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[11] E

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Vogelstein et al.

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[54] **APC GENE AND NUCLEIC ACID PROBES DERIVED THEREFROM**

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Related U.S. Patent Documents

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Jan. 16, 1991	[GB]	United Kingdom	9100974
Jan. 16, 1991	[GB]	United Kingdom	9100975

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C12Q 01/68

[52] **U.S. Cl.** **536/23.5**; 536/24.31; 536/24.33;
536/23.1; 435/6; 935/6; 935/8; 935/9

[58] **Field of Search** 536/23.5, 24.31,
536/23.1, 24.33; 935/6, 8, 9; 435/6

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[57] ABSTRACT

A human gene termed APC is disclosed. Methods and kits are provided for assessing mutations of the APC gene in hum tissues and body samples. APC mutations are found in familial adenomatous polyposis patients as well as in sporadic colorectal cancer patents. APC is expressed in most normal tissue. These results suggest that APC is a tumor suppressor.

10 Claims, 40 Drawing Sheets

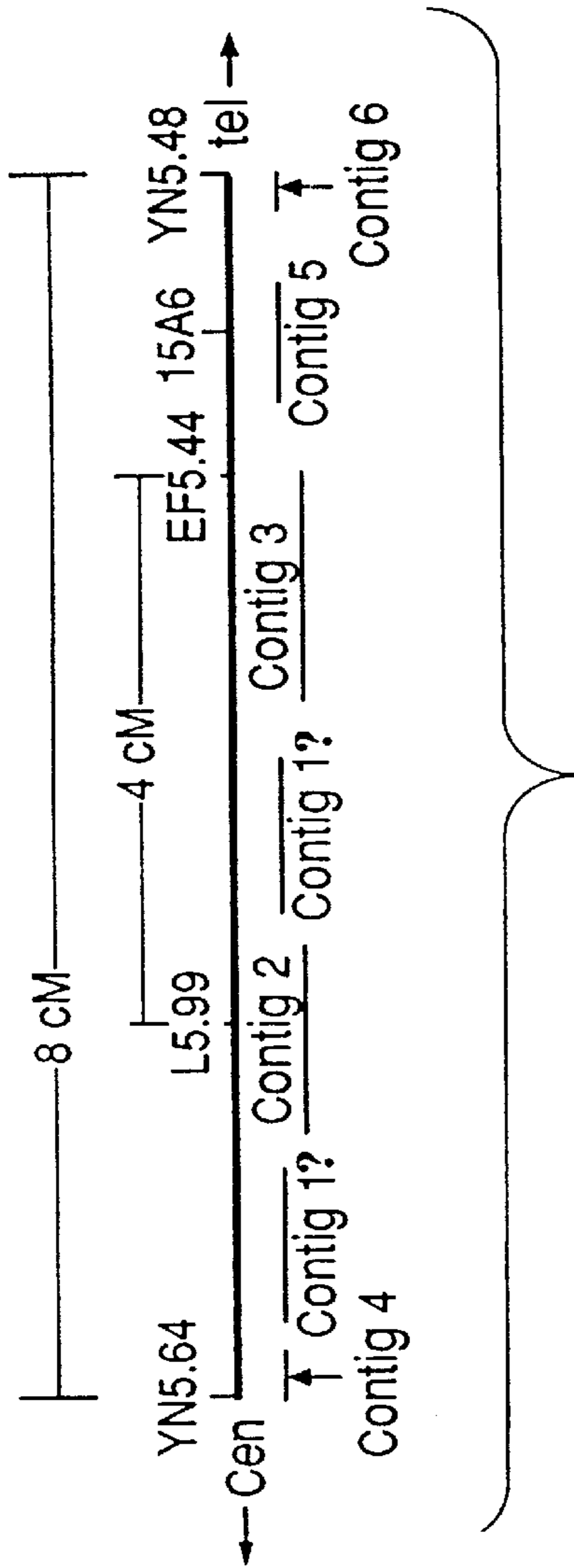


FIG. 1A

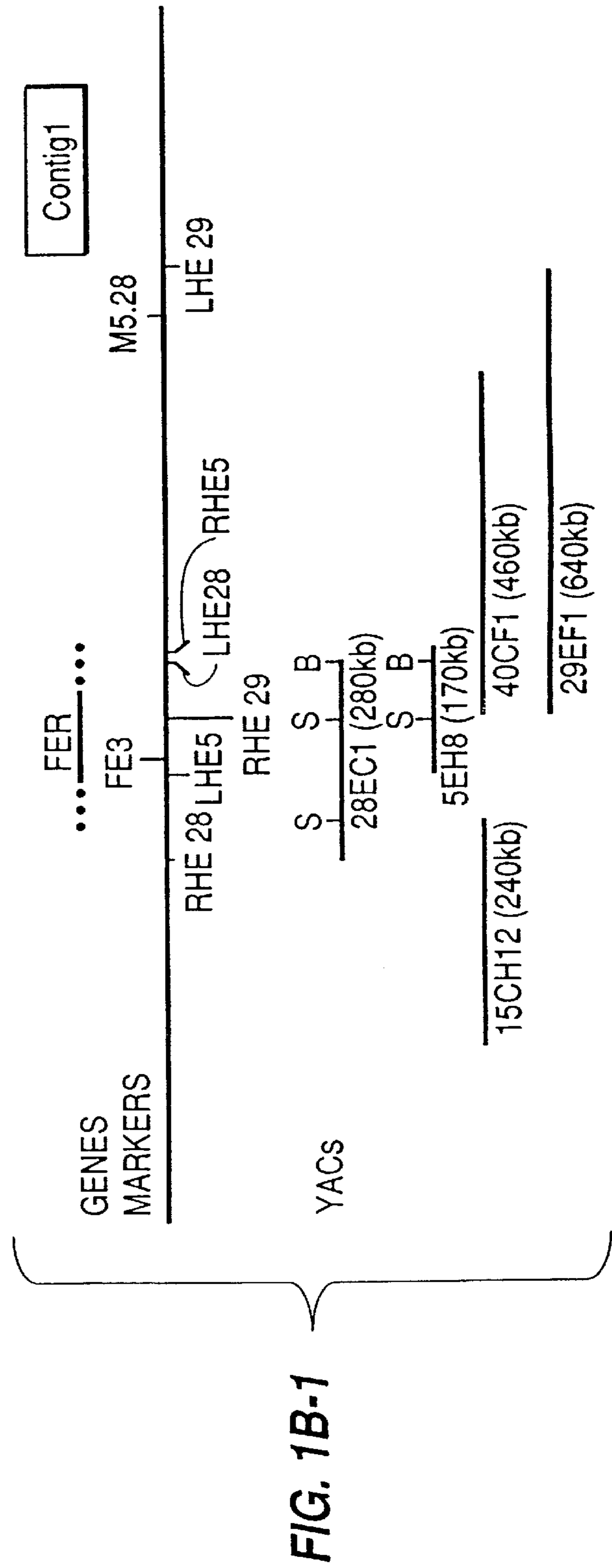


FIG. 1B-1

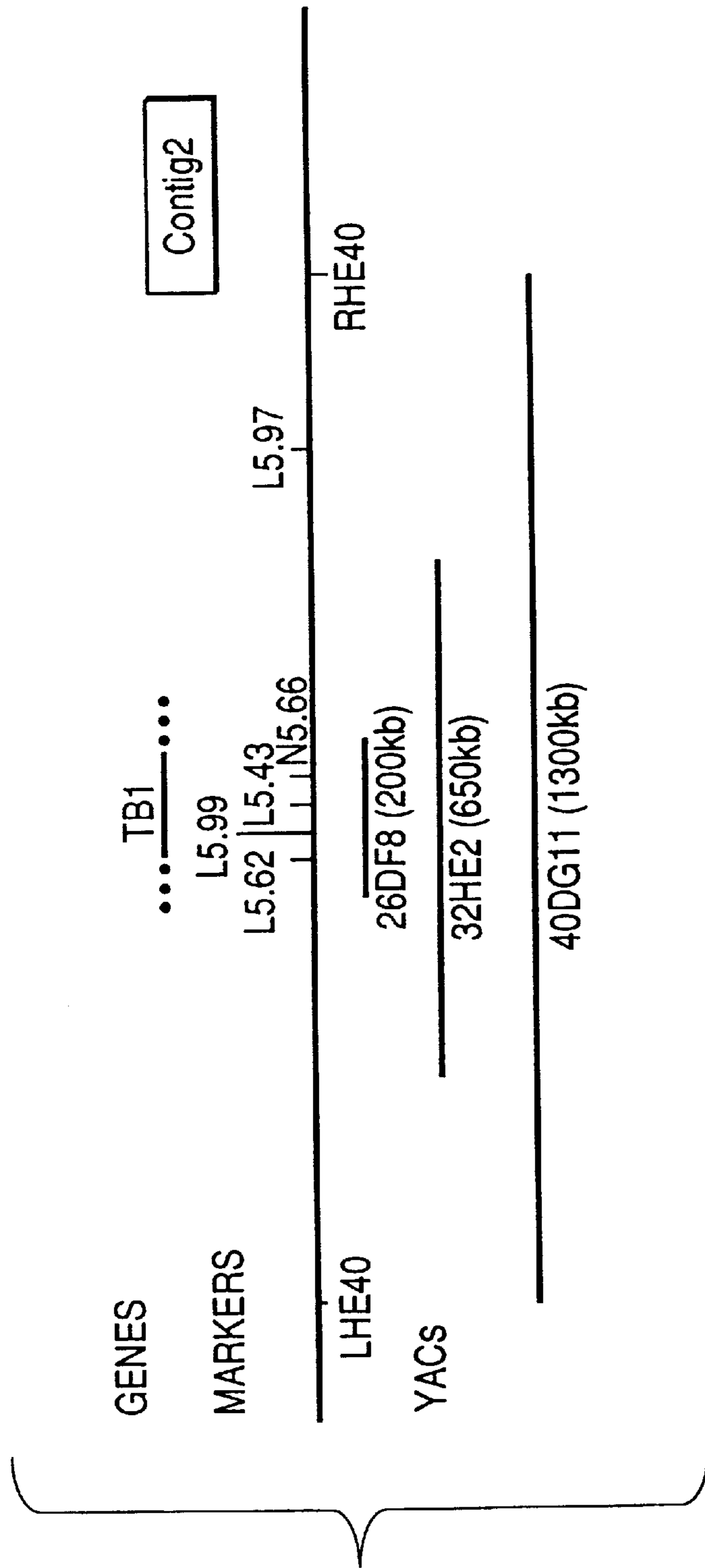


FIG. 1B-2

FIG. 2A**TB1 AMINO ACID SEQUENCE**

VAPVVVGSGR APRHPAPAAM HPRRPOGFDG LGYRGGARDE QGFGGAFPAR SFSTGSDLGH 60
WVTTPPDIPG SRNLHWGEKS PPYGVPTTST PYEGPTEEPF SSGGGGSVQG QSSEQLNRFA 120
GFGIGLASLF TENVLAHPCI VLRROCQVNY HAQHYHLTPF TVINIMYSFN KTOGPRALWK 180
GMGSTFIVQG VTLGAEGIS EFTPLPREVL HKWSPKQIGE HLLKSLTYV VAMPFYSASL 240
IETVQSEIIR DNTGILECVK EGIGRVIGMG VPHSKRLLPL LSLIFPTVLH GVLHYIISV 300
IOKFVLLILK RKTYNSHLAE STSPVQSM LD AYFPELIANF AASLCSDVIL YPLETVLHRL 360
HIQGIRTIID NTDLGYEVLP INTQYEGHRD CINTIRQEEG VFGFYKGFGA VIIQYTLHAA 420
VLOITKIIYS TLLQ 434

FIG. 2B

TB2 AMINO ACID SEQUENCE

ELRRFDRFLH EKNCHTDLLA KLEAKTGVNR SFIALGVIGL VALYLVFGYG ASLLCNLIGF 60
GYPAYISIKA IESPKNEDDT QWLTYNVVYVG VFSIAEFFSD IFLSHFPFY ILKCGFLLHC 120
MAPSPSNGAE LLYKRIIRPF FLKHESQMS VVKDLKDKAK ETADAITKEA KKATVNLIGE 180
EKKST 185

Amended *Figure 3A*

