  L  R  K ·
6371 GCACCCACAT CACTAACCCA AATTAAGGAG AAGGTGTTAG AGCATTCGCA CCGGCCCATA CACCTGAGAA
     · G  D  F  Y  S  Y  L  S  L  S  S  H  D  S  D  C  G  E  V  T  N  Y  I ·
6441 AGGGGGACTT TTACTCCTAC TTATCACTTT CGTCCCACGA CAGTGACTGT GGGGAGGTCA CCAATTACAT
     · D  E  K  S  S  T  P  L  P  P  D  A  V  D  S  G  L  D  D  K  E  D  M
6511 AGATGAGAAG AGCAGTACTC CATTGCCACC GGACGCTGTG GACTCTGGCT TAGATGACAA GGAAGACATG
      D  C  F  F  E  A  C  V  E  D  E  P  V  N  E  E  A  G  L  P  G  A  L  P ·
6581 GACTGCTTCT TTGAAGCTTG TGTTGAGGAT GAGCCTGTCA ATGAGGAAGC TGGTCTCCCC GGTGCCCTTC
     · N  E  S  A  I  E  D  G  A  E  Q  K  S  E  Q  K  T  A  S  S  P  V  L ·
6651 CCAATGAATC AGCCATCGAG GATGGAGCAG AGCAAAAGTC AGAACAAAAG ACAGCCAGCT CTCCTGTGCT
     · S  D  K  T  D  L  V  P  L  S  G  L  S  P  Q  K  G  A  D  D  A  K  E
6721 CAGTGACAAG ACAGACCTGG TGCCTCTTTC AGGACTTTCC CCTCAGAAGG GAGCTGATGA TGCAAAGGAA
      G  D  D  V  S  H  T  S  Q  G  C  A  E  S  T  E  P  T  T  P  S  G  K  A ·
6791 GGAGATGATG TGTCTCACAC TTCCCAGGGC TGTGCAGAGA GCACAGAGCC TACCACCCCC TCAGGAAAGG
     · N  A  E  G  R  S  R  M  Q  G  V  S  A  T  P  E  E  N  A  A  S  A  K ·
6861 CCAATGCAGA GGGGAGGTCA AGAATGCAAG GTGTATCAGC AACGCCAGAA GAAAACGCTG CTTCGGCCAA
     · P  K  I  Q  A  F  S  L  N  A  K  Q  P  K  G  K  V  A  M  R  Y  P  S
6931 ACCGAAAATT CAAGCTTTCT CTTTGAATGC AAAACAGCCA AAAGGCAAGG TTGCCATGAG GTATCCCAGC
      P  Q  T  L  T  C  K  E  K  L  V  N  F  H  E  D  R  H  S  N  M  H  R
7001 CCCCAAACTC TAACCTGTAA AGAGAAGCTC GTAAACTTTC ATGAAGATCG ACACAGTAAC ATGCATAGGT
7071 AGAGTGTAAT GCCCCCACGC ATGGAAATCA TCTCATTGAA AGATAGCCTG GCTGAAGCTC AGGGCTAGCC
7141 CAATCCACCC TGGGCCGGTC TTGGGCTCCA TCCTGTTATC ACTGCCGCCT GTCACATTGA CTTTCTGAAG
7211 ACGAACCTTC CTTCCGAATG CAGTCTGTCC ACGTGGGCCT CTCGACCTGG ATGTGTGCAT TGCTTCTCTT
7281 AGGTGATCAT CCTAGTTCCA CAAAGCTGCT TGTTCTCCCG TGGATTCCTG TCCCAAGCTA CCTCTGGCAA
7351 CCCTGTCTCT CCAGCAAGAC TTCGGTTTTC CCTCCCCCTC CTCCCCCCCC TTAAAGTTCC GCGGCTCACC
7421 AAATTGATGG TCCATCAAAC CCACTGTCTG GAATGATACC CCTCCCATCA GTACTTGACC AATGTTATGT
7491 TTTGCTCTGA AAACTTTCGC TGTATTAGAC CAATGTTTAT TGAAAGAGAT TTACCTAAAA AGCCCGCCCT
7561 TGATTTGGTT GCAGTATAGA GGAGACACAT TGATCCTTCT AACAAAATTA AGTGATGTCT GAAAGCGCCA
7631 TTTTAATTAT TTCTTTTTAA ATAATGATCT ATGCAGCACT TCAAGAAACA ACTATAACAG TGTTGTATCT
7701 TATAAACTGG TACATTCTAC TATTAAGTTT GTTTTTGGTT TCTATGCTTC TTGAGGTGGT GATGAGAAAA
7771 ATGGTTTTTT TTTTAAAACG GTGTGCCTTG CTGTATTACT TATAGCATTT ATTAAAAAGC TGCTTTCATG
7841 GTAAGATTAC ACTGGTTTGA AAGGAGGAAA TAGCAAGGTT AAGATGCGTG CATAATTTCT GTATATATGT
7911 ATAAGCTAGT GCAAACACTG ATGTATGACA GTATAAAATG CTTTCATGTT TGTGATGTCC AGTGGTGTGG
7981 AATATAAGCC TTAAACCCGT TCGATTGCAT GGTAATTAAA ATTGGCATAA TAAAAATAGC TTATTGGGGG
8051 AAAGGAAAAT TAATGATCTC TTCTACCTGT GTTTACCAAT TTCTTTCATG TGGTTCTGGG AAAGAAAAAG
8121 AAACAAACCC CATATATTAG CTTCCAAAAT ATCCATATTG CACAGAAGGC TTAAGTTGCT TAGACTACAG
8191 ACTGGGCCTG AAGACTTCAT GATTTTCCAA ATTTTTCTGT TTCACTATAA ACATCCGAAA TAGCAAAGAT
8261 TTCTTTCCCC TCCATCAACA GCATTTTATT CTGAATGTTT TTATTTCTAC TTGTTAATGG TTTAAAGTTG
8331 TATTTGGAGA TCTCTTACAT GCCCTAATTT ATTTTAAATA TTTGAATGGG TTTGGTGGAT GGTATAGAAA
8401 ATTTAATTAT TATTTTATTT AAACTACAGA TTTCAGGTGT ATTTATTTTG TTAAATATTC CATTTGGTCT
8471 TTTGGTCTTT TTATGACTTG AAAGTTTCAG CTTTTAATTT ATATCATAAC TCCTACTAAA GTGCCTGACA
8541 CACAGTAGGT ATTTCATAGA GTTTCCTGAA TTAGAGTATT GGGTGGTTTA TATATATATA TATATATATG
8611 AGATTCCTGC ATTAAAACTA GAAAAAGATG TGCAAAGTGA ACCAGACACA GCATATTATC AGATTTCAAA
8681 AAGGAAAGAG AACATAGCCA CAGAAATGAC AATCATTCAT TCAGTAGATT AGCATCTTTT GCCTGCAAGT
8751 CACCATTCTA GATTCAGGGA GAGCAGCTAT GACCGATGCA CTGCCTTTGG AGGCTTCTGT GTTAGAGACA
8821 GAGTGACCTC GTGCCGAATT C
```

FIGURE 26

Figure 26. human mAKAPβ mRNA with open reading frame translated:

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   1 GAGTCTGGGA GCTGAGTGAC TGAGGATTTG AAACCTTGCT ATAGTTACAG TTCATAACAA GCGTCTAGGC
  71 AGTTAGACCT TAAGTGTTCA GGTATGGAAA GAAAGTCATA TGTTATGTTT TAGATTCTGT TTGTAAAGCT
 141 GGTTAACTAG AGACAGCTGA TGAAAAACCA AATCGACTTG AGTTACAAGA TCTGGGCTTT CTCTGCTCTG
 211 CTTTCAACCT GTTGGTTGGT GGTGGAGTAG CTGACAGAAG CGAATGGCTT GGCTGAGGGA CATGAAGTGA
 281 CAGCAGCCTG TTTAGGACCA CACCACATTT TGGACCTCTT GCTGTGCAGT TCAGGACATT TGTGAAGATA
 351 TTTCTGATCA TGTTGAGCAA ATCCATGCCC TCCTTGAAAC AGAGTTCTCC CTAAAGCTGC TGTCTTACTC
 421 TGTCAACGTG ATAGTGGACA TCCACGCAGT GCAGCTCCTC TGGCACCAGC TTCGAGTCTC AGTGCTGGTT
 491 CTGCGGGAGC GCATTCTGCA AGGTCTGCAG GACGCCAATG GCAACTACAC TAGGCAGACG GACATTCTGC
 561 AAGCTTTCTC TGAAGAGACA AAAGAGGGCC GGCTTGATTC TCTAACAGAA GTGGATGACT CAGGACAATT
 631 AACCATCAAA TGTTCTCAAA ATTACTTGTC TCTGGATTGT GGCATTACTG CATTCGAACT GTCTGACTAC
                                                 M  T  S  S  Q  V  K  T  K  P  F  D ·
 701 AGTCCAAGTG AGGATTTGCT CAGTGGGCTA GGTGACATGA CCTCTAGCCA AGTCAAAACC AAACCCTTTG
     ·  S  W  S  Y  S  E  M  E  K  E  F  P  E  L  I  R  S  V  G  L  L  T  V ·
 771 ACTCTTGGAG CTACAGTGAG ATGGAAAAGG AGTTTCCTGA GCTTATCCGA AGTGTTGGTT TACTTACGGT
     ·  A  A  D  S  I  S  T  N  G  S  E  A  V  T  E  E  V  S  Q  V  S  L  S
 841 AGCTGCTGAC TCTATCTCTA CCAATGGCAG TGAAGCAGTT ACTGAGGAGG TATCTCAAGT ATCTCTCTCA
      V  D  D  K  G  G  C  E  E  D  N  A  S  A  V  E  E  Q  P  G  L  T  L  G ·
 911 GTAGACGACA AAGGTGGATG TGAGGAAGAC AATGCTTCTG CAGTCGAAGA GCAACCAGGC TTAACACTGG
     ·  V  S  S  S  S  G  E  A  L  T  N  A  A  Q  P  S  S  E  T  V  Q  Q  E ·
 981 GGGTGTCATC ATCTTCAGGA GAAGCTCTGA CAAATGCTGC TCAACCCTCC TCTGAGACTG TGCAGCAAGA
     ·  S  S  S  S  S  H  H  D  A  K  N  Q  Q  P  V  P  C  E  N  A  T  P  K
1051 ATCCAGTTCC TCCTCCCATC ATGATGCAAA GAATCAGCAG CCTGTTCCTT GTGAAAATGC AACCCCCAAA
      R  T  I  R  D  C  F  N  Y  N  E  D  S  P  T  Q  P  T  L  P  K  R  G  L ·
1121 CGAACCATCA GAGATTGCTT TAATTATAAC GAGGACTCTC CCACGCAGCC TACATTGCCA AAAAGAGGAC
     ·  F  L  K  E  E  T  F  K  N  D  L  K  G  N  G  G  K  R  Q  M  V  D  L ·
1191 TTTTTCTTAA AGAGGAAACT TTTAAGAATG ATCTGAAAGG CAATGGTGGA AAGAGGCAAA TGGTTGATCT
     ·  K  P  E  M  S  R  S  T  P  S  L  V  D  P  P  D  R  S  K  L  C  L  V
1261 AAAGCCTGAG ATGAGCAGAA GCACCCCTTC GCTAGTAGAT CCTCCTGACA GATCCAAACT TTGCCTGGTA
      L  Q  S  S  Y  P  N  S  P  S  A  A  S  Q  S  Y  E  C  L  H  K  V  G  N ·
1331 TTGCAGTCTT CTTACCCCAA CAGCCCTTCT GCTGCCAGCC AGTCTTATGA GTGTTTACAC AAGGTGGGGA
     ·  G  N  L  E  N  T  V  K  F  H  I  K  E  I  S  S  S  L  G  R  L  N  D ·
1401 ATGGGAACCT TGAAAACACA GTCAAATTTC ACATTAAAGA AATTTCTTCC AGCCTGGGAA GGCTTAACGA
     ·  C  Y  K  E  K  S  R  L  K  K  P  H  K  T  S  E  E  V  P  P  C  R  T
1471 CTGCTATAAA GAGAAATCTC GACTTAAAAA GCCACACAAG ACCTCAGAAG AGGTGCCTCC ATGCCGAACA
      P  K  R  G  T  G  S  G  K  Q  A  K  N  T  K  S  S  A  V  P  N  G  E  L ·
1541 CCTAAACGGG GGACTGGTTC AGGCAAACAA GCTAAAAATA CAAAGAGCTC AGCAGTGCCA AATGGAGAGC
     ·  S  Y  T  S  K  A  I  E  G  P  Q  T  N  S  A  S  T  S  S  L  E  P  C ·
1611 TTTCTTATAC TTCCAAGGCC ATAGAGGGGC CACAAACAAA TTCTGCTTCC ACATCCTCAC TTGAGCCTTG
     ·  N  Q  R  S  W  N  A  K  L  Q  L  Q  S  E  T  S  S  S  P  A  F  T  Q
1681 TAATCAGAGA AGTTGGAATG CCAAATTGCA ATTGCAGTCA GAAACATCCA GTTCACCAGC TTTTACTCAG
      S  S  E  S  S  V  G  S  D  N  I  M  S  P  V  P  L  L  S  K  H  K  S  K ·
1751 AGCAGTGAAT CCTCTGTTGG CTCAGACAAC ATCATGTCTC CGGTGCCACT TCTTTCAAAA CACAAAAGCA
     ·  K  G  Q  A  S  S  P  S  H  V  T  R  N  G  E  V  V  E  A  W  Y  G  S ·
1821 AAAAAGGTCA AGCCTCCTCT CCAAGTCACG TCACTAGGAA TGGTGAGGTT GTGGAGGCCT GGTATGGCTC
     ·  D  E  Y  L  A  L  P  S  H  L  K  Q  T  E  V  L  A  L  K  L  E  N  L
1891 TGATGAATAC CTAGCACTGC CCTCTCACCT TAAGCAGACA GAAGTATTGG CTTTGAAGTT GGAAAACCTA
      T  K  L  L  P  Q  K  P  R  G  E  T  I  Q  N  I  D  D  W  E  L  S  E  M ·
1961 ACAAAGCTTC TGCCTCAGAA ACCCAGAGGA GAAACCATCC AGAATATTGA TGACTGGGAA CTGTCTGAAA
     ·  N  S  D  S  E  I  Y  P  T  Y  H  V  K  K  K  H  T  R  L  G  R  V  S ·
2031 TGAATTCAGA TTCTGAAATC TATCCAACCT ATCATGTCAA AAAGAAGCAT ACAAGGCTAG GCAGGGTGTC
     ·  P  S  S  S  S  D  I  A  S  S  L  G  E  S  I  E  S  G  P  L  S  D  I
2101 TCCAAGCTCA TCTAGTGACA TAGCCTCTTC ACTAGGGGAG AGCATTGAAT CTGGGCCCCT GAGTGACATT
      L  S  D  E  E  S  S  M  P  L  A  G  M  K  K  Y  A  D  E  K  S  E  R  A ·
2171 CTTTCTGATG AGGAGTCCAG TATGCCTCTC GCTGGCATGA AAAAGTATGC TGATGAGAAG TCAGAAAGAG
     ·  S  S  S  E  K  N  E  S  H  S  A  T  K  S  A  L  I  Q  K  L  M  Q  D ·
2241 CTTCATCCTC TGAGAAAAAT GAGAGCCATT CTGCCACTAA ATCAGCTTTA ATTCAGAAAC TGATGCAAGA
     ·  I  Q  H  Q  D  N  Y  E  A  I  W  E  K  I  E  G  F  V  N  K  L  D  E
```

FIGURE 26 (cont.)