10	20	30	40	50	60
MAAASYDQLL	KQVEALKMEN	SNLRQELEDN	SNHLTKLETE	ASNMKEVLKQ	LQGSIEDEAM
70	80	90	100	110	120
ASSGQIDLLE	RLKELNLDSS	NFPGVKLRSK	MSLRSYGSRE	GSVSSRSGEC	SPVPMGSFPR
130	140	150	160	170	180
RGFVNGSRES	TGYLEELEKE	RLLLLADLDK	EEKEKDWYYA	QLQNLTKRID	SLPLTENFSL
190	200	210	220	230	240
QTMTRRQLE	YEARQIRVAM	EEQLGTCQDM	EKRAQRRIAR	IQQIEKDILR	IRQLLOSQAT
250	260	270	280	290	300
EAERSSQNKH	ETGSHDAERQ	NEGQGVGEIN	MATSGNGQGS	TTRMDHETAS	VLSSSSTHSA
310	320	330	340	350	360
PRRLTSHLGT	KVEMVYSLLS	MLGTHDKDDM	SRTLLAMSSS	QDSCISMRQS	GCLPLLIQLL
370	380	390	400	410	420
HGNDKDSVLL	GNSRGSKEAR	ARASAALHNI	IHSQPDDKRG	RREIRVLHLL	EQIRAYCETC
430	440	450	460	470	480
WEWQEAHEPG	MDQDKNPMPA	PVEHQICPAV	CVLMKLSFDE	EHRHAMNELG	GLQAI AELLQ
490	500	510	520	530	540
VDCEMYGLTN	DHYSITLRRY	AGMALTNLTF	GDVANKATLC	SMKGCMRALV	AQLKSESEDL
550	560	570	580	590	600
QQVIASVLRN	LSWRADVNSK	KTLREVGSVK	ALMECALEVK	KESTLKSVLS	ALWNLSAHCT
610	620	630	640	650	660
ENKADICAVD	GALAFVLVGT	TYRSQTNTLA	IIESGGGILR	NVSSLIATNE	DHRQILRENN
670	680	690	700	710	720
CLQTLLOHLK	SHSLTIVSNA	CGTLWNLSAR	NPKDQEALWD	MGAVSMLKNL	IHSKHKMIAM
730	740	750	760	770	780
GSAAALRNLM	ANRPAKYKDA	NIMSPGSSLP	SLHVRKQKAL	EAELDAQHLS	ETFDNIDNLS
790	800	810	820	830	840
PKASHRSKQR	HKQSLYGDYV	FDTNRHDDNR	SDNFNTGNMT	VLSPYLNTTV	LPSSSSSRGS
850	860	870	880	890	900
LDSSRSEKDR	SLERERGIGL	GNYHPATENP	GTSSKRGLQI	STTAAQIAKV	MEEVSAIHTS
910	920	930	940	950	960
QEDRSSGSTT	ELHCVTDERN	ALRRSSAAHT	HSNTYNFTKS	ENSNRTCSMP	YAKLEYKRSS
970	980	990	1000	1010	1020
NDSLNSVSSS	DGYGKRGQMK	PSIESYSEDD	ESKFCSYGQY	PADLAHKIHS	ANHMDDNDGE
1030	1040	1050	1060	1070	1080
LDTPINYSLK	YSDEQLNSGR	QSPSQNERWA	RPKHIEDEI	KQSEQRQSRN	QSTTYPVYTE
1090	1100	1110	1120	1130	1140
STDDKHLKFQ	PHFGQOECVS	PYRSRGANGS	ETNRVGSNHG	INQNVSQSLC	QEDDYEDDKP
1150	1160	1170	1180	1190	1200
TNYSERYSEE	EQHEEEERPT	NYSIKYNEEK	RHVDQPIDYS	LKYATDIPSS	QKQSF SFSKS
1210	1220	1230	1240	1250	1260
SSGQSSKTEH	MSSSENTST	PSSNAKRQNO	LHPSSAQSR	GQPQKAATCK	VSSINQETIQ
1270	1280	1290	1300	1310	1320
TYCVEDTPIC	FSRCSSLSSL	SSAEDEIGCN	QTTQEADSAN	TLQIAEIKEK	IGTRSAEDPV
1330	1340	1350	1360	1370	1380
HP	RTKSSRLQGS	SLSSESARHK	AVEFSSGAKS	PSKSGAQTPK	SPPEHYVQET
90	1400	1410	1420	1430	1440