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2311 TATTCAGCAC CAAGACAACT ATGAAGCCAT ATGGGAAAAA ATAGAGGGGT TTGTAAACAA ACTGGATGAA
      F  I  Q  W  L  N  E  A  M  E  T  T  E  N  W  T  P  P  K  A  E  M  D  D  ·
2381 TTCATTCAAT GGTTAAATGA AGCCATGGAA ACTACAGAGA ATTGGACTCC CCCTAAAGCA GAGATGGATG
      ·  L  K  L  Y  L  E  T  H  L  S  F  K  L  N  V  D  S  H  C  A  L  K  E  ·
2451 ACCTTAAACT GTATCTGGAG ACACACTTGA GTTTTAAGTT GAATGTAGAC AGTCATTGTG CTCTCAAGGA
      ·  A  V  E  E  E  G  H  Q  L  L  E  L  I  A  S  H  K  A  G  L  K  D  M
2521 AGCTGTGGAG GAGGAAGGAC ACCAACTTCT TGAGCTTATT GCATCTCACA AAGCAGGACT GAAGGACATG
      L  R  M  I  A  S  Q  W  K  E  L  Q  R  Q  I  K  R  Q  H  S  W  I  L  R  ·
2591 CTGCGGATGA TTGCAAGTCA ATGGAAGGAG CTGCAGAGGC AAATCAAACG GCAGCACAGC TGGATTCTCA
      ·  A  L  D  T  I  K  A  E  I  L  A  T  D  V  S  V  E  D  E  E  G  T  G  ·
2661 GGGCTCTGGA TACCATCAAA GCCGAGATAC TGGCTACTGA TGTGTCTGTG GAGGATGAGG AAGGGACTGG
      ·  S  P  K  A  E  V  Q  L  C  Y  L  E  A  Q  R  D  A  V  E  Q  M  S  L
2731 AAGCCCCAAG GCTGAGGTTC AACTATGCTA CCTGGAAGCA CAAAGAGATG CTGTTGAGCA GATGTCCCTC
      K  L  Y  S  E  Q  Y  T  S  S  S  K  R  K  E  E  F  A  D  M  S  K  V  H  ·
2801 AAGCTGTACA GCGAGCAGTA TACCAGCAGC AGCAAGCGAA AGGAAGAGTT TGCTGATATG TCAAAAGTTC
      ·  S  V  G  S  N  G  L  L  D  F  D  S  E  Y  Q  E  L  W  D  C  L  I  D  ·
2871 ATTCAGTGGG AAGCAATGGG CTTCTGGACT TTGATTCAGA ATATCAGGAG CTCTGGGATT GCTTGATTGA
      ·  M  E  S  L  V  M  D  S  H  D  L  M  M  S  E  E  Q  Q  Q  H  L  Y  K
2941 CATGGAGTCC CTTGTGATGG ACAGCCACGA CCTGATGATG TCAGAGGAGC AGCAGCAGCA TCTTTACAAG
      R  Y  S  V  E  M  S  I  R  H  L  K  K  T  E  L  L  S  K  V  E  A  L  K  ·
3011 CGATACAGTG TGGAAATGTC CATCAGACAC CTGAAAAAGA CGGAGCTGCT TAGTAAGGTT GAAGCTTTGA
      ·  K  G  G  V  L  L  P  N  D  L  L  E  K  V  D  S  I  N  E  K  W  E  L  ·
3081 AGAAAGGTGG CGTTTTACTA CCAAATGATC TCCTTGAAAA AGTGGATTCA ATTAATGAAA AATGGGAACT
      ·  L  G  K  T  L  G  E  K  I  Q  D  T  M  A  G  H  S  G  S  S  P  R  D
3151 GCTTGGGAAA ACCCTAGGAG AGAAGATCCA GGACACAATG GCAGGGCACA GTGGGTCGAG TCCACGTGAC
      L  L  S  P  E  S  G  S  L  V  R  Q  L  E  V  R  I  K  E  L  K  G  W  L  ·
3221 CTGCTCTCTC CTGAAAGTGG AAGCCTGGTA AGGCAGCTGG AGGTCAGGAT CAAAGAACTG AAAGGATGGC
      ·  R  D  T  E  L  F  I  F  N  S  C  L  R  Q  E  K  E  G  T  M  N  T  E  ·
3291 TAAGAGATAC AGAGCTTTTC ATCTTCAATT CCTGTCTGAG ACAAGAAAAG GAAGGAACAA TGAATACTGA
      ·  K  Q  L  Q  Y  F  K  S  L  C  R  E  I  K  Q  R  R  R  G  V  A  S  I
3361 GAAACAACTG CAATACTTTA AGTCCCTCTG TCGTGAAATC AAGCAACGAC GTCGAGGAGT TGCCTCCATT
      L  R  L  C  Q  H  L  L  D  D  R  E  T  C  N  L  N  A  D  H  Q  P  M  Q  ·
3431 CTGCGACTAT GCCAGCATCT TTTGGATGAC CGGGAGACTT GCAATCTGAA TGCAGACCAC CAGCCCATGC
      ·  L  I  I  V  N  L  E  R  R  W  E  A  I  V  M  Q  A  V  Q  W  Q  T  R  ·
3501 AGCTGATCAT TGTAAATCTT GAAAGAAGGT GGGAAGCCAT TGTCATGCAA GCCGTCCAGT GGCAAACACG
      ·  L  Q  K  K  M  G  K  E  S  E  T  L  N  V  I  D  P  G  L  M  D  L  N
3571 TCTACAAAAG AAGATGGGAA AGGAATCTGA GACTTTGAAT GTGATTGATC CTGGCTTGAT GGACCTAAAT
      G  M  S  E  D  A  L  E  W  D  E  M  D  I  S  N  K  L  I  S  L  N  E  E  ·
3641 GGGATGAGTG AGGATGCCCT GGAATGGGAT GAAATGGACA TAAGTAACAA GTTAATTAGT TTGAATGAGG
      ·  S  N  D  L  D  Q  E  L  Q  P  V  I  P  S  L  K  L  G  E  T  S  N  E  ·
3711 AATCAAATGA CCTTGATCAA GAACTCCAAC CTGTTATCCC TTCCTTGAAG CTTGGAGAGA CAAGTAATGA
      ·  D  P  G  Y  D  E  E  A  D  N  H  G  G  S  Q  Y  A  S  N  I  T  A  P
3781 GGACCCTGGT TATGACGAGG AGGCTGATAA CCATGGGGGA TCTCAGTATG CCTCAAATAT TACTGCCCCC
      S  S  P  H  I  Y  Q  V  Y  S  L  H  N  V  E  L  Y  E  D  N  H  M  P  F  ·
3851 TCTAGTCCAC ACATTTACCA GGTGTACAGC CTCCACAATG TTGAACTCTA TGAGGACAAC CACATGCCAT
      ·  L  K  N  N  P  K  V  T  G  M  T  Q  P  N  V  L  T  K  S  L  S  K  D  ·
3921 TTCTGAAAAA CAATCCAAAG GTCACTGGCA TGACACAGCC TAATGTTTTA ACTAAGAGTC TCAGTAAAGA
      ·  S  S  F  S  S  T  K  S  L  P  D  L  L  G  G  S  N  L  V  K  P  C  A
3991 CTCTTCATTT TCATCTACCA AATCTTTGCC AGATCTTCTA GGTGGTTCCA ATTTGGTAAA GCCCTGCGCA
      C  H  G  G  D  M  S  Q  N  S  G  S  E  S  G  I  V  S  E  G  D  T  E  T  ·
4061 TGTCATGGAG GAGACATGAG CCAGAATTCA GGCAGTGAGA GTGGAATTGT CAGTGAAGGA GACACAGAAA
      ·  T  T  N  S  E  M  C  L  L  N  A  V  D  G  S  P  S  N  L  E  T  E  H  ·
4131 CCACTACCAA CTCTGAAATG TGCTTGCTCA ATGCAGTGGA TGGGTCCCCA AGTAACCTTG AAACTGAACA
      ·  L  D  P  Q  M  G  D  A  V  N  V  L  K  Q  K  F  T  D  E  G  E  S  I
4201 TCTGGACCCA CAAATGGGAG ATGCAGTTAA CGTGTTAAAG CAAAAATTTA CAGATGAGGG GGAAAGCATT
      K  L  P  N  S  S  Q  S  S  I  S  P  V  G  C  V  N  G  K  V  G  D  L  N  ·
4271 AAGCTTCCAA ATAGCTCTCA GTCGTCCATT TCACCAGTGG GTTGTGTAAA TGGAAAAGTT GGAGATTTAA
      ·  S  I  T  K  H  T  P  D  C  L  G  E  E  L  Q  G  K  H  D  V  F  T  F  ·
4341 ACAGTATTAC CAAACATACC CCTGACTGTT TGGGAGAAGA ATTACAAGGA AAACATGATG TGTTTACATT
      ·  Y  D  Y  S  Y  L  Q  G  S  K  L  K  L  P  M  I  M  K  Q  S  Q  S  E
```

FIGURE 26 (cont.)