Amended *Figure 3B*

PLMFSRCTSV 1450	SSLDSFESRS 1460	IASSVQSEPC 1470	SGMVSGIISP 1480	SDLPDSPGQT 1490	MPPSRSKTPP 1500
PPPQTAQTKR 1510	EVPKNKAPTA 1520	EKRESGPKQA 1530	AVNAAVQRVQ 1540	VLPDADTLLH 1550	FATESTPDGF 1560
SCSSLSALS 1570	LDEPFIQKDV 1580	ELRIMPPVQE 1590	NDNGNETESE 1600	QPKESNENQE 1610	KEAEKTIDSE 1620
KDLLDSDDD 1630	DIEILEECII 1640	SAMPTKSSRK 1650	AKKPAQTASK 1660	LPPPVARKPS 1670	QLPVYKLLPS 1680
QNRLQPQKHV 1690	SFTPGDDMPR 1700	VYCVGTPIN 1710	FSTATSLSDL 1720	TIESPPNELA 1730	AGEGVRGGAQ 1740
SGEFEKRDTI 1750	PTEGRSTDEA 1760	QGGKTSSVTI 1770	PELDDNKAAE 1780	GDILAEICINS 1790	AMPKGKSHKP 1800
FRVKKIMDQV 1810	QQASASSSAP 1820	NKNQLDGKKK 1830	KPTSPVKPIP 1840	QNTYRTRVR - 1850	KNADSKNNLN 1860
AERVFSDNKD 1870	SKKQNLKNS 1880	KDFNDKLPNN 1890	EDRVRGSFAF 1900	DSPHHTPIE 1910	GTPYCFSRND 1920
SLSSLDFDDD 1930	DVDLSREKAE 1940	LRKAKENKES 1950	EAKVTSHTL 1960	TSNQOSANKT 1970	QAIKQPINR 1980
GQPKPILQKQ 1990	STFPQSSKDI 2000	PDRGAATDEK 2010	LQNFIENTP 2020	VCFSHNSSLS 2030	SLSDIDQENN 2040
NKENAPIKET 2050	EPPDSQGEPS 2060	KPQASGYAPK 2070	SFHVEDTPVC 2080	FSRNSSLSSL 2090	SIDSEDDLQ 2100
ECISSAMPKK 2110	KKPSRLKGDN 2120	EKHSPRNMGG 2130	ILGEDLTLDL 2140	KDIQRPDSEH 2150	GLSPDSENF 2160
WKAIQEGANS 2170	IVSSLHQAAA 2180	AACLSRQASS 2190	DSDSLILSKS 2200	GISLGSPFHL 2210	TPDQEEKPFT 2220
SNKGPRILKP 2230	GEKSTLETKK 2240	IESESKGIK 2250	GKKVYKSLIT 2260	GKVRNSEIS 2270	GOMKQPLQAN 2280
MPSISRGRM 2290	IHIPGVRNSS 2300	SSTSPVSKKG 2310	PPLKTPASKS 2320	PSEGQTATTS 2330	PRGAKPSVKS 2340
ELSPVARQTS 2350	QIGGSSKAPS 2360	RSGSRDSTPS 2370	RPAQQPLSRP 2380	IQSPGRNSIS 2390	PGRNGISPPN 2400
KLSQLPRTSS 2410	PSTASTKSSG 2420	SGKMSYTSPG 2430	ROMSQONLTK 2440	QTGLSKNASS 2450	IPRSESASKG 2460
LNQMNGNGA 2470	NKKVELSRMS 2480	STKSSGSED 2490	RSERPVLVRQ 2500	STFIKEAPSP 2510	TLRRKLEESA 2520
SFESLSPSSR 2530	PASPTRSQAQ 2540	TPVLSPSLPD 2550	MSLSTHSSVQ 2560	AGGWRKLPPN 2570	LSPTIEYNDG 2580
RPAKRHDIA 2590	SHSEPSRLP 2600	INRSGTWKRE 2610	HSKHSSSLPR 2620	VSTWRRTGSS 2630	SSILSASSES 2640
SEKAKSEDEK 2650	HVNSISGTKQ 2660	SKENQVSAK 2670	TWRKIKENEF 2680	SPTNSTSQTV 2690	SSGATNGAES 2700
KTLIYQMAPA 2710	VSKTEDVWVR 2720	IEDCPINNPR 2730	SGRSPTGNT 2740	PVIDSVSEKA 2750	NPNIKDSKDN 2760
QAKQNVGNGS 2770	VPMRTVGLEN 2780	RLNSFIQVDA 2790	PDQKGTEIKP 2800	GQNNPVPVSE 2810	TNESSIVERT 2820
PFSSSSSSKH	SSPSGTVAAR	VTPFNYNPSP	RKSSADSTSA	RPSQIPTPVN	NNTKKRDSKT

Amended *Figure 3C*

2830 2840
DSTESSGTQS PKRHSGSYLV TSV*

FIG. 4A

APC	203	LGTCODMEKRAORRIARIOOIEKDILRIROL	233
		: :	
RAL2	576	LTGAKGLQLRALRRRIARIEQGGTAISPTSPL	606

FIG. 4B

APC	453	MKLSFDEEHRHAMNELGGLOAIAELLOVD	481
		: :	
M3	249	LYWRIYKETEKRTELKELAGLOASGTEAETE	277
		: :	
MCC	220	LYPNLAEERSRWEKELAGLREENESLTAM	248
		: :	
APC	453	MKLSFDEEHRHAMNELGGLOAIAELLOVD	481