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4411 TTATGATTAC TCATACCTCC AAGGCTCAAA ACTCAAATTA CCAATGATAA TGAAACAGTC ACAAAGCGAA
      K  V  H  V  E  D  P  L  L  R  G  F  Y  F  D  K  K  S  C  K  S  K  H  Q  ·
4481 AAAGTGCATG TGGAGGATCC CCTGCTTCGT GGTTTTTATT TTGATAAAAA ATCATGCAAA TCTAAACATC
      ·  T  T  E  L  Q  P  D  V  P  P  H  E  R  I  L  A  S  A  S  H  E  M  D  ·
4551 AGACTACAGA GTTACAACCA GATGTACCTC CCCATGAAAG GATTTTGGCA AGTGCATCTC ATGAAATGGA
      ·  R  I  S  Y  K  S  G  N  I  E  K  T  F  T  G  M  Q  N  A  K  Q  L  S
4621 TCGCATTTCA TATAAAAGTG GCAATATAGA AAAGACATTC ACTGGCATGC AGAATGCCAA ACAGCTCTCC
      L  L  S  H  S  S  S  I  E  S  L  S  P  G  G  D  L  F  G  L  G  I  F  K  ·
4691 CTTTTATCTC ATAGTTCATC TATTGAGTCC CTTTCTCCAG GGGGTGATTT ATTTGGATTG GGCATCTTTA
      ·  N  G  S  D  S  L  Q  R  S  T  S  L  E  S  W  L  T  S  Y  K  S  N  E  ·
4761 AAAATGGCAG TGACAGCCTC CAGCGAAGCA CTTCTTTAGA AAGTTGGTTG ACTTCCTATA AAAGCAATGA
      ·  D  L  F  S  C  H  S  S  G  D  I  S  V  S  S  G  S  V  G  E  L  S  K
4831 AGATCTCTTT AGCTGTCACA GCTCTGGGGA TATAAGCGTG AGCAGTGGCT CAGTTGGTGA ACTAAGTAAA
      R  T  L  D  L  L  N  R  L  E  N  I  Q  S  P  S  E  Q  K  I  K  R  S  V  ·
4901 AGAACATTAG ATCTCCTGAA TCGTTTGGAG AATATCCAGA GCCCCTCAGA GCAAAAGATA AAACGAAGTG
      ·  S  D  I  T  L  Q  S  S  S  Q  K  M  S  F  T  G  Q  M  S  L  D  I  A  ·
4971 TTTCTGATAT CACTCTTCAA AGCAGTTCCC AAAAGATGTC CTTTACTGGC CAGATGTCAT TGGACATAGC
      ·  S  S  I  N  E  D  S  A  A  S  L  T  E  L  S  S  S  D  E  L  S  L  C
5041 ATCTTCTATC AATGAAGACT CAGCGGCATC TCTAACAGAA CTTAGCAGCA GTGACGAGCT CTCTCTTTGC
      S  E  D  I  V  L  H  K  N  K  I  P  E  S  N  A  S  F  R  K  R  L  T  R  ·
5111 TCAGAGGATA TTGTGTTACA CAAGAACAAG ATCCCGGAAT CGAATGCATC GTTCAGGAAG CGTCTGACTC
      ·  S  V  A  D  E  S  D  V  N  V  S  M  I  V  N  V  S  C  T  S  A  C  T  ·
5181 GTTCAGTGGC TGATGAAAGC GATGTCAATG TCAGCATGAT TGTTAATGTC TCTTGCACCT CTGCTTGCAC
      ·  D  D  E  D  D  S  D  L  L  S  S  S  T  L  T  L  T  E  E  E  L  C  I
5251 TGATGATGAA GATGACAGCG ACCTGCTCTC CAGCTCTACC CTTACCTTGA CTGAAGAAGA GCTGTGCATC
      K  D  E  D  D  D  S  S  I  A  T  D  D  E  I  Y  E  D  C  T  L  M  S  G  ·
5321 AAAGATGAGG ATGACGACTC CAGTATTGCA ACAGATGATG AAATTTATGA AGACTGCACC TTGATGTCAG
      ·  L  D  Y  I  K  N  E  L  Q  T  W  I  R  P  K  L  S  L  T  R  D  K  K  ·
5391 GGCTAGACTA CATAAAGAAT GAATTACAGA CCTGGATTAG GCCAAAATTG TCTTTGACAA GAGATAAGAA
      ·  R  C  N  V  S  D  E  M  K  G  S  K  D  I  S  S  S  E  M  T  N  P  S
5461 AAGGTGCAAT GTCAGTGATG AGATGAAGGG CAGTAAAGAT ATAAGTAGCA GTGAGATGAC CAATCCCTCT
      D  T  L  N  I  E  T  L  L  N  G  S  V  K  R  V  S  E  N  N  G  N  G  K  ·
5531 GATACTCTGA ATATTGAGAC CCTTCTAAAT GGCTCTGTAA AACGTGTCTC TGAAAATAAT GGAAATGGTA
      ·  N  S  S  H  T  H  E  L  G  T  K  R  E  N  K  K  T  I  F  K  V  N  K  ·
5601 AGAATTCATC TCATACCCAT GAGTTAGGGA CAAAGCGTGA AAATAAGAAA ACTATTTTCA AAGTTAATAA
      ·  D  P  Y  V  A  D  M  E  N  G  N  I  E  G  I  P  E  R  Q  K  G  K  P
5671 AGATCCATAT GTGGCTGACA TGGAAAATGG CAATATTGAA GGTATTCCAG AAAGGCAAAA GGGCAAACCG
      N  V  T  S  K  V  S  E  N  L  G  S  H  G  K  E  I  S  E  S  E  H  C  K  ·
5741 AATGTGACTT CAAAGGTATC AGAAAATCTT GGTTCACATG GGAAAGAGAT TTCAGAGAGT GAGCATTGTA
      ·  C  K  A  L  M  D  S  L  D  D  S  N  T  A  G  K  E  F  V  S  Q  D  V  ·
5811 AGTGTAAAGC ACTTATGGAT AGTTTAGATG ATTCAAATAC TGCTGGCAAG GAATTTGTTT CCCAAGATGT
      ·  R  H  L  P  K  K  C  P  N  H  H  H  F  E  N  Q  S  T  A  S  T  P  T
5881 TAGACATCTT CCAAAGAAAT GTCCAAATCA CCACCATTTT GAAAATCAAA GCACTGCCTC TACTCCCACT
      E  K  S  F  S  E  L  A  L  E  T  R  F  N  N  R  Q  D  S  D  A  L  K  S  ·
5951 GAGAAGTCTT TCTCAGAACT GGCTTTAGAA ACCAGGTTTA ACAACAGACA AGACTCTGAT GCACTGAAAT
      ·  S  D  D  A  P  S  M  A  G  K  S  A  G  C  C  L  A  L  E  Q  N  G  T  ·
6021 CATCTGATGA TGCACCGAGT ATGGCTGGAA AATCTGCTGG TTGTTGCCTA GCACTTGAAC AAAACGGAAC
      ·  E  E  N  A  S  I  S  N  I  S  C  C  N  C  E  P  D  V  F  H  Q  K  D
6091 AGAGGAAAAT GCTTCTATCA GCAACATTTC CTGTTGCAAC TGTGAGCCAG ATGTTTTCCA TCAAAAAGAT
      A  E  D  C  S  V  H  N  F  V  K  E  I  I  D  M  A  S  T  A  L  K  S  K  ·
6161 GCCGAAGATT GTTCAGTACA CAACTTTGTT AAGGAAATCA TTGACATGGC TTCGACAGCC CTAAAAAGTA
      ·  S  Q  P  E  N  E  V  A  A  P  T  S  L  T  Q  I  K  E  K  V  L  E  H  ·
6231 AATCTCAACC TGAAAACGAG GTGGCTGCTC CTACTTCATT AACTCAAATC AAGGAGAAAG TGTTGGAGCA
      ·  S  H  R  P  I  Q  L  R  K  G  D  F  Y  S  Y  L  S  L  S  S  H  D  S
6301 TTCTCACCGG CCCATCCAGC TGAGAAAAGG GGACTTTTAT TCGTACTTAT CTCTCTCATC TCATGACAGT
      D  C  G  E  V  T  N  Y  I  E  E  K  S  S  T  P  L  P  L  D  T  T  D  S  ·
6371 GATTGTGGGG AGGTCACCAA TTACATAGAA GAGAAAAGCA GCACTCCATT GCCACTAGAC ACCACTGACT
      ·  G  L  D  D  K  E  D  I  E  C  F  F  E  A  C  V  E  G  D  S  D  G  E  ·
6441 CGGGCTTAGA TGACAAGGAA GATATTGAAT GCTTTTTTGA GGCCTGTGTT GAGGGTGACT CTGATGGAGA
      ·  E  P  C  F  S  S  A  P  P  N  E  S  A  V  P  S  E  A  A  M  P  L  Q
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FIGURE 26 (cont.)

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6511 GGAGCCTTGT TTCTCTAGTG CTCCTCCAAA TGAATCTGCA GTTCCCAGCG AAGCTGCAAT GCCACTACAA
      A  T  A  C   S  S  E   F  S  D   S  S  L  S   A  D  D   A  D  T   V  A  L  S  ·
6581 GCAACAGCAT GTTCTTCTGA GTTCAGTGAT AGTTCTCTTT CAGCTGATGA TGCAGATACA GTGGCTCTTT
      ·  S  P  S   S  Q  E   R  A  E  V   G  K  E   V  N  G   L  P  Q  T   S  S  G  ·
6651 CAAGTCCTTC CTCTCAGGAA AGAGCTGAGG TTGGAAAGGA AGTGAATGGT TTGCCCCAAA CTTCCAGTGG
      ·  C  A  E   N  L  E  F   T  P  S   K  L  D   S  E  K  E   S  S  G   K  P  G
6721 CTGTGCAGAA AACTTAGAGT TTACTCCTTC AAAGCTTGAC AGTGAAAAGG AAAGTTCCGG AAAACCAGGT
      E  S  G  M   P  E  E   H  N  A   A  S  A  K   S  K  V   Q  D  L   S  L  K  A  ·
6791 GAATCTGGAA TGCCAGAAGA ACATAATGCT GCTTCAGCCA AATCTAAAGT TCAAGACCTC TCCTTGAAGG
      ·  N  Q  P   T  D  K   A  A  L  H   P  S  P   K  T  L   T  C  E  E   N  L  L  ·
6861 CAAATCAGCC AACAGACAAG GCCGCATTGC ATCCCAGCCC CAAAACTTTA ACCTGTGAAG AAAATCTTCT
      ·  N  L  H   E  K  R  H   R  N  M   H  R
6931 AAACCTTCAT GAAAAACGAC ATAGAAATAT GCATAGGTAG AATGTACCCC CTCCCCAAGC ATGAAAATCA
7001 TCTCACTGAA AGATACGCCT GGCTGCAACT CAGGGGTGGC CTCATCCTCC CGCCCTGGGC TGGCCTCTGG
7071 TTCCATCACG TTTGTCACTG CCGTTTATTA CATTGACTTC TCCCAAGATG AATCTTCCTT CCAAATGTGT
7141 TTTCTCCACA CAAGCCTTGT GATCTGAATG TGTGCGCTGG TTCTCTTTAG GTGATCGTCT TTGAAGTTCA
7211 GCAAAGCTGC TTGTTCTCCC ATGGATTCCT GTCCCAAGCT ACCTCTACCA ACCCTCTCTC TCCAGCTAGA
7281 CTTTTCTCTT TGCCTCCTCC CTTCCCTTCC ACTCTTTAAA GTTCTGCAGT TCACCAACTG GTAGTCCATT
7351 AAATTCTCCT GTCTAGAATG ACCCCCCCAC CAGTACTTGA CCAATTTCAT GTATCAATCT GGATTTTTTT
7421 TTTAACGGTA TAATGACTGT GCTTATTGAA AGAGTTTTAC CTAAAAAGCC AACATTTGAA TTGGTTGCAG
7491 CATAGAGAAG AAACACTGGT CCTTCTTTCA AAATTAAGCA ACTATTAAAA GCGCCATTTT ATTTATTTCA
7561 TTTAAAAAAT AATCTATGCA GCATTTCAAG AAACAACCAT ATGGTGTTGT ATATTATAAA CTGGTGACAT
7631 TCTACTATTG AATTATGTAC AACATTTTCA TTTTTTATGC TTCTTGAGGT GGTAATGAGA AAAAAGTTTT
7701 TTAAAAAAGT GTGCCTTGCT GTATTTCTTA TACCATTTAT TAAAAAGCTG CTTTCACGGT AAAATTATGT
7771 TGGTTTGAAA GGAGGAAATA GCAAGGTTAA GATGTGTGAA TAATTTCTGT ATATATGTAT AACCAAGTAC
7841 AAACATTGAT GTATAATGAC AGTATAAAAT GCTTTCATGT TTGTGATGTC TAGTGATGTG GAAAATATAA
7911 GCCTTAAATC CATTAGATTG CATGGTAATT AAAATTGGCA TAATAAACAC AGATTATTGG GGGAAAAGGA
7981 AAATTAGTGA TCTCTTCTAC TATGTTCTTT ACCAAATTGT TGCATCTGGT TCTGAAAAAG TATAGCATGT
8051 AGCAGCTTCC AAACATATTC ATATTGCTTA AGAGGCTTAA CATTACCTAA ACTAGAGACT AGACGTAAAG
8121 CCTTCAGTTT TCAAAATCTT TCTGGTCACT ATAAAGATCT TGGAACAGCA AATGATTAAA TGTCAGTTCC
8191 CCTAAACCAA TAAACATTTA TACTAGATTT TTTATTTCCA CTTATCATTA ATGATTTAAT GTTGGATTTC
8261 AGGTACCTTG TATGTCTTAA TTTATTTTAA ATATTTATTT TGAATGAGTT TGATAGAAAG CTAGTAGAAA
8331 AGTACAGAAA ATTTGACTAT TATTTATAGA TTTCAGGTAT ATTTATATGT GTAAAAGAAA TTGACAAAGA
8401 AATATTTCAT CTGGCCTTTA CTGACTCCTG TTAAATGCAG TTTTAAATTT ATATCGTAAC ACCTACTTAA
8471 GTGCCTGACA CAGTAGGTAT TCAATAAAAA TTTACTGAAT TAAAGGATTA AATTAGGTGA CATGGTGACA
8541 TCTATCCCTT TATTTTGACA CTAAAACATG GACACAACTA GAAAGAGGTA CAATGCAATA TAAAGTCACA
8611 ATAGATAATA TATATCAAAT TTCTAAAAGG TAAAGAATGT TGTGGGTTCA TGCAGTCACA GGAATGACAA
8681 TCATTCAACA GATAGTTCAG AAACACTTTT TATCTGCAAG GCACTATTCT AGATCCAGAA GATGCAATGT
8751 TGAACAAACA GACAAAGCCC TGCCCTCAGA AGGCTGTCCT GCATTAGGAA CAAGTGAACA CGCAAATGAC