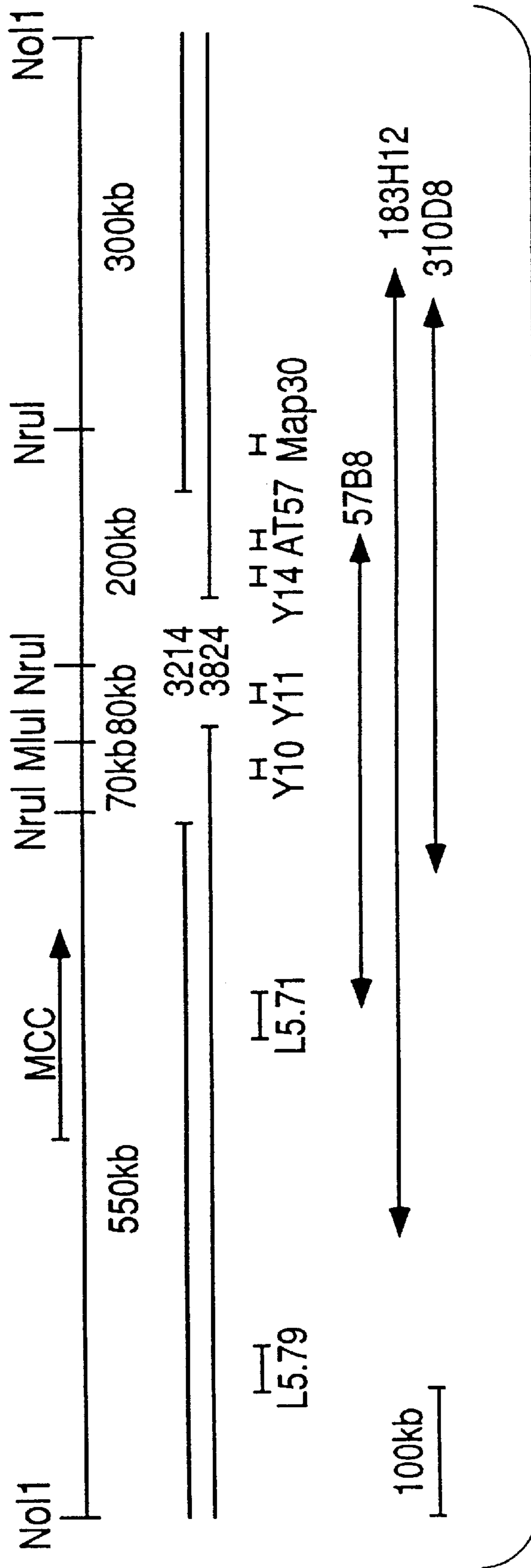


FIG. 6A

GCA	GTC	GCC	GCT	CCA	GTC	TAT	CCG	GCA	CTA	GGA	ACA	GCC	CCG	CCG	GGN	GGC	GAG	ACG	55
Ala	Val	Ala	Ala	Pro	Val	Tyr	Pro	Ala	Leu	Gly	Thr	Ala	Pro	Pro	Gly	Gly	Glu	Thr	109
GTC	CCC	GCC	ATG	TCT	GCG	GCC	ATG	AGG	GAG	AGG	TTC	GAC	CGG	TTC	TTC	CTG	CAC	GAG	163
Val	Pro	Ala	MET	Ser	Ala	Ala	MET	Arg	Glu	Arg	Phe	Asp	Arg	Phe	Phe	Leu	His	Glu	163
AAG	AAC	TGC	ATG	ACT	GAC	CTT	CTG	GCC	AAG	CTC	GAG	GCC	AAA	ACC	GGC	GTG	AAC	217	
Lys	Asn	Cys	MET	Thr	Asp	Leu	Leu	Ala	Lys	Leu	Glu	Ala	Lys	Thr	Gly	Val	Asn	217	
AGG	AGC	TTC	ATC	GCT	CTT	GGT	GTC	ATC	GGA	CTG	GTG	GCC	TTG	TAC	CTG	GTG	TTC	271	
Arg	Ser	Phe	Ile	Ala	Leu	Gly	Val	Ile	Gly	Leu	Val	Ala	Leu	Tyr	Leu	Val	Phe	271	
GGT	TAT	GGA	GCC	TCT	CTC	TGC	TGC	AAC	CTG	ATA	GGA	TTT	GGC	TAC	CCA	GCC	TAC	271	
Gly	Tyr	Gly	Ala	Ser	Leu	Leu	Cys	Asn	Leu	Ile	Gly	Phe	Gly	Tyr	Pro	Ala	Tyr	325	
ATC	TCA	ATT	AAA	GCT	ATA	GAG	AGT	CCC	AAC	AAA	GAA	GAT	GAT	ACC	CAG	TGG	CTG	325	
Ile	Ser	Ile	Lys	Ala	Ile	Glu	Ser	Pro	Asn	Lys	Glu	Asp	Asp	Thr	Gln	Trp	Leu	379	
ACC	TAC	TGG	GTA	GTG	TAT	GGT	GTG	TTC	AGC	ATT	GCT	GAA	TTC	TTC	TCT	GAT	ATC	379	
Thr	Tyr	Trp	Val	Val	Tyr	Gly	Val	Phe	Ser	Ile	Ala	Glu	Phe	Phe	Ser	Asp	Ile	433	
TTC	CTG	TCA	TGG	TTC	CCC	TTC	TAC	TAC	ATG	CTG	AAG	TGT	GGC	TTC	CTG	TTG	TGG	433	
Phe	Leu	Ser	Trp	Phe	Pro	Phe	Tyr	Tyr	MET	Leu	Lys	Cys	Gly	Phe	Leu	Leu	Trp	487	
TGC	ATG	GCC	CCG	AGC	CCT	TCT	AAT	GGG	GCT	GAA	CTG	CTC	TAC	AAG	CGC	ATC	ATC	487	
Cys	MET	Ala	Pro	Ser	Pro	Ser	Asn	Gly	Ala	Glu	Leu	Leu	Tyr	Lys	Arg	Ile	Ile	541	
CGT	CCT	TTC	TTC	CTG	AAG	CAC	GAG	TCC	CAG	ATG	GAC	AGT	GTG	GTC	AAG	GAC	CTT	541	
Arg	Pro	Phe	Phe	Leu	Lys	His	Glu	Ser	Gln	MET	Asp	Ser	Val	Val	Lys	Asp	Leu		

FIG. 6B

AAA GAC AAG TCC AAA GAG ACT GCA GAT GCC ATC ACT AAA GAA GCG AAG AAA GCT	568	595
Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr Lys Glu Ala Lys Lys Ala		
ACC GTG AAT TTA CTG GGT GAA GAA AAG AAG AGC ACC TAA ACC AGA	622	700
Thr Val Asn Leu Leu Gly Glu Glu Lys Lys Ser Thr		
CTAAACCAGA CTGGATGGAA ACTTCCTGCC CTCCTGTAC CTCCTACTG GAGCTTGATG TTATATTAGG	640	690
710	730	750
GACTGTGGTA TAATTATTTT AATAATGTTG CCTTGGAAAC ATTTTGGAGA TATTAAGAT TGGAAATGTGT		770
780	790	800
TGTAAGTTTC TTTGCTTACT TTTACTGTCT ATATATATAG GGAGCACTTT AAACCTAATG CAGTGGGCAG		830
850	860	870
TGTCCACGTT TTTGGAAAAT GTATTTTGCC TCTGGGTAGG AAAAGATGTA TGTTGCTATC CTGCAGGAAA		910
920	930	940
TATAAACTTA AAATAAAAT ATATACCCCA CAGGCTGTGT ACTTTACTGG GCTCTCCCTG CACGSATTTT		970
990	1000	1010
CTCTGTAGTT ACATTTAGGR TAATCTTTAT GGTCTACTT CTRTAATGT ACAATTTTAT ATAATTCNGR		1040
1060	1070	1080
AATGTTTTTA ATGTATTTGT GCACATGTAC ATATGGAAAT GTTACTGTCT GACTACANCA TGCATCATGC		1110
1130	1140	1150
TCATGGGGAG GGAGCAGGG AAGGTTGTAT GTGTCATTTA TAACTTCTGT ACAGTAAGAC CACCTGCCAA		1180
1200	1210	1220
AAGCTGGAG AACCATTTGT CTGGTGTGGT CTAATAATA ATACTTTAGG AAATACGTGA TTAATATGCA		1250
1270	1280	1290
AGTGAACAAA GTGAGAAATG AAATCGAATG GAGATTGGCC TGGTTGTTTC CGTAGTATAT GGCATATGAA		1320
1340	1350	1360
	1370	1380
	1390	1400