8821 ATGAAGTATT TGTTGCAGAG CTGAGGAACA GAGCAAATGT AGTGATAGAA GCGCAATGAG AGAAGCAGCA
8891 GTGGGTACAA GGAGGAAGAA AAAGGGCTTG CAGAGAGTGG AAAGTTAGTG GAATATTCAT GAAACTTCAT
8961 TGCAGGGGTA ATAGAAGAAA AAGTAAATTG GGAGGACTTA ATGGAAGGTC TTTTAAAAAG TTAACTTGGA
9031 GCTTCTGTAT GTAAAATGCT AGGTAATAAG GACACTTTGT ACAGGCTGTT TTGCACCTGA TTTTATTTAT
9101 CATTAGTGCC ACGCCAAGAT CATTTAGACG ATGCTTATCT GTAATTCTAC CACTTTAATA ACTATTTGTA
9171 TTTTTATGCC CCTTCTGATC TTTTCCATAT GTATTTCTAA ATGGATAAAT TATTCTAGGC TTCTTAATAG
9241 GTAGTAATTT GTTCAAAAGC GGTTTTAGCC AGACATCTAG TTGCAGTGTT CAAGAGGATT ATGGGGGAAA
9311 GAGATTAGAG ATAATTGTCT AGTTAGGGGG CAGCTGGAGA AAATAAGCTA AGTTTGCAAT AACAGAGTAC
9381 ACAAGTATAG TGGCCCAGGA TGTAGTGAAA GAACAAATCC TAGAGTCTTT GAAATTTCTA AGGGCATTCT
9451 AGACCTCTGT TGGGATATGG TATTATTTTA CATACTGACA CAACCTAAAT TTTCTTTGGG TAGTAACTAA
9521 TGTCAAGTCT ACATCGACTG GTAAAACATT CAAAGAACAA ACTGACAATG ATGTTCTACC TACTTGTTAC
9591 ATGCTCATGG AAGACCGTGC AGTATTGAAA GTATTTGTTA ATTATCTGCT TAGTATTAAC ACTAAATTTG
9661 TAGAATGACT TTCAGGTTTG TTGAACAATG CCTTTTCAGG TTGGAAGAAG AAAAATAGCC TCAATCTCCC
9731 ACCCCATGTA GGCACTACCT CCCCAATTAC CCTTAGAAAA TGATCACACC AACTCTGCCT ACACACTTCC
9801 AGTGATAGTG GCTCATTGTC TGTTAAGGCA AACTGTTCCA CTGTTGGGCA TATCTCTTTG TTAGAAAGTT
9871 CTTTCTTAGG TTGCTAAAAT CTGCCTAGTA CCCCGCTACC CTGTTCTGTC TTATGGAGCA GCCCAGATTA
9941 TCTTTACTCC CTCTTTCTCA TGGCAACCCT GAAGATAATC AAGGCCAGTT ACTCATCATC TCCCAACCAC
10011 TGTTTCCTCA ACTGCCCTTC ATATGTCATG GTTTTCAGAT CCATTCCAAC CTGACTGAAT GTTAACAGAC
10081 AGAATTCTTC ACATTAAGGA ACTGTCTTCA TCATCATACA TGTAGAAAAG AATCTGAACA TTTAAGTGCG
10151 AAGTTTTCTC TAGAAATATA TTCAAGATAT GTTTATTCTA TTATTGTAAA TTTCAAACAA TAAATAAATA
10221 AGAATCC
```

FIGURE 27

Figure 27. human mAKAPα mRNA with open reading frame translated:

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   1 CATCATGCAG CAGGTCAAAC AAGGCATCTC CTAGTATTGC ATCCTACAGA TGTGCTGTAA ACATCAAAAG
                                                                 M  L  T  M  S  ·
  71 AAGACGGTGG GATCAGGAGA TGCTGTTTTG GAAAGAAGTG AGGTTTAGAC TTCTCCATGT TAACCATGAG
     ·  V  T  L  S  P  L  R  S  Q  D  L  D  P  M  A  T  D  A  S  P  M  A  I
 141 CGTGACACTT TCCCCCCTGA GGTCACAGGA CCTGGATCCC ATGGCTACTG ATGCTTCACC CATGGCCATC
      N  M  T  P  T  V  E  Q  G  E  G  E  E  A  M  K  D  M  D  S  D  Q  Q  Y  ·
 211 AACATGACAC CCACTGTGGA GCAGGGTGAG GGAGAAGAGG CAATGAAGGA CATGGACTCT GACCAGCAGT
     ·  E  K  P  P  P  L  H  T  G  A  D  W  K  I  V  L  H  L  P  E  I  E  T  ·
 281 ATGAAAAGCC ACCCCCACTA CACACAGGGG CTGACTGGAA GATTGTCCTC CACTTACCTG AAATTGAGAC
     ·  W  L  R  M  T  S  E  R  V  R  D  L  T  Y  S  V  Q  Q  D  S  D  S  K
 351 CTGGCTCCGG ATGACCTCAG AGAGGGTCCG AGACCTAACC TATTCAGTCC AGCAGGATTC GGACAGCAAG
      H  V  D  V  H  L  V  Q  L  K  D  I  C  E  D  I  S  D  H  V  E  Q  I  H  ·
 421 CATGTGGATG TACATCTAGT TCAACTAAAG GACATTTGTG AAGATATTTC TGATCATGTT GAGCAAATCC
     ·  A  L  L  E  T  E  F  S  L  K  L  L  S  Y  S  V  N  V  I  V  D  I  H  ·
 491 ATGCCCTCCT TGAAACAGAG TTCTCCCTAA AGCTGCTGTC TTACTCTGTC AACGTGATAG TGGACATCCA
     ·  A  V  Q  L  L  W  H  Q  L  R  V  S  V  L  V  L  R  E  R  I  L  Q  G
 561 CGCAGTGCAG CTCCTCTGGC ACCAGCTTCG AGTCTCAGTG CTGGTTCTGC GGGAGCGCAT TCTGCAAGGT
      L  Q  D  A  N  G  N  Y  T  R  Q  T  D  I  L  Q  A  F  S  E  E  T  K  E  ·
 631 CTGCAGGACG CCAATGGCAA CTACACTAGG CAGACGGACA TTCTGCAAGC TTTCTCTGAA GAGACAAAAG
     ·  G  R  L  D  S  L  T  E  V  D  D  S  G  Q  L  T  I  K  C  S  Q  N  Y  ·
 701 AGGGCCGGCT TGATTCTCTA ACAGAAGTGG ATGACTCAGG ACAATTAACC ATCAAATGTT CTCAAAATTA
     ·  L  S  L  D  C  G  I  T  A  F  E  L  S  D  Y  S  P  S  E  D  L  L  S
 771 CTTGTCTCTG GATTGTGGCA TTACTGCATT CGAACTGTCT GACTACAGTC CAAGTGAGGA TTTGCTCAGT
      G  L  G  D  M  T  S  S  Q  V  K  T  K  P  F  D  S  W  S  Y  S  E  M  E  ·
 841 GGGCTAGGTG ACATGACCTC TAGCCAAGTC AAAACCAAAC CCTTTGACTC TTGGAGCTAC AGTGAGATGG
     ·  K  E  F  P  E  L  I  R  S  V  G  L  L  T  V  A  A  D  S  I  S  T  N  ·
 911 AAAAGGAGTT TCCTGAGCTT ATCCGAAGTG TTGGTTTACT TACGGTAGCT GCTGACTCTA TCTCTACCAA
     ·  G  S  E  A  V  T  E  E  V  S  Q  V  S  L  S  V  D  D  K  G  G  C  E
 981 TGGCAGTGAA GCAGTTACTG AGGAGGTATC TCAAGTATCT CTCTCAGTAG ACGACAAAGG TGGATGTGAG
      E  D  N  A  S  A  V  E  E  Q  P  G  L  T  L  G  V  S  S  S  S  G  E  A  ·
1051 GAAGACAATG CTTCTGCAGT CGAAGAGCAA CCAGGCTTAA CACTGGGGGT GTCATCATCT TCAGGAGAAG
     ·  L  T  N  A  A  Q  P  S  S  E  T  V  Q  Q  E  S  S  S  S  S  H  H  D  ·
1121 CTCTGACAAA TGCTGCTCAA CCCTCCTCTG AGACTGTGCA GCAAGAATCC AGTTCCTCCT CCCATCATGA
     ·  A  K  N  Q  Q  P  V  P  C  E  N  A  T  P  K  R  T  I  R  D  C  F  N
1191 TGCAAAGAAT CAGCAGCCTG TTCCTTGTGA AAATGCAACC CCCAAACGAA CCATCAGAGA TTGCTTTAAT
      Y  N  E  D  S  P  T  Q  P  T  L  P  K  R  G  L  F  L  K  E  E  T  F  K  ·
1261 TATAACGAGG ACTCTCCCAC GCAGCCTACA TTGCCAAAAA GAGGACTTTT TCTTAAAGAG GAAACTTTTA
     ·  N  D  L  K  G  N  G  G  K  R  Q  M  V  D  L  K  P  E  M  S  R  S  T  ·
1331 AGAATGATCT GAAAGGCAAT GGTGGAAAGA GGCAAATGGT TGATCTAAAG CCTGAGATGA GCAGAAGCAC
     ·  P  S  L  V  D  P  P  D  R  S  K  L  C  L  V  L  Q  S  S  Y  P  N  S
1401 CCCTTCGCTA GTAGATCCTC CTGACAGATC CAAACTTTGC CTGGTATTGC AGTCTTCTTA CCCCAACAGC
      P  S  A  A  S  Q  S  Y  E  C  L  H  K  V  G  N  G  N  L  E  N  T  V  K  ·
1471 CCTTCTGCTG CCAGCCAGTC TTATGAGTGT TTACACAAGG TGGGGAATGG GAACCTTGAA AACACAGTCA
     ·  F  H  I  K  E  I  S  S  S  L  G  R  L  N  D  C  Y  K  E  K  S  R  L  ·
1541 AATTTCACAT TAAAGAAATT TCTTCCAGCC TGGGAAGGCT TAACGACTGC TATAAAGAGA AATCTCGACT
     ·  K  K  P  H  K  T  S  E  E  V  P  P  C  R  T  P  K  R  G  T  G  S  G
1611 TAAAAAGCCA CACAAGACCT CAGAAGAGGT GCCTCCATGC CGAACACCTA AACGGGGGAC TGGTTCAGGC
      K  Q  A  K  N  T  K  S  S  A  V  P  N  G  E  L  S  Y  T  S  K  A  I  E  ·
1681 AAACAAGCTA AAAATACAAA GAGCTCAGCA GTGCCAAATG GAGAGCTTTC TTATACTTCC AAGGCCATAG
     ·  G  P  Q  T  N  S  A  S  T  S  S  L  E  P  C  N  Q  R  S  W  N  A  K  ·
1751 AGGGGCCACA AACAAATTCT GCTTCCACAT CCTCACTTGA GCCTTGTAAT CAGAGAAGTT GGAATGCCAA
     ·  L  Q  L  Q  S  E  T  S  S  S  P  A  F  T  Q  S  S  E  S  S  V  G  S
1821 ATTGCAATTG CAGTCAGAAA CATCCAGTTC ACCAGCTTTT ACTCAGAGCA GTGAATCCTC TGTTGGCTCA
      D  N  I  M  S  P  V  P  L  L  S  K  H  K  S  K  K  G  Q  A  S  S  P  S  ·
1891 GACAACATCA TGTCTCCGGT GCCACTTCTT TCAAAACACA AAAGCAAAAA AGGTCAAGCC TCCTCTCCAA
     ·  H  V  T  R  N  G  E  V  V  E  A  W  Y  G  S  D  E  Y  L  A  L  P  S  ·
1961 GTCACGTCAC TAGGAATGGT GAGGTTGTGG AGGCCTGGTA TGGCTCTGAT GAATACCTAG CACTGCCCTC
     ·  H  L  K  Q  T  E  V  L  A  L  K  L  E  N  L  T  K  L  L  P  Q  K  P
```

FIGURE 27 (cont.)

```
2031 TCACCTTAAG CAGACAGAAG TATTGGCTTT GAAGTTGGAA AACCTAACAA AGCTTCTGCC TCAGAAACCC
      R  G  E  T  I  Q  N  I  D  D  W  E  L  S  E  M  N  S  D  S  E  I  Y  P  ·
2101 AGAGGAGAAA CCATCCAGAA TATTGATGAC TGGGAACTGT CTGAAATGAA TTCAGATTCT GAAATCTATC
      ·  T  Y  H  V  K  K  K  H  T  R  L  G  R  V  S  P  S  S  S  S  D  I  A  ·
2171 CAACCTATCA TGTCAAAAAG AAGCATACAA GGCTAGGCAG GGTGTCTCCA AGCTCATCTA GTGACATAGC
      ·  S  S  L  G  E  S  I  E  S  G  P  L  S  D  I  L  S  D  E  E  S  S  M
2241 CTCTTCACTA GGGGAGAGCA TTGAATCTGG GCCCCTGAGT GACATTCTTT CTGATGAGGA GTCCAGTATG
      P  L  A  G  M  K  K  Y  A  D  E  K  S  E  R  A  S  S  S  E  K  N  E  S  ·
2311 CCTCTCGCTG GCATGAAAAA GTATGCTGAT GAGAAGTCAG AAAGAGCTTC ATCCTCTGAG AAAAATGAGA
      ·  H  S  A  T  K  S  A  L  I  Q  K  L  M  Q  D  I  Q  H  Q  D  N  Y  E  ·
2381 GCCATTCTGC CACTAAATCA GCTTTAATTC AGAAACTGAT GCAAGATATT CAGCACCAAG ACAACTATGA
      ·  A  I  W  E  K  I  E  G  F  V  N  K  L  D  E  F  I  Q  W  L  N  E  A
2451 AGCCATATGG GAAAAAATAG AGGGGTTTGT AAACAAACTG GATGAATTCA TTCAATGGTT AAATGAAGCC
      M  E  T  T  E  N  W  T  P  P  K  A  E  M  D  D  L  K  L  Y  L  E  T  H  ·
2521 ATGGAAACTA CAGAGAATTG GACTCCCCCT AAAGCAGAGA TGGATGACCT TAAACTGTAT CTGGAGACAC
      ·  L  S  F  K  L  N  V  D  S  H  C  A  L  K  E  A  V  E  E  E  G  H  Q  ·
2591 ACTTGAGTTT TAAGTTGAAT GTAGACAGTC ATTGTGCTCT CAAGGAAGCT GTGGAGGAGG AAGGACACCA
      ·  L  L  E  L  I  A  S  H  K  A  G  L  K  D  M  L  R  M  I  A  S  Q  W
2661 ACTTCTTGAG CTTATTGCAT CTCACAAAGC AGGACTGAAG GACATGCTGC GGATGATTGC AAGTCAATGG
      K  E  L  Q  R  Q  I  K  R  Q  H  S  W  I  L  R  A  L  D  T  I  K  A  E  ·