FIG. 6C

TACCAGGATA GCTTTATAAA GCAGTTAGTT AGTTAGTTAC TCACCTCTAGT GATAAATCGG GAAATTTTACA
1410 1420 1430 1440 1450 1460 1470
CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA GAGTACCCTG TAACTCTCAA
1480 1490 1500 1510 1520 1530 1540
TTCCCTGAAA AACTAGTAAT ACTGTCTTAT CTGCTATAAA CTTTACATAT TTGTCTATTG TCAAGATGCT
1550 1560 1570 1580 1590 1600 1610
ACANTGGAMN CCATTCTGG TTTTATCTTC ANAGSGGAGA NACATGTTGA TTTAGTCTTC TTTCCCAATC
1620 1630 1640 1650 1660 1670 1680
TTCTTTTTA AMCCAGTTN AGMNCTTCT GRAGATTGY CCACCTCTGA TTACATGTAT GTTCTYGTTT
1690 1700 1710 1720 1730 1740 1750
GTATCATKAG CAACAACATG CTAATGRCGA CACCTAGCTC TRAGMGCAAT TCTGGGAGAN TGARAGGNWG
1760 1770 1780 1790 1800 1810 1820
TATARAGTMN CCCATAATCT GCTTGGCAAT AGTTAAGTCA ATCTATCTTC AGTTTTTCTC TGGCCTTTAA
1830 1840 1850 1860 1870 1880 1890
GGTCAAACAC AAGAGGCTC CCTAGTTTAC AAGTCAGAGT CACTTGAGT CCATTTAAAT GCCCTCATCC
1900 1910 1920 1930 1940 1950 1960
GTATTCITTG TGTGATAAG CTGCACAKGA CTACATAGTA AGTACAGANC AGTAAAGTTA ANNCGGATGT
1970 1980 1990 2000 2010 2020 2030
CTCCATTGAT CTGCCAANTC GNTATAGAGA GCAATTGTC TGGACTAGAA AATCTGAGTT TTACACCATA
2040 2050 2060 2070 2080 2090 2100
CTGTTAAGAG TCCTTTTGAA TTAAACTAGA CTAAACAAG TGTATAACTA AACTAACAAAG ATTAATAATC
2110 2120 2130 2140 2150 2160 2170
CAGCCAGTAC AGTATTTTTT AAGGCAAATA AAGATGATTA GCTCACCTTG AGNTAACAAAT CAGGTAAGAT
2180 2190 2200 2210 2220 2230 2240
CATNACAATG TCTCATGATG TNAANAATAT TAAAGATATC AATACTAAGT GACAGTATCA CNNCTAATAT

FIG. 6D

2250 AATATGGATC 2260 AGAGCATTTA 2270 TTTTGGGGAG 2280 GAAACACAGTG 2290 GTGATTACCG 2300 GCATTTTATT 2310 AAACCTTAAAA
 2320 CTTTGTAGAA 2330 AGCAAACAAA 2340 ATTGTTCTTG 2350 GGAGAAAATC 2360 AACTTTTAGA 2370 TTAAAAAAT 2380 TTTAAGTAWC
 2390 TAGGAGTATT 2400 TAAATCCTTT 2410 TCCCATAAAT 2420 AAAAGTACAG 2430 TTTTCTTGGT 2440 GGCAGAAATGA 2450 AAATCAGCAA
 2460 CNTCTAGCAT 2470 ATAGACTATA 2480 TAATCAGATT 2490 GACAGCATAT 2500 AGAATATATT 2510 ATCAGACAAG 2520 ATGAGGAGGT
 2530 ACAAAAAGTTA 2540 CTATTGCTCA 2550 TAATGACTTA 2560 CAGGCTAAAA 2570 NTAGNTNTAA 2580 AATACTATAT 2590 TAAAATCTGA
 2600 ATGCAATTTT 2610 TTTTGTGCC 2620 CTTGAGACCA 2630 AAATTTAAGT 2640 TAACTGTTGC 2650 TGGCAGTCTA 2660 AGTGTAATG
 2670 TTAACAGCAG 2680 GAGAAGTTAA 2690 GAATTGAGCA 2700 GTTCTGTTGC 2710 ATGATTTCCC 2720 AAATGAAATA 2730 CTGCCCTTGGC
 2740 TAGAGTTTGA 2750 AAAACTAATT 2760 GAGCCTGTGC 2770 CTGGCTAGAA 2780 AACAAAGCGTT 2790 TATTTGAATG 2800 TGAATAGTGT
 2810 TTCAAAGGTA 2820 TGTAGTTACA 2830 GAATTCCTAC 2840 CAAACAGCCTT 2850 AAATTCITCA 2860 AGAAAGAATT 2870 CCTGCAGCAG
 2880 TTATTCCCCTT 2890 ACCTGAAGGC 2900 TTCAATCATT 2910 TGGATCAACA 2920 ACTGCTACTC 2930 TCGGGAAGAC 2940 TCCTCTACTC
 2950 ACAGCTGAAG 2960 AAAATGAGCA 2970 CACCCTTCAC 2980 ACTGTTATCA 2990 CCTATCCTGA 3000 AGATGTGATA 3010 CACTGAATGG
 3020 AAAATAAATAG 3030 ATGTAATAAA 3040 AATTGAGWTC 3050 TCATTTAAAA 3060 AAAACCATGT 3070 GCCCAATGGG 3080 AAAATGACCT
 3090 CATGTTGTGG 3100 TTTAAACAGC 3110 AACTGCACCC 3120 ACTAGCACAG 3130 CCCATTGAGC 3140 TANCCTATAT 3150 ATACATCTCT
 3160 GTCAGTGCCC CTC