2731 AAGGAGCTGC AGAGGCAAAT CAAACGGCAG CACAGCTGGA TTCTCAGGGC TCTGGATACC ATCAAAGCCG
      ·  I  L  A  T  D  V  S  V  E  D  E  E  G  T  G  S  P  K  A  E  V  Q  L  ·
2801 AGATACTGGC TACTGATGTG TCTGTGGAGG ATGAGGAAGG GACTGGAAGC CCCAAGGCTG AGGTTCAACT
      ·  C  Y  L  E  A  Q  R  D  A  V  E  Q  M  S  L  K  L  Y  S  E  Q  Y  T
2871 ATGCTACCTG GAAGCACAAA GAGATGCTGT TGAGCAGATG TCCCTCAAGC TGTACAGCGA GCAGTATACC
      S  S  S  K  R  K  E  E  F  A  D  M  S  K  V  H  S  V  G  S  N  G  L  L  ·
2941 AGCAGCAGCA AGCGAAAGGA AGAGTTTGCT GATATGTCAA AAGTTCATTC AGTGGGAAGC AATGGGCTTC
      ·  D  F  D  S  E  Y  Q  E  L  W  D  C  L  I  D  M  E  S  L  V  M  D  S  ·
3011 TGGACTTTGA TTCAGAATAT CAGGAGCTCT GGGATTGCTT GATTGACATG GAGTCCCTTG TGATGGACAG
      ·  H  D  L  M  M  S  E  E  Q  Q  Q  H  L  Y  K  R  Y  S  V  E  M  S  I
3081 CCACGACCTG ATGATGTCAG AGGAGCAGCA GCAGCATCTT TACAAGCGAT ACAGTGTGGA AATGTCCATC
      R  H  L  K  K  T  E  L  L  S  K  V  E  A  L  K  K  G  G  V  L  L  P  N  ·
3151 AGACACCTGA AAAAGACGGA GCTGCTTAGT AAGGTTGAAG CTTTGAAGAA AGGTGGCGTT TTACTACCAA
      ·  D  L  L  E  K  V  D  S  I  N  E  K  W  E  L  L  G  K  T  L  G  E  K  ·
3221 ATGATCTCCT TGAAAAAGTG GATTCAATTA ATGAAAAATG GGAACTGCTT GGGAAAACCC TAGGAGAGAA
      ·  I  Q  D  T  M  A  G  H  S  G  S  S  P  R  D  L  L  S  P  E  S  G  S
3291 GATCCAGGAC ACAATGGCAG GGCACAGTGG GTCGAGTCCA CGTGACCTGC TCTCTCCTGA AAGTGGAAGC
      L  V  R  Q  L  E  V  R  I  K  E  L  K  G  W  L  R  D  T  E  L  F  I  F  ·
3361 CTGGTAAGGC AGCTGGAGGT CAGGATCAAA GAACTGAAAG GATGGCTAAG AGATACAGAG CTTTTCATCT
      ·  N  S  C  L  R  Q  E  K  E  G  T  M  N  T  E  K  Q  L  Q  Y  F  K  S  ·
3431 TCAATTCCTG TCTGAGACAA GAAAAGGAAG GAACAATGAA TACTGAGAAA CAACTGCAAT ACTTTAAGTC
      ·  L  C  R  E  I  K  Q  R  R  R  G  V  A  S  I  L  R  L  C  Q  H  L  L
3501 CCTCTGTCGT GAAATCAAGC AACGACGTCG AGGAGTTGCC TCCATTCTGC GACTATGCCA GCATCTTTTG
      D  D  R  E  T  C  N  L  N  A  D  H  Q  P  M  Q  L  I  I  V  N  L  E  R  ·
3571 GATGACCGGG AGACTTGCAA TCTGAATGCA GACCACCAGC CCATGCAGCT GATCATTGTA AATCTTGAAA
      ·  R  W  E  A  I  V  M  Q  A  V  Q  W  Q  T  R  L  Q  K  K  M  G  K  E  ·
3641 GAAGGTGGGA AGCCATTGTC ATGCAAGCCG TCCAGTGGCA AACACGTCTA CAAAAGAAGA TGGGAAAGGA
      ·  S  E  T  L  N  V  I  D  P  G  L  M  D  L  N  G  M  S  E  D  A  L  E
3711 ATCTGAGACT TTGAATGTGA TTGATCCTGG CTTGATGGAC CTAAATGGGA TGAGTGAGGA TGCCCTGGAA
      W  D  E  M  D  I  S  N  K  L  I  S  L  N  E  E  S  N  D  L  D  Q  E  L  ·
3781 TGGGATGAAA TGGACATAAG TAACAAGTTA ATTAGTTTGA ATGAGGAATC AAATGACCTT GATCAAGAAC
      ·  Q  P  V  I  P  S  L  K  L  G  E  T  S  N  E  D  P  G  Y  D  E  E  A  ·
3851 TCCAACCTGT TATCCCTTCC TTGAAGCTTG GAGAGACAAG TAATGAGGAC CCTGGTTATG ACGAGGAGGC
      ·  D  N  H  G  G  S  Q  Y  A  S  N  I  T  A  P  S  S  P  H  I  Y  Q  V
3921 TGATAACCAT GGGGGATCTC AGTATGCCTC AAATATTACT GCCCCCTCTA GTCCACACAT TTACCAGGTG
      Y  S  L  H  N  V  E  L  Y  E  D  N  H  M  P  F  L  K  N  N  P  K  V  T  ·
3991 TACAGCCTCC ACAATGTTGA ACTCTATGAG GACAACCACA TGCCATTTCT GAAAAACAAT CCAAAGGTCA
      ·  G  M  T  Q  P  N  V  L  T  K  S  L  S  K  D  S  S  F  S  S  T  K  S  ·
4061 CTGGCATGAC ACAGCCTAAT GTTTTAACTA AGAGTCTCAG TAAAGACTCT TCATTTTCAT CTACCAAATC
      ·  L  P  D  L  L  G  G  S  N  L  V  K  P  C  A  C  H  G  G  D  M  S  Q
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FIGURE 27 (cont.)

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4131 TTTGCCAGAT CTTCTAGGTG GTTCCAATTT GGTAAAGCCC TGCGCATGTC ATGGAGGAGA CATGAGCCAG
      N  S  G  S  E  S  G  I  V  S  E  G  D  T  E  T  T  T  N  S  E  M  C  L  ·
4201 AATTCAGGCA GTGAGAGTGG AATTGTCAGT GAAGGAGACA CAGAAACCAC TACCAACTCT GAAATGTGCT
      ·  L  N  A  V  D  G  S  P  S  N  L  E  T  E  H  L  D  P  Q  M  G  D  A  ·
4271 TGCTCAATGC AGTGGATGGG TCCCCAAGTA ACCTTGAAAC TGAACATCTG GACCCACAAA TGGGAGATGC
      ·  V  N  V  L  K  Q  K  F  T  D  E  G  E  S  I  K  L  P  N  S  S  Q  S
4341 AGTTAACGTG TTAAAGCAAA AATTTACAGA TGAGGGGGAA AGCATTAAGC TTCCAAATAG CTCTCAGTCG
      S  I  S  P  V  G  C  V  N  G  K  V  G  D  L  N  S  I  T  K  H  T  P  D  ·
4411 TCCATTTCAC CAGTGGGTTG TGTAAATGGA AAAGTTGGAG ATTTAAACAG TATTACCAAA CATACCCCTG
      ·  C  L  G  E  E  L  Q  G  K  H  D  V  F  T  F  Y  D  Y  S  Y  L  Q  G  ·
4481 ACTGTTTGGG AGAAGAATTA CAAGGAAAAC ATGATGTGTT TACATTTTAT GATTACTCAT ACCTCCAAGG
      ·  S  K  L  K  L  P  M  I  M  K  Q  S  Q  S  E  K  V  H  V  E  D  P  L
4551 CTCAAAACTC AAATTACCAA TGATAATGAA ACAGTCACAA AGCGAAAAAG TGCATGTGGA GGATCCCCTG
      L  R  G  F  Y  F  D  K  K  S  C  K  S  K  H  Q  T  T  E  L  Q  P  D  V  ·
4621 CTTCGTGGTT TTTATTTTGA TAAAAAATCA TGCAAATCTA AACATCAGAC TACAGAGTTA CAACCAGATG
      ·  P  P  H  E  R  I  L  A  S  A  S  H  E  M  D  R  I  S  Y  K  S  G  N  ·
4691 TACCTCCCCA TGAAAGGATT TTGGCAAGTG CATCTCATGA AATGGATCGC ATTTCATATA AAAGTGGCAA
      ·  I  E  K  T  F  T  G  M  Q  N  A  K  Q  L  S  L  L  S  H  S  S  S  I
4761 TATAGAAAAG ACATTCACTG GCATGCAGAA TGCCAAACAG CTCTCCCTTT TATCTCATAG TTCATCTATT
      E  S  L  S  P  G  G  D  L  F  G  L  G  I  F  K  N  G  S  D  S  L  Q  R  ·
4831 GAGTCCCTTT CTCCAGGGGG TGATTTATTT GGATTGGGCA TCTTTAAAAA TGGCAGTGAC AGCCTCCAGC
      ·  S  T  S  L  E  S  W  L  T  S  Y  K  S  N  E  D  L  F  S  C  H  S  S  ·
4901 GAAGCACTTC TTTAGAAAGT TGGTTGACTT CCTATAAAAG CAATGAAGAT CTCTTTAGCT GTCACAGCTC
      ·  G  D  I  S  V  S  S  G  S  V  G  E  L  S  K  R  T  L  D  L  L  N  R
4971 TGGGGATATA AGCGTGAGCA GTGGCTCAGT TGGTGAACTA AGTAAAAGAA CATTAGATCT CCTGAATCGT
      L  E  N  I  Q  S  P  S  E  Q  K  I  K  R  S  V  S  D  I  T  L  Q  S  S  ·
5041 TTGGAGAATA TCCAGAGCCC CTCAGAGCAA AAGATAAAAC GAAGTGTTTC TGATATCACT CTTCAAAGCA
      ·  S  Q  K  M  S  F  T  G  Q  M  S  L  D  I  A  S  S  I  N  E  D  S  A  ·
5111 GTTCCCAAAA GATGTCCTTT ACTGGCCAGA TGTCATTGGA CATAGCATCT TCTATCAATG AAGACTCAGC
      ·  A  S  L  T  E  L  S  S  S  D  E  L  S  L  C  S  E  D  I  V  L  H  K
5181 GGCATCTCTA ACAGAACTTA GCAGCAGTGA CGAGCTCTCT CTTTGCTCAG AGGATATTGT GTTACACAAG
      N  K  I  P  E  S  N  A  S  F  R  K  R  L  T  R  S  V  A  D  E  S  D  V  ·
5251 AACAAGATCC CGGAATCGAA TGCATCGTTC AGGAAGCGTC TGACTCGTTC AGTGGCTGAT GAAAGCGATG
      ·  N  V  S  M  I  V  N  V  S  C  T  S  A  C  T  D  D  E  D  D  S  D  L  ·
5321 TCAATGTCAG CATGATTGTT AATGTCTCTT GCACCTCTGC TTGCACTGAT GATGAAGATG ACAGCGACCT
      ·  L  S  S  S  T  L  T  L  T  E  E  E  L  C  I  K  D  E  D  D  D  S  S
5391 GCTCTCCAGC TCTACCCTTA CCTTGACTGA AGAAGAGCTG TGCATCAAAG ATGAGGATGA CGACTCCAGT
      I  A  T  D  D  E  I  Y  E  D  C  T  L  M  S  G  L  D  Y  I  K  N  E  L  ·
5461 ATTGCAACAG ATGATGAAAT TTATGAAGAC TGCACCTTGA TGTCAGGGCT AGACTACATA AAGAATGAAT
      ·  Q  T  W  I  R  P  K  L  S  L  T  R  D  K  K  R  C  N  V  S  D  E  M  ·
5531 TACAGACCTG GATTAGGCCA AAATTGTCTT TGACAAGAGA TAAGAAAAGG TGCAATGTCA GTGATGAGAT
      ·  K  G  S  K  D  I  S  S  S  E  M  T  N  P  S  D  T  L  N  I  E  T  L
5601 GAAGGGCAGT AAAGATATAA GTAGCAGTGA GATGACCAAT CCCTCTGATA CTCTGAATAT TGAGACCCTT
      L  N  G  S  V  K  R  V  S  E  N  N  G  N  G  K  N  S  S  H  T  H  E  L  ·
5671 CTAAATGGCT CTGTAAAACG TGTCTCTGAA AATAATGGAA ATGGTAAGAA TTCATCTCAT ACCCATGAGT
      ·  G  T  K  R  E  N  K  K  T  I  F  K  V  N  K  D  P  Y  V  A  D  M  E  ·
5741 TAGGGACAAA GCGTGAAAAT AAGAAAACTA TTTTCAAAGT TAATAAAGAT CCATATGTGG CTGACATGGA
      ·  N  G  N  I  E  G  I  P  E  R  Q  K  G  K  P  N  V  T  S  K  V  S  E
5811 AAATGGCAAT ATTGAAGGTA TTCCAGAAAG GCAAAAGGGC AAACCGAATG TGACTTCAAA GGTATCAGAA
      N  L  G  S  H  G  K  E  I  S  E  S  E  H  C  K  C  K  A  L  M  D  S  L  ·
5881 AATCTTGGTT CACATGGGAA AGAGATTTCA GAGAGTGAGC ATTGTAAGTG TAAAGCACTT ATGGATAGTT
      ·  D  D  S  N  T  A  G  K  E  F  V  S  Q  D  V  R  H  L  P  K  K  C  P  ·
5951 TAGATGATTC AAATACTGCT GGCAAGGAAT TTGTTTCCCA AGATGTTAGA CATCTTCCAA AGAAATGTCC
      ·  N  H  H  H  F  E  N  Q  S  T  A  S  T  P  T  E  K  S  F  S  E  L  A
6021 AAATCACCAC CATTTTGAAA ATCAAAGCAC TGCCTCTACT CCCACTGAGA AGTCTTTCTC AGAACTGGCT
      L  E  T  R  F  N  N  R  Q  D  S  D  A  L  K  S  S  D  D  A  P  S  M  A  ·
6091 TTAGAAACCA GGTTTAACAA CAGACAAGAC TCTGATGCAC TGAAATCATC TGATGATGCA CCGAGTATGG
      ·  G  K  S  A  G  C  C  L  A  L  E  Q  N  G  T  E  E  N  A  S  I  S  N  ·
6161 CTGGAAAATC TGCTGGTTGT TGCCTAGCAC TTGAACAAAA CGGAACAGAG GAAAATGCTT CTATCAGCAA
      ·  I  S  C  C  N  C  E  P  D  V  F  H  Q  K  D  A  E  D  C  S  V  H  N
```

FIGURE 27 (cont.)

```
6231 CATTTCCTGT TGCAACTGTG AGCCAGATGT TTTCCATCAA AAAGATGCCG AAGATTGTTC AGTACACAAC
      F  V  K  E  I  I  D  M  A  S  T  A  L  K  S  K  S  Q  P  E  N  E  V  A  ·
6301 TTTGTTAAGG AAATCATTGA CATGGCTTCG ACAGCCCTAA AAAGTAAATC TCAACCTGAA AACGAGGTGG
      ·  A  P  T  S  L  T  Q  I  K  E  K  V  L  E  H  S  H  R  P  I  Q  L  R  ·
6371 CTGCTCCTAC TTCATTAACT CAAATCAAGG AGAAAGTGTT GGAGCATTCT CACCGGCCCA TCCAGCTGAG
      ·  K  G  D  F  Y  S  Y  L  S  L  S  S  H  D  S  D  C  G  E  V  T  N  Y
6441 AAAAGGGGAC TTTTATTCGT ACTTATCTCT CTCATCTCAT GACAGTGATT GTGGGGAGGT CACCAATTAC
      I  E  E  K  S  S  T  P  L  P  L  D  T  T  D  S  G  L  D  D  K  E  D  I  ·
6511 ATAGAAGAGA AAAGCAGCAC TCCATTGCCA CTAGACACCA CTGACTCGGG CTTAGATGAC AAGGAAGATA
      ·  E  C  F  F  E  A  C  V  E  G  D  S  D  G  E  E  P  C  F  S  S  A  P  ·
6581 TTGAATGCTT TTTTGAGGCC TGTGTTGAGG GTGACTCTGA TGGAGAGGAG CCTTGTTTCT CTAGTGCTCC
      ·  P  N  E  S  A  V  P  S  E  A  A  M  P  L  Q  A  T  A  C  S  S  E  F
6651 TCCAAATGAA TCTGCAGTTC CCAGCGAAGC TGCAATGCCA CTACAAGCAA CAGCATGTTC TTCTGAGTTC
      S  D  S  S  L  S  A  D  D  A  D  T  V  A  L  S  S  P  S  S  Q  E  R  A  ·
6721 AGTGATAGTT CTCTTTCAGC TGATGATGCA GATACAGTGG CTCTTTCAAG TCCTTCCTCT CAGGAAAGAG
      ·  E  V  G  K  E  V  N  G  L  P  Q  T  S  S  G  C  A  E  N  L  E  F  T  ·
6791 CTGAGGTTGG AAAGGAAGTG AATGGTTTGC CCCAAACTTC CAGTGGCTGT GCAGAAAACT TAGAGTTTAC
      ·  P  S  K  L  D  S  E  K  E  S  S  G  K  P  G  E  S  G  M  P  E  E  H
6861 TCCTTCAAAG CTTGACAGTG AAAAGGAAAG TTCCGGAAAA CCAGGTGAAT CTGGAATGCC AGAAGAACAT
      N  A  A  S  A  K  S  K  V  Q  D  L  S  L  K  A  N  Q  P  T  D  K  A  A  ·
6931 AATGCTGCTT CAGCCAAATC TAAAGTTCAA GACCTCTCCT TGAAGGCAAA TCAGCCAACA GACAAGGCCG
      ·  L  H  P  S  P  K  T  L  T  C  E  E  N  L  L  N  L  H  E  K  R  H  R  ·
7001 CATTGCATCC CAGCCCCAAA ACTTTAACCT GTGAAGAAAA TCTTCTAAAC CTTCATGAAA AACGACATAG
      ·  N  M  H  R
7071 AAATATGCAT AGGTAGAATG TACCCCCTCC CCAAGCATGA AAATCATCTC ACTGAAAGAT ACGCCTGGCT
7141 GCAACTCAGG GGTGGCCTCA TCCTCCCGCC CTGGGCTGGC CTCTGGTTCC ATCACGTTTG TCACTGCCGT
7211 TTATTACATT GACTTCTCCC AAGATGAATC TTCCTTCCAA ATGTGTTTTC TCCACACAAG CCTTGTGATC
7281 TGAATGTGTG CGCTGGTTCT CTTTAGGTGA TCGTCTTTGA AGTTCAGCAA AGCTGCTTGT TCTCCCATGG
7351 ATTCCTGTCC CAAGCTACCT CTACCAACCC TCTCTCTCCA GCTAGACTTT TCTCTTTGCC TCCTCCCTTC
7421 CCTTCCACTC TTTAAAGTTC TGCAGTTCAC CAACTGGTAG TCCATTAAAT TCTCCTGTCT AGAATGACCC
7491 CCCCACCAGT ACTTGACCAA TTTCATGTAT CAATCTGGAT TTTTTTTTTA ACGGTATAAT GACTGTGCTT
7561 ATTGAAAGAG TTTTACCTAA AAAGCCAACA TTTGAATTGG TTGCAGCATA GAGAAGAAAC ACTGGTCCTT
7631 CTTTCAAAAT TAAGCAACTA TTAAAAGCGC CATTTTATTT ATTTCATTTA AAAAATAATC TATGCAGCAT
7701 TTCAAGAAAC AACCATATGG TGTTGTATAT TATAAACTGG TGACATTCTA CTATTGAATT ATGTACAACA
7771 TTTTCATTTT TTATGCTTCT TGAGGTGGTA ATGAGAAAAA AGTTTTTTAA AAAAGTGTGC CTTGCTGTAT
7841 TTCTTATACC ATTTATTAAA AAGCTGCTTT CACGGTAAAA TTATGTTGGT TTGAAAGGAG GAAATAGCAA
7911 GGTTAAGATG TGTGAATAAT TTCTGTATAT ATGTATAACC AAGTACAAAC ATTGATGTAT AATGACAGTA
7981 TAAAATGCTT TCATGTTTGT GATGTCTAGT GATGTGGAAA ATATAAGCCT TAAATCCATT AGATTGCATG
8051 GTAATTAAAA TTGGCATAAT AAACACAGAT TATTGGGGGA AAAGGAAAAT TAGTGATCTC TTCTACTATG
8121 TTCTTTACCA AATTGTTGCA TCTGGTTCTG AAAAAGTATA GCATGTAGCA GCTTCCAAAC ATATTCATAT
8191 TGCTTAAGAG GCTTAACATT ACCTAAACTA GAGACTAGAC GTAAAGCCTT CAGTTTTCAA AATCTTTCTG
8261 GTCACTATAA AGATCTTGGA ACAGCAAATG ATTAAATGTC AGTTCCCCTA AACCAATAAA CATTTATACT
8331 AGATTTTTTA TTTCCACTTA TCATTAATGA TTTAATGTTG GATTTCAGGT ACCTTGTATG TCTTAATTTA
8401 TTTTAAATAT TTATTTTGAA TGAGTTTGAT AGAAAGCTAG TAGAAAAGTA CAGAAAATTT GACTATTATT
8471 TATAGATTTC AGGTATATTT ATATGTGTAA AAGAAATTGA CAAAGAAATA TTTCATCTGG CCTTTACTGA
8541 CTCCTGTTAA ATGCAGTTTT AAATTTATAT CGTAACACCT ACTTAAGTGC CTGACACAGT AGGTATTCAA
8611 TAAAAATTTA CTGAATTAAA GGATTAAATT AGGTGACATG GTGACATCTA TCCCTTTATT TTGACACTAA
8681 AACATGGACA CAACTAGAAA GAGGTACAAT GCAATATAAA GTCACAATAG ATAATATATA TCAAATTTCT
8751 AAAAGGTAAA GAATGTTGTG GGTTCATGCA GTCACAGGAA TGACAATCAT TCAACAGATA GTTCAGAAAC
8821 ACTTTTTATC TGCAAGGCAC TATTCTAGAT CCAGAAGATG CAATGTTGAA CAAACAGACA AAGCCCTGCC
8891 CTCAGAAGGC TGTCCTGCAT TAGGAACAAG TGAACACGCA AATGACATGA AGTATTTGTT GCAGAGCTGA
8961 GGAACAGAGC AAATGTAGTG ATAGAAGCGC AATGAGAGAA GCAGCAGTGG GTACAAGGAG GAAGAAAAAG
9031 GGCTTGCAGA GAGTGGAAAG TTAGTGGAAT ATTCATGAAA CTTCATTGCA GGGGTAATAG AAGAAAAAGT
9101 AAATTGGGAG GACTTAATGG AAGGTCTTTT AAAAAGTTAA CTTGGAGCTT CTGTATGTAA AATGCTAGGT
9171 AATAAGGACA CTTTGTACAG GCTGTTTTGC ACCTGATTTT ATTTATCATT AGTGCCACGC CAAGATCATT
9241 TAGACGATGC TTATCTGTAA TTCTACCACT TTAATAACTA TTTGTATTTT TATGCCCCTT CTGATCTTTT
9311 CCATATGTAT TTCTAAATGG ATAAATTATT CTAGGCTTCT TAATAGGTAG TAATTTGTTC AAAAGCGGTT
9381 TTAGCCAGAC ATCTAGTTGC AGTGTTCAAG AGGATTATGG GGGAAAGAGA TTAGAGATAA TTGTCTAGTT
9451 AGGGGGCAGC TGGAGAAAAT AAGCTAAGTT TGCAATAACA GAGTACACAA GTATAGTGGC CCAGGATGTA
9521 GTGAAAGAAC AAATCCTAGA GTCTTTGAAA TTTCTAAGGG CATTCTAGAC CTCTGTTGGG ATATGGTATT
```

FIGURE 27 (cont.)

```
 9591 ATTTTACATA CTGACACAAC CTAAATTTTC TTTGGGTAGT AACTAATGTC AAGTCTACAT CGACTGGTAA
 9661 AACATTCAAA GAACAAACTG ACAATGATGT TCTACCTACT TGTTACATGC TCATGGAAGA CCGTGCAGTA
 9731 TTGAAAGTAT TTGTTAATTA TCTGCTTAGT ATTAACACTA AATTTGTAGA ATGACTTTCA GGTTTGTTGA
 9801 ACAATGCCTT TTCAGGTTGG AAGAAGAAAA ATAGCCTCAA TCTCCCACCC CATGTAGGCA CTACCTCCCC
 9871 AATTACCCTT AGAAAATGAT CACACCAACT CTGCCTACAC ACTTCCAGTG ATAGTGGCTC ATTGTCTGTT
 9941 AAGGCAAACT GTTCCACTGT TGGGCATATC TCTTTGTTAG AAAGTTCTTT CTTAGGTTGC TAAAATCTGC
10011 CTAGTACCCC GCTACCCTGT TCTGTCTTAT GGAGCAGCCC AGATTATCTT TACTCCCTCT TTCTCATGGC
10081 AACCCTGAAG ATAATCAAGG CCAGTTACTC ATCATCTCCC AACCACTGTT TCCTCAACTG CCCTTCATAT
10151 GTCATGGTTT TCAGATCCAT TCCAACCTGA CTGAATGTTA ACAGACAGAA TTCTTCACAT TAAGGAACTG
10221 TCTTCATCAT CATACATGTA GAAAAGAATC TGAACATTTA AGTGCGAAGT TTTCTCTAGA AATATATTCA
10291 AGATATGTTT ATTCTATTAT TGTAAATTTC AAACAATAAA TAAATAAGAA TCC
```

FIGURE 28

Figure 28. human mAKAP sequence (PBD in bold)

```
   1  MLTMSVTLSP LRSQDLDPMA TDASPMAINM TPTVEQGEGE EAMKDMDSDQ
  51  QYEKPPPLHT GADWKIVLHL PEIETWLRMT SERVRDLTYS VQQDSDSKHV
 101  DVHLVQLKDI CEDISDHVEQ IHALLETEFS LKLLSYSVNV IVDIHAVQLL
 151  WHQLRVSVLV LRERILQGLQ DANGNYTRQT DILQAFSEET KEGRLDSLTE
 201  VDDSGQLTIK CSQNYLSLDC GITAFELSDY SPSEDLLSGL GDMTSSQVKT
 251  KPFDSWSYSE MEKEFPELIR SVGLLTVAAD SISTNGSEAV TEEVSQVSLS
 301  VDDKGGCEED NASAVEEQPG LTLGVSSSSG EALTNAAQPS SETVQQESSS
 351  SSHHDAKNQQ PVPCENATPK RTIRDCFNYN EDSPTQPTLP KRGLFLKEET
 401  FKNDLKGNGG KRQMVDLKPE MSRSTPSLVD PPDRSKLCLV LQSSYPNSPS
 451  AASQSYECLH KVGNGNLENT VKFHIKEISS SLGRLNDCYK EKSRLKKPHK
 501  TSEEVPPCRT PKRGTGSGKQ AKNTKSSAVP NGELSYTSKA IEGPQTNSAS
 551  TSSLEPCNQR SWNAKLQLQS ETSSSPAFTQ SSESSVGSDN IMSPVPLLSK
 601  HKSKKGQASS PSHVTRNGEV VEAWYGSDEY LALPSHLKQT EVLALKLENL
 651  TKLLPQKPRG ETIQNIDDWE LSEMNSDSEI YPTYHVKKKH TRLGRVSPSS
 701  SSDIASSLGE SIESGPLSDI LSDEESSMPL AGMKKYADEK SERASSSEKN
 751  ESHSATKSAL IQKLMQDIQH QDNYEAIWEK IEGFVNKLDE FIQWLNEAME
 801  TTENWTPPKA EMDDLKLYLE THLSFKLNVD SHCALKEAVE EEGHQLLELI
 851  ASHKAGLKDM LRMIASQWKE LQRQIKRQHS WILRALDTIK AEILATDVSV
 901  EDEEGTGSPK AEVQLCYLEA QRDAVEQMSL KLYSEQYTSS SKRKEEFADM
 951  SKVHSVGSNG LLDFDSEYQE LWDCLIDMES LVMDSHDLMM SEEQQQHLYK
1001  RYSVEMSIRH LKKTELLSKV EALKKGGVLL PNDLLEKVDS INEKWELLGK
1051  TLGEKIQDTM AGHSGSSPRD LLSPESGSLV RQLEVRIKEL KGWLRDTELF
1101  IFNSCLRQEK EGTMNTEKQL QYFKSLCREI KQRRRGVASI LRLCQHLLDD
1151  RETCNLNADH QPMQLIIVNL ERRWEAIVMQ AVQWQTRLQK KMGKESETLN
1201  VIDPGLMDLN GMSEDALEWD EMDISNKLIS LNEESNDLDQ ELQPVIPSLK
1251  LGETSNEDPG YDEEADNHGG SQYASNITAP SSPHIYQVYS LHNVELYEDN
1301  HMPFLKNNPK VTGMTQPNVL TKSLSKDSSF SSTKSLPDLL GGSNLVKPCA
1351  CHGGDMSQNS GSESGIVSEG DTETTTNSEM CLLNAVDGSP SNLETEHLDP
1401  QMGDAVNVLK QKFTDEGESI KLPNSSQSSI SPVGCVNGKV GDLNSITKHT
1451  PDCLGEELQG KHDVFTFYDY SYLQGSKLKL PMIMKQSQSE KVHVEDPLLR
1501  GFYFDKKSCK SKHQTTELQP DVPPHERILA SASHEMDRIS YKSGNIEKTF
1551  TGMQNAKQLS LLSHSSSIES LSPGGDLFGL GIFKNGSDSL QRSTSLESWL
1601  TSYKSNEDLF SCHSSGDISV SSGSVGELSK RTLDLLNRLE NIQSPSEQKI
1651  KRSVSDITLQ SSSQKMSFTG QMSLDIASSI NEDSAASLTE LSSSDELSLC
1701  SEDIVLHKNK IPESNASFRK RLTRSVADES DVNVSMIVNV SCTSACTDDE
1751  DDSDLLSSST LTLTEEELCI KDEDDDSSIA TDDEIYEDCT LMSGLDYIKN
1801  ELQTWIRPKL SLTRDKKRCN VSDEMKGSKD ISSSEMTNPS DTLNIETLLN
1851  GSVKRVSENN GNGKNSSHTH ELGTKRENKK TIFKVNKDPY VADMENGNIE
1901  GIPERQKGKP NVTSKVSENL GSHGKEISES EHCKCKALMD SLDDSNTAGK
1951  EFVSQDVRHL PKKCPNHHHF ENQSTASTPT EKSFSELALE TRFNNRQDSD
2001  ALKSSDDAPS MAGKSAGCCL ALEQNGTEEN ASISNISCCN CEPDVFHQKD
2051  AEDCSVHNFV KEIIDMASTA LKSKSQPENE VAAPTSLTQI KEKVLEHSHR
```

FIGURE 28 (cont.)