Amended *Figure 7A*

23 ATGGCTGCAGCTTCATATGATCAGTTGTTAAAGCAAGTTGAGGCACTGAAGATGGAGAAC 82

1 M A A A S Y D Q L L K Q V E A L K M E N 20

83 TCAAATCTTCGACAAGAGCTAGAAGATAATCCAATCATCTTACAAAACCTGGAAACTGAG 142

21 S N L R Q E L E D N S N H L T K L E T E 40

143 GCATCTAATATGAAGGAAGTACTTAAACAACCTACAAGGAAGTATTGAAGATGAAGCTATG 202

41 A S N M K E V L K Q L Q G S I E D E A M 60

203 GCTTCTTCTGGACAGATTGATTTATTAGAGCGTCTTAAAGAGCTTAACTTAGATAGCAGT 262

61 A S S G Q I D L L E R L K E L N L D S S 80

263 AATTTCCCTGGAGTAAAACCTGCGGTCAAAAATGTCCCTCCGTTCTTATGGAAGCCGGGAA 322

81 N F P G V K L R S K M S L R S Y G S R E 100

323 GGATCTGTATCAAGCCGTTCTGGAGAGTGCAGTCCTGTTCCCTATGGGTTTCATTTCCAAGA 382

101 G S V S S R S G E C S P V P M G S F P R 120

383 AGAGGGTTTGTAAATGGAAGCAGAGAAAGTACTGGATATTTAGAAGAACTTGAGAAAGAG 442

Amended *Figure 7B*

121 R G F V N G S R E S T G Y L E E L E K E 140

443 AGGTCATTGCTTCTTGCTGATCTTGACAAAGAAGAAAAGGAAAAGACTGGTATTACGCT 502

141 R S L L L A D L D K E E K E K D W Y Y A 160

503 CAACTTCAGAATCTCACTAAAAGAATAGATAGTCTTCCTTTAACTGAAAATTTTTCCTTA 562

161 Q L Q N L T K R I D S L P L T E N F S L 180

563 CAAACAGATATGACCAGAAGGCAATTGGAATATGAAGCAAGGCAAATCAGAGTTGCGATG 622

181 Q T D M T R R Q L E Y E A R Q I R V A M 200

623 GAAGAACAACCTAGGTACCTGCCAGGATATGGAAAACGAGCACAGCGAAGAATAGCCAGA 682

201 E E Q L G T C Q D M E K R A Q R R I A R 220

683 ATTCAGCAAATCGAAAAGGACATACTTCGTATACGACAGCTTTTACAGTCCCAAGCAACA 742

221 I Q Q I E K D I L R I R Q L L Q S Q A T 240

743 GAAGCAGAGAGGTCATCTCAGAACAAGCATGAAACCGGCTCACATGATGCTGAGCGGCAG 802

241 E A E R S S Q N K H E T G S H D A E R Q 260

Amended *Figure 7C*

803 AATGAAGGTCAAGGAGTGGGAGAAATCAACATGGCAACTTCTGGTAATGGTCAGGGTTCA 862

261 N E G Q G V G E I N M A T S G N G Q G S 280

863 ACTACACGAATGGACCATGAAACAGCCAGTGTTTTGAGTTCTAGTAGCACACACTCTGCA 922

281 T T R M D H E T A S V L S S S S T H S A 300

923 CCTCGAAGGCTGACAAGTCATCTGGGAACCAAGgtggaaatggtgtattcattgttgtca 982

301 p r r l t s h l g t k v e m v y s l l s 320

983 atgcttggtactcatgataaggatgatatgtcgcgaaactttgctagctatgtctagctcc 1042

321 m l g t h d k d d m s r t l l a m s s s 340

1043 caagacagctgtatatccatgcgacagtctggatgtcttcctctcctcatccagctttta 1102

341 q d s c i s m r q s g c l p l l i q l l 360

1103 catggcaatgacaaagactctgtattggtgggaattcccggggcagtaaagaggctcgg 1162

361 h g n d k d s v l l g n s r g s k e a r 380

1163 gccagggccagtgcagcactccacaacatcattcactcacagcctgatgacaagagaggc 1222

Amended *Figure 7D*

381 a r a s a a l h n i i h s q p d d k r g 400

1223 aggcgtgaaatccgagtccttcatcttttggaacagATACGCGCTTACTGTGAAACCTGT 1282

401 r r e i r v l h l l e q I R A Y C E T C 420

1283 TGGGAGTGGCAGGAAGCTCATGAACCAGGCATGGACCAGGACAAAAATCCAATGCCAGCT 1342

421 W E W Q E A H E P G M D Q D K N P M P A 440

1343 CCTGTTGAACATCAGATCTGTCCTGCTGTGTGTGTTCTAATGAACTTTCATTTGATGAA 1402

441 P V E H Q I C P A V C V L M K L S F D E 460

1403 GAGCATAGACATGCAATGAATGAACTAGGGGGACTACAGGCCATTGCAGAATTATTGCAA 1462

461 E H R H A M N E L G G L Q A I A E L L Q 480

1463 GTGGACTGTGAAATGTACGGGCTTACTAATGACCACTACAGTATTACACTAAGACGATAT 1522

481 V D C E M Y G L T N D H Y S I T L R R Y 500

1523 GCTGGAATGGCTTTGACAACTTGACTTTTGGAGATGTAGCCAACAAGGCTACGCTATGC 1582

501 A G M A L T N L T F G D V A N K A T L C 520

Amended *Figure 7E*

1583 TCTATGAAAGGCTGCATGAGAGCACTTGTGGCCCACTAAAATCTGAAAGTGAAGACTTA 1642

521 S M K G C M R A L V A Q L K S E S E D L 540

1643 CAGCAGGTTATTGCAAGTGTTTTGAGGAATTTGTCTTGCCGAGCAGATGTAAATAGTAAA 1702

541 Q Q V I A S V L R N L S W R A D V N S K 560

1703 AAGACGTTGCGAGAAGTTGGAAGTGTGAAAGCATTGATGGAATGTGCTTTAGAAGTTAAA 1762

561 K T L R E V G S V K A L M E C A L E V K 580

1763 AAGGAATCAACCCTCAAAAGCGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACT 1822

581 K E S T L K S V L S A L W N L S A H C T 600

1823 GAGAATAAAGCTGATATATGTGCTGTAGATGGTGCACTTGCATTTTTGGTTGGCACTCTT 1882

601 E N K A D I C A V D G A L A F L V G T L 620

1883 ACTTACCGGAGCCAGACAAACACTTTAGCCATTATTGAAAGTGGAGGTGGGATATTACGG 1942

621 T Y R S Q T N T L A I I E S G G G I L R 640

Amended *Figure 7F*

1943 AATGTGTCCAGCTTGATAGCTACAAATGAGGACCACAGGCAAATCCTAAGAGAGAACAAC 2002

641 N V S S L I A T N E D H R Q I L R E N N 660

2003 TGTCTACAACTTTATTACAACACTTAAAATCTCATAGTTTGACAATAGTCAGTAATGCA 2062

661 C L Q T L L Q H L K S H S L T I V S N A 680

2063 TGTGGAACCTTGTGGAATCTCTCAGCAAGAAATCCTAAAGACCAGGAAGCATTATGGGAC 2122

681 C G T L W N L S A R N P K D Q E A L W D 700

2123 ATGGGGGCAGTTAGCATGCTCAAGAACCTCATTCATTCAAAGCACAAAATGATTGCTATG 2182

701 M G A V S M L K N L I H S K H K M I A M 720