```
2101  PIQLRKGDFY SYLSLSSHDS DCGEVTNYIE EKSSTPLPLD TTDSGLDDKE
2151  DIECFFEACV EGDSDGEEPC FSSAPPNESA VPSEAAMPLQ ATACSSEFSD
2201  SSLSADDADT VALSSPSSQE RAEVGKEVNG LPQTSSGCAE NLEFTPSKLD
2251  SEKESSGKPG ESGMPEEHNA ASAKSKVQDL SLKANQPTDK AALHPSPKTL
2301  TCEENLLNLH EKRHRNMHR
```

FIGURE 29

Figure 29. human PBD sequence:

```
       1  MGKSSTPLPL DTTDSGLDDK EDIECFFEAC VEGDSDGEEP CFSSAPPNES
      51  AVPSEAAMPL QATACSSEFS DSSLSADDAD TVALSSPSSQ ERAEVGKEVN
     101  GLPQTSSGCA ENLEFTPSKL DSEKESSGKP GESGMPEEHN AASAKSKVQD
     151  LSLKANQPTD KAALHPSPKT LTCEENLLNL HEKRHRNMHR
```

FIGURE 30

Figure 30. Alignment of human and rat PBD sequences

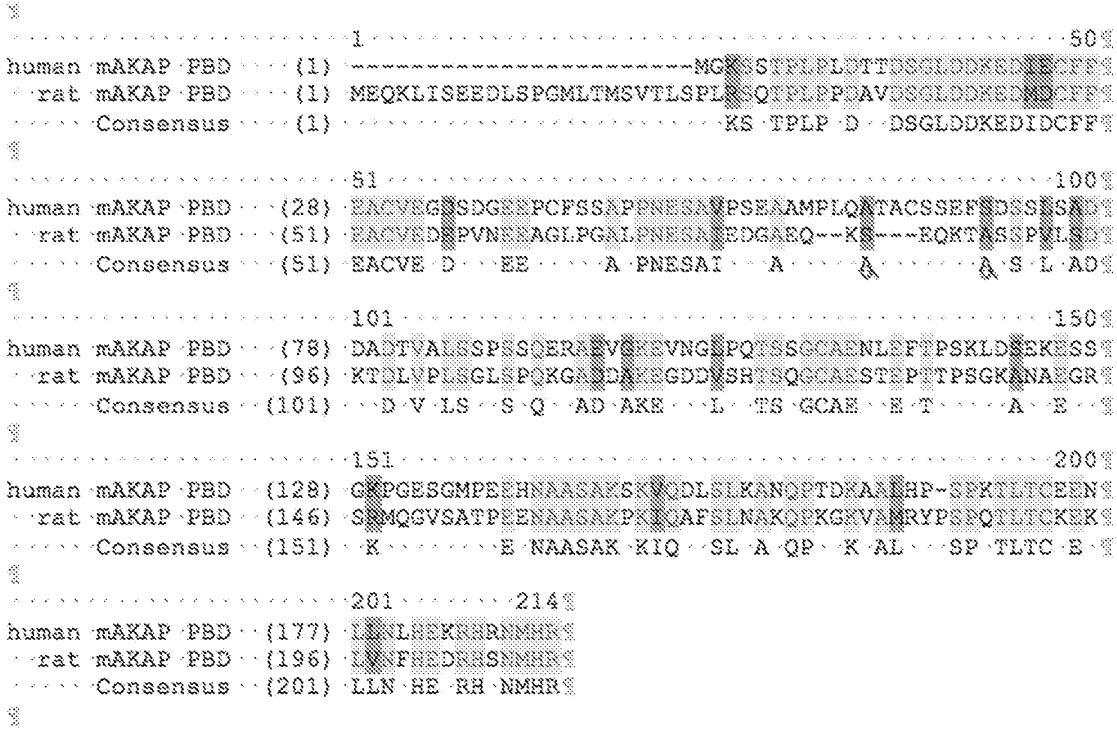


FIGURE 31

Figure 31. Map of human PBD shuttle plasmid.

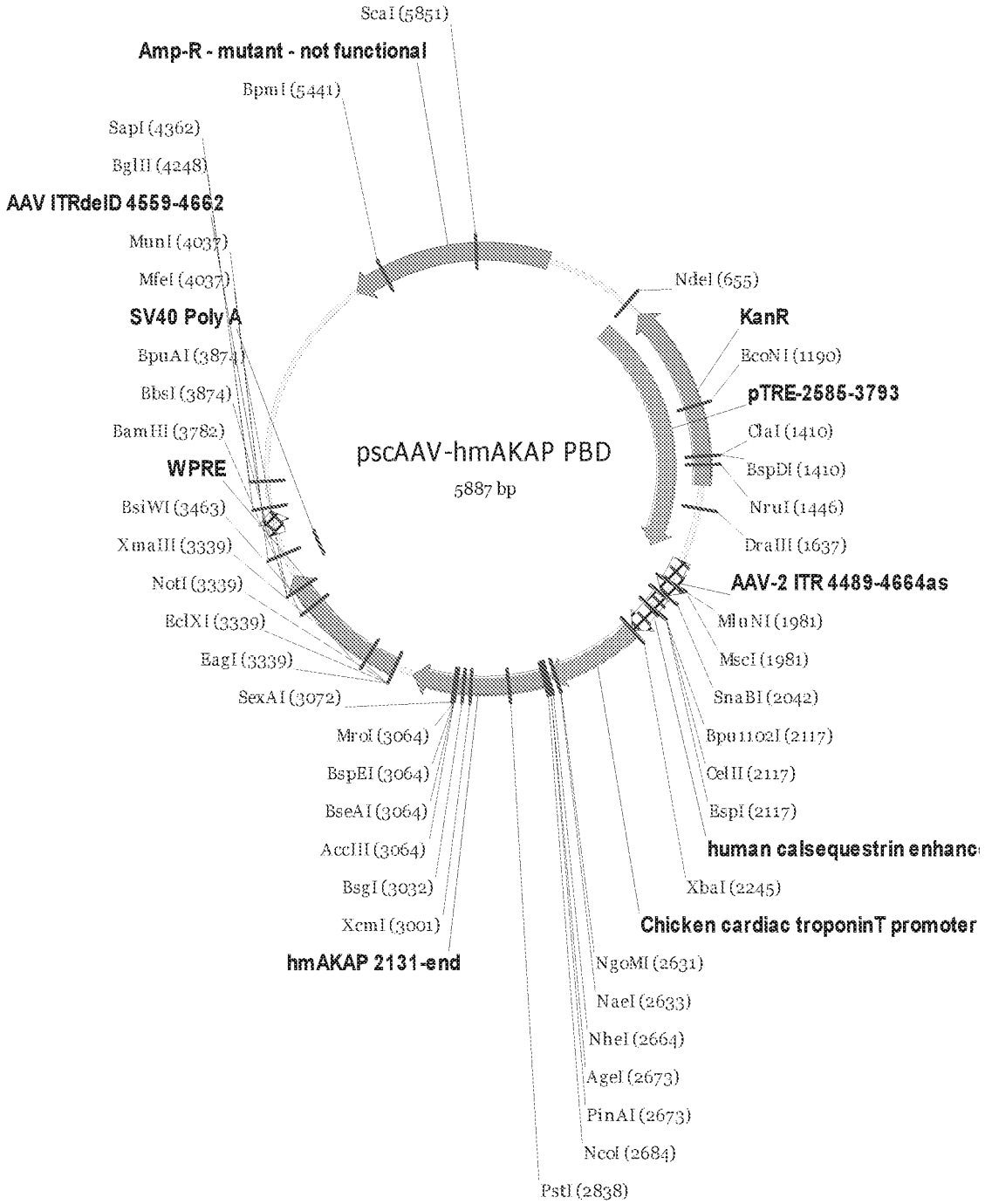


FIGURE 32

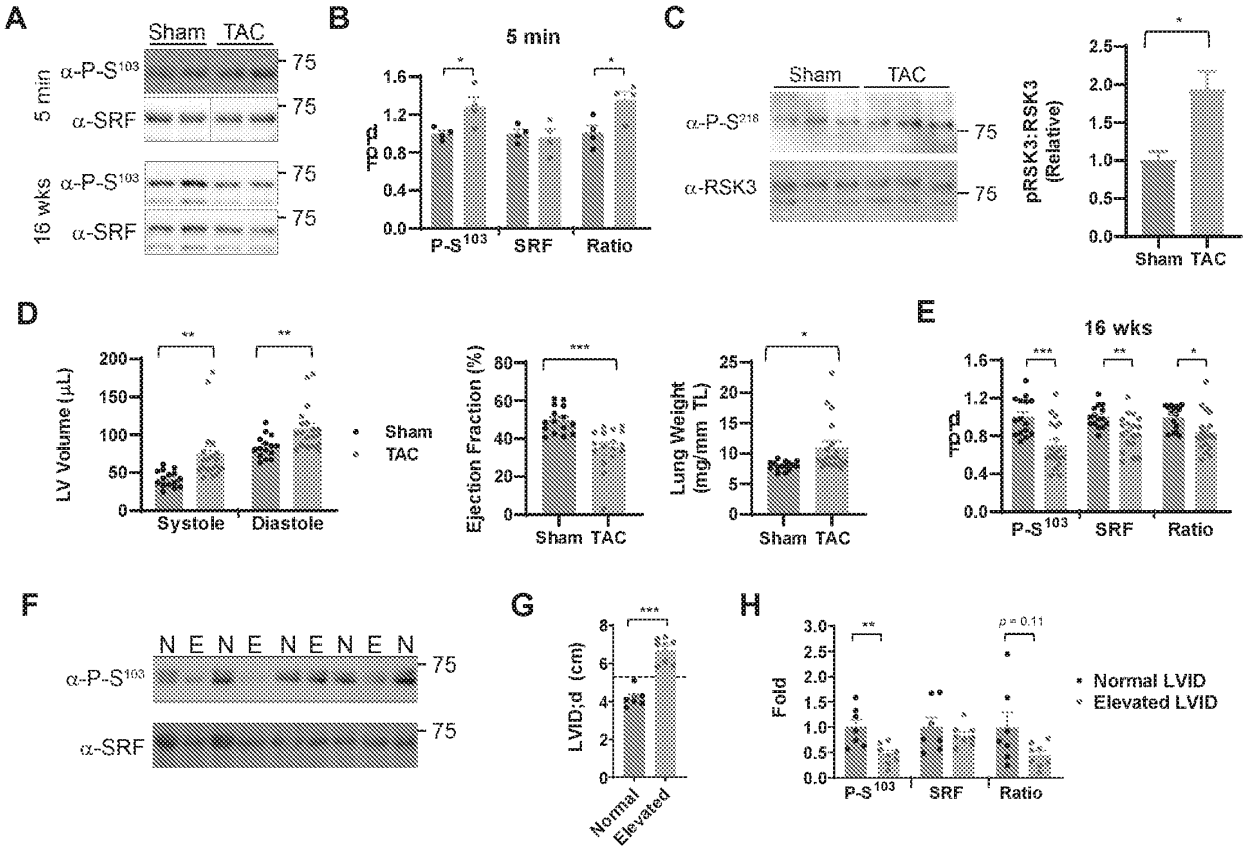
Figure 32. Sequence of pscAAV-hmAKAP PBD

```
   1 ACCGAGTTGC TCTCACCCGG CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTGGAA
  81 AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTTCGATGT AACCCACTCG TGCACCCAAC
 161 TGATCTTCAG CATCTTTTAC TTTCACCAGC GTTTCTGGGT GAGCAAAAAC AGGAAGGCAA AATGCCGCAA AAAAGGGAAT
 241 AAGGGCGACA CGGAAATGTT CAATTCAACT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA
 321 TGAGCGGATA CATATTTGAA TGTATTTAGA AAAATAAACA AATAGGGGTT CCGCGCACAT TTCCCCGAAA AGTGCCACCT
 401 GACGTCTAAG AAACCATTAT TATCATGACA TTAACCTATA AAAATAGGCG TATCACGAGG CCCTTTCGTC TCGCGCGTTT
 481 CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA
 561 GACAAGCCCG TCAGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA
 641 CTGAGAGTGC ACCATATGGC CGTCCCGTCA AGTCAGCGTA ATGCTCTGCC AGTGTTACAA CCAATTAACC AATTCTGATT
 721 AGAAAAACTC ATCGAGCATC AAATGAAACT GCAATTTATT CATATCAGGA TTATCAATAC CATATTTTTG AAAAAGCCGT
 801 TTCTGTAATG AAGGAGAAAA CTCACCGAGG CAGTTCCATA GGATGGCAAG ATCCTGGTAT CGGTCTGCGA TTCCGACTCG
 881 TCCAACATCA ATACAACCTA TTAATTTCCC CTCGTCAAAA ATAAGGTTAT CAAGTGAGAA ATCACCATGA GTGACGACTG
 961 AATCCGGTGA GAATGGCAAA AGCTTATGCA TTTCTTTCCA GACTTGTTCA ACAGGCCAGC CATTACGCTC GTCATCAAAA
1041 TCACTCGCAT CAACCAAACC GTTATTCATT CGTGATTGCG CCTGAGCGAG ACGAAATACG CGATCGCTGT TAAAAGGACA
1121 ATTACAAACA GGAATCGAAT GCAACCGGCG CAGGAACACT GCCAGCGCAT CAACAATATT TTCACCTGAA TCAGGATATT
1201 CTTCTAATAC CTGGAATGCT GTTTTCCCGG GGATCGCAGT GGTGAGTAAC CATGCATCAT CAGGAGTACG GATAAAATGC
1281 TTGATGGTCG GAAGAGGCAT AAATTCCGTC AGCCAGTTTA GTCTGACCAT CTCATCTGTA ACATCATTGG CAACGCTACC
1361 TTTGCCATGT TTCAGAAACA ACTCTGGCGC ATCGGGCTTC CCATACAATC GATAGATTGT CGCACCTGAT TGCCCGACAT
1441 TATCGCGAGC CCATTTATAC CCATATAAAT CAGCATCCAT GTTGGAATTT AATCGCGGCC TCGAGCAAGA CGTTTCCCGT
1521 TGAATATGGC TCATAACACC CCTTGTATTA CTGTTTATGT AAGCAGACAG TTTTATTGTT CATGATGATA TATTTTTATC
1601 TTGTGCAATG TAACATCAGA GATTTTGAGA CACAACGTGG CTTTGTTGAA TAAATCGAAC TTTTGCTGAG TTGAAGGATC
1681 AGATCACGCA TCTTCCCGAC AACGCAGACC GTTCCGTGGC AAAGCAAAAG TTCAAAATCA CCAACTGGTC CACCTACAAC
1761 AAAGCTCTCA TCAACCGTGG CTCCCTCACT TTCTGGCTGG ATGATGGGGC GATTCAGGCC TGGTATGAGT CAGCAACACC
1841 TTCTTCACGA GGCAGACCTC AGCGCTACTC GAGCCTGCGC GCTCGCTCGC TCACTGAGGC CGCCCGGGCA AAGCCCGGGC
1921 GTCGGGCGAC CTTTGGTCGC CCGGCCTCAG TGAGCGAGCG AGCGCGCAGA GAGGGAGTGG CCAACTCCAT CACTAGGGGT
2001 TCCTTGTAGT TAATGATTAA CCCGCCATGC TACTTATCTA CGTAGCCATG CAGTAGAAAA ACAGCCAAGC TAGGGAGGCT
2081 GGGAGGCCAA GCCCCAGATA CCTTACATAG CTCTGCTCAG CCTCTGTCTC ATTAGGAACT CCATTTTTAG GATGCAGTTG
2161 TTTCAGGCTA AAAATAAATC ATGCAATGAA TAAAAAAGTT AGATACGACA CTGTAGAGGG ATTCGCTGAT ACAGTCTGTC
2241 CGATCTAGAG CAGTCTGGGC TTTCACAAGA CAGCATCTGG GGCTGCGGCA GAGGGTCGGG TCCGAAGCGC TGCCTTATCA
2321 GCGTCCCCAG CCCTGGGAGG TGACAGCTGG CTGGCTTGTG TCAGCCCCTC GGGCACTCAC GTATCTCCGT CCGACGGGTT
2401 TAAAATAGCA AAACTCTGAG GCCACACAAT AGCTTGGGCT TATATGGGCT CCTGTGGGGG AAGGGGGAGC ACGGAGGGGG
2481 CCGGGGCCGC TGCTGCCAAA ATAGCAGCTC ACAAGTGTTG CATTCCTCTC TGGGCGCCGG GCACATTCCT GCTGGCTCTG
2561 CCCGCCCCGG GGTGGGCGCC GGGGGGACCT TAAAGCCTCT GCCCCCCAAG GAGCCCTTCC CAGACAGCCG CCGGCACCCA
                                                    M  G  K  S  S  T  P  L  P  L  D  T
2641 CCGCTCCGTG GGACCTAAGC TTGCTAGCGC TACCGGTCGC CACCATGGGT AAAAGCAGCA CTCCATTGCC ACTAGACACC
      T  D  S  G  L  D  D  K  E  D  I  E  C  F  F  E  A  C  V  E  G  D  S  D  G  E  E  ·
2721 ACTGACTCGG GCTTAGATGA CAAGGAAGAT ATTGAATGCT TTTTTGAGGC CTGTGTTGAG GGTGACTCTG ATGGAGAGGA
     ·  P  C  F  S  S  A  P  P  N  E  S  A  V  P  S  E  A  A  M  P  L  Q  A  T  A  C  S  ·
2801 GCCTTGTTTC TCTAGTGCTC CTCCAAATGA ATCTGCAGTT CCCAGCGAAG CTGCAATGCC ACTACAAGCA ACAGCATGTT