2183 GGAAGTGCTGCAGCTTTAAGGAATCTCATGGCAAATAGGCCTGCGAAGTACAAGGATGCC 2242

721 G S A A A L R N L M A N R P A K Y K D A 740

2243 AATATTATGTCTCCTGGCTCAAGCTTGCCATCTCTTCATGTTAGGAAACAAAAGCCCTA 2302

741 N I M S P G S S L P S L H V R K Q K A L 760

2303 GAAGCAGAATTAGATGCTCAGCACTTATCAGAACTTTTGACAATATAGACAATTTAAGT 2362

Amended *Figure 7G*

761 E A E L D A Q H L S E T F D N I D N L S 780

2363 CCCAAGGCATCTCATCGTAGTAAGCAGAGACACAAGCAAAGTCTCTATGGTGATTATGTT 2422

781 P K A S H R S K Q R H K Q S L Y G D Y V 800

2423 TTTGACACCAATCGACATGATGATAATAGGTCAGACAATTTTAATACTGGCAACATGACT 2482

801 F D T N R H D D N R S D N F N T G N M T 820

2483 GTCCTTTCACCATATTTGAATACTACAGTGTTACCCAGCTCCTCTTCATCAAGAGGAAGC 2542

821 V L S P Y L N T T V L P S S S S S R G S 840

2543 TTAGATAGTTCTCGTTCTGAAAAAGATAGAAGTTTGGAGAGAGAACGCGGAATTGGTCTA 2602

841 L D S S R S E K D R S L E R E R G I G L 860

2603 GGCAACTACCATCCAGCAACAGAAAATCCAGGAACTTCTTCAAAGCGAGGTTTGAGATC 2662

861 G N Y H P A T E N P G T S S K R G L Q I 880

2663 TCCACCACTGCAGCCCAGATTGCCAAAGTCATGGAAGAAGTGTCAGCCATTCATACCTCT 2722

881 S T T A A Q I A K V M E E V S A I H T S 900

Amended *Figure 7H*

2723 CAGGAAGACAGAAGTTCTGGGTCTACCACTGAATTACATTGTGTGACAGATGAGAGAAAT 2782

901 Q E D R S S G S T T E L H C V T D E R N 920

2783 GCACTTAGAAGAAGCTCTGCTGCCCATACACATTCAAACACTTACAATTTCACTAAGTCG 2842

921 A L R R S S A A H T H S N T Y N F T K S 940

2843 GAAAATTCAAATAGGACATGTTCTATGCCTTATGCCAAATTAGAATACAAGAGATCTTCA 2902

941 E N S N R T C S M P Y A K L E Y K R S S 960

2903 AATGATAGTTTAAATAGTGTCAGTAGTAGTGATGGTTATGGTAAAAGAGGTCAAATGAAA 2962

961 N D S L N S V S S S D G Y G K R G Q M K 980

2963 CCCTCGATTGAATCCTATTCTGAAGATGATGAAAGTAAGTTTTGCAGTTATGGTCAATAC 3022

981 P S I E S Y S E D D E S K F C S Y G Q Y 1000

3023 CCAGCCGACCTAGCCCATAAAATACATAGTGCAAATCATATGGATGATAATGATGGAGAA 3082

1001 P A D L A H K I H S A N H M D D N D G E 1020

3083 CTAGATACACCAATPAATTATAGTCTTAAATATTCAGATGAGCAGTTGAACTCTGGAAGG 3142

Amended *Figure 7I*

1021 L D T P I N Y S L K Y S D E Q L N S G R 1040

3143 CAAAGTCCTTCACAGAATGAAAGATGGGCAAGACCCAAACACATAATAGAAGATGAAATA 3202

1041 Q S P S Q N E R W A R P K H I I E D E I 1060

3203 AAACAAAGTGAGCAAAGACAATCAAGGAATCAAAGTACAACCTTATCCTGTTTATACTGAG 3262

1061 K Q S E Q R Q S R N Q S T T Y P V Y T E 1080

3263 AGCACTGATGATAAACACCTCAAGTTCCAACCACATTTTGGACAGCAGGAATGTGTTTCT 3322

1081 S T D D K H L K F Q P H F G Q Q E C V S 1100

3323 CCATACAGGTCACGGGGAGCCAATGGTTCAGAAACAAATCGAGTGGGTTCTAATCATGGA 3382

1101 P Y R S R G A N G S E T N R V G S N H G 1120

3383 ATTAATCAAATGTAAGCCAGTCTTTGTGTCAAGAAGATGACTATGAAGATGATAAGCCT 3442

1121 I N Q N V S Q S L C Q E D D Y E D D K P 1140

3443 ACCAATTATAGTGAACGTTACTCTGAAGAAGAACAGCATGAAGAAGAAGAGAGACCAACA 3502

1141 T N Y S E R Y S E E E Q H E E E E R P T 1160

Amended *Figure 7J*

3503 AATTATAGCATAAAATATAATGAAGAGAAACGTCATGTGGATCAGCCTATTGATTATAGT 3562

1161 N Y S I K Y N E E K R H V D Q P I D Y S 1180

3563 TTAAAATATGCCACAGATATTCCTTCATCACAGAAACAGTCATTTTCATTCTCAAAGAGT 3622

1181 L K Y A T D I P S S Q K Q S F S F S K S 1200

3623 TCATCTGGACAAAGCAGTAAAACCGAACATATGTCTTCAAGCAGTGAGAATACGTCCACA 3682

1201 S S G Q S S K T E H M S S S S E N T S T 1220

3683 CCTTCATCTAATGCCAAGAGGCAGAATCAGCTCCATCCAAGTTCTGCACAGAGTAGAAGT 3742

1221 P S S N A K R Q N Q L H P S S A Q S R S 1240

3743 GGTCAGCCTCAAAGGCTGCCACTTGCAAAGTTTCTTCTATTAACCAAGAAACAATACAG 3802

1241 G Q P Q K A A T C K V S S I N Q E T I Q 1260

3803 ACTTATTGTGTAGAAGATACTCCAATATGTTTTTCAAGATGTAGTTCATTATCATCTTTG 3862

1261 T Y C V E D T P I C F S R C S S L S S L 1280

3863 TCATCAGCTGAAGATGAAATAGGATGTAATCAGACGACACAGGAAGCAGATTCTGCTAAT 3922

Amended *Figure 7K*

1281 S S A E D E I G C N Q T T Q E A D S A N 1300

3923 ACCCTGCAAATAGCAGAAATAAAAGAAAAGATTGGAACTAGGTCAGCTGAAGATCCTGTG 3982

1301 T L Q I A E I K E K I G T R S A E D P V 1320

3983 AGCGAAGTTCAGCAGTGTACAGCACCCCTAGAACCAAATCCAGCAGACTGCAGGGTTCT 4042

1321 S E V P A V S Q H P R T K S S R L Q G S 1340

4043 AGTTTATCTTCAGAATCAGCCAGGCACAAAGCTGTTGAATTTTCTTCAGGAGCGAAATCT 4102

1341 S L S S E S A R H K A V E F S S G A K S 1360

4103 CCCTCCAAAAGTGGTGCTCAGACACCCAAAAGTCCACCTGAACACTATGTTTCAGGAGACC 4162

1361 P S K S G A Q T P K S P P E H Y V Q E T 1380

4163 CCACTCATGTTTAGCAGATGTACTTCTGTCAGTTCACTTGATAGTTTTGAGAGTCGTTCCG 4222

1381 P L M F S R C T S V S S L D S F E S R S 1400

4223 ATTGCCAGCTCCGTTTCAGAGTGAACCATGCAGTGGAAATGGTAAGTGGCATTATAAGCCCC 4282

1401 I A S S V Q S E P C S G M V S G I I S P 1420

Amended *Figure 7L*

4283 AGTGATCTTCCAGATAGCCCTGGACAAACCATGCCACCAAGCAGAAGTAAAACACCTCCA 4342