     ·  S  E  F  S  D  S  S  L  S  A  D  D  A  D  T  V  A  L  S  S  P  S  S  Q  E  R
2881 CTTCTGAGTT CAGTGATAGT TCTCTTTCAG CTGATGATGC AGATACAGTG GCTCTTTCAA GTCCTTCCTC TCAGGAAAGA
      A  E  V  G  K  E  V  N  G  L  P  Q  T  S  S  G  C  A  E  N  L  E  F  T  P  S  K  ·
2961 GCTGAGGTTG GAAAGGAAGT GAATGGTTTG CCCCAAACTT CCAGTGGCTG TGCAGAAAAC TTAGAGTTTA CTCCTTCAAA
     ·  L  D  S  E  K  E  S  S  G  K  P  G  E  S  G  M  P  E  E  H  N  A  A  S  A  K  S  ·
3041 GCTTGACAGT GAAAAGGAAA GTTCCGGAAA ACCAGGTGAA TCTGGAATGC CAGAAGAACA TAATGCTGCT TCAGCCAAAT
     ·  K  V  Q  D  L  S  L  K  A  N  Q  P  T  D  K  A  A  L  H  P  S  P  K  T  L  T
3121 CTAAAGTTCA AGACCTCTCC TTGAAGGCAA ATCAGCCAAC AGACAAGGCC GCATTGCATC CCAGCCCCAA AACTTTAACC
      C  E  E  N  L  L  N  L  H  E  K  R  H  R  N  M  H  R
3201 TGTGAAGAAA ATCTTCTAAA CCTTCATGAA AAACGACATA GAAATATGCA TAGGTAGAGT GTAATGCCCC CACGCATGGA
3281 AATCATCTCA TTGAAAGATA GCCTGGCTGA AGCTCAGGGC TAGTTAAGTT TGATCCGCGG CCGCAATCAA CCTCTGGATT
3361 ACAAAATTTG TGAAAGATTG ACTGATATTC TTAACTATGT TGCTCCTTTT ACGCTGTGTG GATATGCTGC TTTAATACCT
3441 CTGTATCGTG CTATTGCTTC CCGTACGGCT TTCGTTTTCT CCTCCTTGTA TAAATCCTGG TTGCTGTCTC TTTATAAGGA
3521 GTTGTGGCCC GTTGTCCGTC AACGTGGCGT GGTGTGCTCT GTGTTTGCTG ACGCAACCCC CACTGGCTGG GGCATTGCCA
3601 CCACCTGTCA ACTCCTTTCT GGGACTTTCG CTTTCCCCCT CCCGATCGCC ACGGCAGAAC TCATCGCCGC CTGCCTTGCC
3681 CGCTGCTGGA CAGGGGCTAG GTTGCTGGGC ACTGATAATT CCGTGGTGTT GTCGGGGAAA TCATCGTCCT TTCCTTGGCT
3761 GCTCGCCTGT GTTGCCAACT GGATCCTGCG CGGGACGTCC TTCTGCTACG TCCCTTCGGC TCTCAATCCA GCGGACCTCC
3841 CTTCCCGCGG CCTTCTGCCG GTTCTGCGGC CTCTCCCGCG TCTTCGCTTT CGGCCTCCGA CGAGTCGGAT CTCCCTTTGG
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FIGURE 32 (cont.)

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3921 GCCGCCTCCC CGCCTGTAGG CCTCACCTGC GATCTCGATG CTTTATTTGT GAAATTTGTG ATGCTATTGC TTTATTTGTA
4001 ACCATTATAA GCTGCAATAA ACAAGTTAAC AACAACAATT GCATTCATTT TATGTTTCAG GTTCAGGGGG AGGTGTGGGA
4081 GGTTTTTTAA AGCAAGTAAA ACCTCTACAA ATGTGGTATG GCTGATTACC ACTCCCTCTC TGCGCGCTCG CTCGCTCACT
4161 GAGGCCGGGC GACCAAAGGT CGCCCGACGC CCGGGCTTTG CCCGGGCGGC CTCAGTGAGC GAGCGAGCGC GCCAGCTGAA
4241 GCTATCAGAT CTGCCGGTCT CCCTATAGTG AGTCGTATTA ATTTCGATAA GCCAGGTTAA CCTGCATTAA TGAATCGGCC
4321 AACGCGCGGG GAGAGGCGGT TTGCGTATTG GGCGCTCTTC CGCTTCCTCG CTCACTGACT CGCTGCGCTC GGTCGTTCGG
4401 CTGCGGCGAG CGGTATCAGC TCACTCAAAG GCGGTAATAC GGTTATCCAC AGAATCAGGG GATAACGCAG GAAAGAACAT
4481 GTGAGCAAAA GGCCAGCAAA AGGCCAGGAA CCGTAAAAAG GCCGCGTTGC TGGCGTTTTT CCATAGGCTC CGCCCCCCTG
4561 ACGAGCATCA CAAAAATCGA CGCTCAAGTC AGAGGTGGCG AAACCCGACA GGACTATAAA GATACCAGGC GTTTCCCCCT
4641 GGAAGCTCCC TCGTGCGCTC TCCTGTTCCG ACCCTGCCGC TTACCGGATA CCTGTCCGCC TTTCTCCCTT CGGGAAGCGT
4721 GGCGCTTTCT CATAGCTCAC GCTGTAGGTA TCTCAGTTCG GTGTAGGTCG TTCGCTCCAA GCTGGGCTGT GTGCACGAAC
4801 CCCCCGTTCA GCCCGACCGC TGCGCCTTAT CCGGTAACTA TCGTCTTGAG TCCAACCCGG TAAGACACGA CTTATCGCCA
4881 CTGGCAGCAG CCACTGGTAA CAGGATTAGC AGAGCGAGGT ATGTAGGCGG TGCTACAGAG TTCTTGAAGT GGTGGCCTAA
4961 CTACGGCTAC ACTAGAAGAA CAGTATTTGG TATCTGCGCT CTGCTGAAGC CAGTTACCTT CGGAAAAAGA GTTGGTAGCT
5041 CTTGATCCGG CAAACAAACC ACCGCTGGTA GCGGTGGTTT TTTTGTTTGC AAGCAGCAGA TTACGCGCAG AAAAAAAGGA
5121 TCTCAAGAAG ATCCTTTGAT CTTTTCTACG GGGTCTGACG CTCAGTGGAA CGAAAACTCA CGTTAAGGGA TTTTGGTCAT
5201 GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTTAAAT TAAAAATGAA GTTTTAAATC AATCTAAAGT ATATATGAGT
5281 AAACTTGGTC TGACAGTTAC CAATGCTTAA TCAGTGAGGC ACCTATCTCA GCGATCTGTC TATTTCGTTC ATCCATAGTT
5361 GCCTGACTCC CCGTCGTGTA GATAACTACG ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA
5441 CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAATCAG CCAGCCGGAA GGGCCGAGCG CAGAAGTGGT CCTGCAACTT
5521 TATCCGCCTC CATCCAGTCT ATTCATTGTT GCCGGGAAGC TAGAGTAAGT AGTTCGCCAG TTAATAGTTT TCACAACGTT
5601 GTTGCCATTG CTACAGGCAT CGTGGTGTCA CGCTCGTCGT TTGGTATGGC TTCATTCAGC TCCGGTTCCC AACGATCAAG
5681 GCGAGTTACA TGTCACCCCA TGTTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT CGTTGTCAGA AGTAAGTTGG
5761 CCGCAGTGTT ATCACTCATG GTTATGGCAG CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTTCTGTG
5841 ACTGGTGAGT ACTCAACCAA GTCATTCTGA GAATAGTGTA TGCGGCG
```

FIGURE 33


A
Sham
TAC
5 min
α-P-S103
α-SRF
16 wks
75
B
5 min
P-S103
SRF
Ratio
C
α-P-S218
α-RSK3
pRSK3:RSK3 (Relative)
Sham
TAC
D
LV Volume (μL)
Systole
Diastole
Ejection Fraction (%)
Lung Weight (mg/mm TL)
E
16 wks
F
N E N E N E N E N
G
LVID;d (cm)
Normal
Elevated
H
Fold
p = 0.11
Normal LVID
Elevated LVID