1421 S D L P D S P G Q T M P P S R S K T P P 1440

4343 CCACCTCCTCAAACAGCTCAAACCAAGCGAGAAGTACCTAAAAATAAAGCACCTACTGCT 4402

1441 P P P Q T A Q T K R E V P K N K A P T A 1460

4403 GAAAAGAGAGAGAGTGGACCTAAGCAAGCTGCAGTAAATGCTGCAGTTCAGAGGGTCCAG 4462

1461 E K R E S G P K Q A A V N A A V Q R V Q 1480

4463 GTTCTTCCAGATGCTGATACTTTATTACATTTTGCCACGGAAAGTACTCCAGATGGATTT 4522

1481 V L P D A D T L L H F A T E S T P D G F 1500

4523 TCTTGTTTCATCCAGCCTGAGTGCTCTGAGCCTCGATGAGCCATTTATACAGAAAGATGTG 4582

1501 S C S S S L S A L S L D E P F I Q K D V 1520

4583 GAATTAAGAATAATGCCTCCAGTTCAGGAAAATGACAATGGGAATGAAACAGAATCAGAG 4642

1521 E L R I M P P V Q E N D N G N E T E S E 1540

4643 CAGCCTAAAGAATCAAATGAAAACCAAGAGAAAGAGGCAGAAAAAACTATTGATTCTGAA 4702

Amended *Figure 7M*

1541 Q P K E S N E N Q E K E A E K T I D S E 1560

4703 AAGGACCTATTAGATGATTCAGATGATGATGATATTGAAATACTAGAAGAATGTATTATT 4762

1561 K D L L D D S D D D D I E I L E E C I I 1580

4763 TCTGCCATGCCAACAAAGTCATCACGTAAAGCAAAAAGCCAGCCCAGACTGCTTCAAAA 4822

1581 S A M P T K S S R K A K K P A Q T A S K 1600

4823 TTACCTCCACCTGTGGCAAGGAAACCAAGTCAGCTGCCTGTGTACAAACTTCTACCATCA 4882

1601 L P P P V A R K P S Q L P V Y K L L P S 1620

4883 CAAAACAGGTTGCAACCCCAAAGCATGTTAGTTTTACACCGGGGGATGATATGCCACGG 4942

1621 Q N R L Q P Q K H V S F T P G D D M P R 1640

4943 GTGTATTGTGTTGAAGGGACACCTATAAACTTTCCACAGCTACATCTCTAAGTGATCTA 5002

1641 V Y C V E G T P I N F S T A T S L S D L 1660

5003 ACAATCGAATCCCCTCCAAATGAGTTAGCTGCTGGAGAAGGAGTTAGAGGAGGAGCACAG 5062

1661 T I E S P P N E L A A G E G V R G G A Q 1680

Amended *Figure 7N*

5063 TCAGGTGAATTTGAAAAACGAGATAACCATTCTACAGAAGGCAGAAGTACAGATGAGGCT 5122

1681 S G E F E K R D T I P T E G R S T D E A 1700

5123 CAAGGAGGAAAAACCTCATCTGTAACCATACCTGAATTGGATGACAATAAAGCAGAGGAA 5182

1701 Q G G K T S S V T I P E L D D N K A E E 1720

5183 GGTGATATTCTTGCAGAATGCATTAATTCTGCTATGCCCAAAGGGAAAAGTCACAAGCCT 5242

1721 G D I L A E C I N S A M P K G K S H K P 1740

5243 TTCCGTGTGAAAAGATAATGGACCAGGTCCAGCAAGCATCTGCGTCGTCTTCTGCACCC 5302

1741 F R V K K I M D Q V Q Q A S A S S S A P 1760

5303 AACAAAAATCAGTTAGATGGTAAGAAAAAGAAACCAACTTCACCAGTAAACCTATACCA 5362

1761 N K N Q L D G K K K K P T S P V K P I P 1780

5363 CAAAATACTGAATATAGGACACGTGTAAGAAAAAATGCAGACTCAAAAAATAATTTAAAT 5422

1781 Q N T E Y R T R V R K N A D S K N N L N 1800

5423 GCTGAGAGAGTTTTCTCAGACAACAAAGATTCAAAGAAACAGAATTTGAAAAATAATTCC 5482

Amended *Figure 70*

1801 A E R V F S D N K D S K K Q N L K N N S 1820

5483 AAGGACTTCAATGATAAGCTCCCAAATAATGAAGATAGAGTCAGAGGAAGTTTTGCTTTT 5542

1821 K D F N D K L P N N E D R V R G S F A F 1840

5543 GATTCACCTCATCATTACACGCCTATTGAAGGAACTCCTTACTGTTTTTCACGAAATGAT 5602

1841 D S P H H Y T P I E G T P Y C F S R N D 1860

5603 TCTTTGAGTTCTCTAGATTTTGATGATGATGATGTTGACCTTCCAGGGAAAAGGCTGAA 5662

1861 S L S S L D F D D D D V D L S R E K A E 1880

5663 TTAAGAAAGGCAAAAGAAAATAAGGAATCAGAGGCTAAAGTTACCAGCCACACAGAACTA 5722

1881 L R K A K E N K E S E A K V T S H T E L 1900

5723 ACCTCCAACCAACAATCAGCTAATAAGACACAAGCTATTGCAAAGCAGCCAATAAATCGA 5782

1901 T S N Q Q S A N K T Q A I A K Q P I N R 1920

5783 GGTCAGCCTAAACCCATACTTCAGAAACAATCCACTTTTCCCAGTCATCCAAGACATA 5842

1921 G Q P K P I L Q K Q S T F P Q S S K D I 1940

Amended *Figure 7P*

5843 CCAGACAGAGGGGCAGCAACTGATGAAAAGTTACAGAATTTTGCTATTGAAAATACTCCA 5902

1941 P D R G A A T D E K L Q N F A I E N T P 1960

5903 GTTTGCTTTTCTCATAATTCCTCTCTGAGTTCTCTCAGTGACATTGACCAAGAAAACAAC 5962

1961 V C F S H N S S L S S L S D I D Q E N N 1980

5963 AATAAAGAAAATGAACCTATCAAAGAGACTGAGCCCCCTGACTCACAGGGAGAACCAAGT 6022

1981 N K E N E P I K E T E P P D S Q G E P S 2000

6023 AAACCTCAAGCATCAGGCTATGCTCCTAAATCATTTTCATGTTGAAGATACCCAGTTTGT 6082

2001 K P Q A S G Y A P K S F H V E D T P V C 2020

6083 TTCTCAAGAAACAGTTCTCTCAGTTCTCTTAGTATTGACTCTGAAGATGACCTGTTGCAG 6142

2021 F S R N S S L S S L S I D S E D D L L Q 2040

6143 GAATGTATAAGCTCCGCAATGCCAAAAAAGAAAAAGCCTTCAAGACTCAAGGGTGATAAT 6202

2041 E C I S S A M P K K K K P S R L K G D N 2060

6203 GAAAACATAGTCCCAGAAATATGGGTGGCATATTAGGTGAAGATCTGACACTTGATTTG 6262

Amended *Figure 7Q*

2061 E K H S P R N M G G I L G E D L T L D L 2080

6263 AAAGATATACAGAGACCAGATTCAGAACATGGTCTATCCCCTGATTCAGAAAATTTTGAT 6322

2081 K D I Q R P D S E H G L S P D S E N F D 2100

6323 TGGAAAGCTATTCAGGAAGGTGCAAATTCATAGTAAGTAGTTTACATCAAGCTGCTGCT 6382

2101 W K A I Q E G A N S I V S S L H Q A A A 2120

6383 GCTGCATGTTTATCTAGACAAGCTTCGTCTGATTCAGATTCATCCTTTCCCTGAAATCA 6442

2121 A A C L S R Q A S S D S D S I L S L K S 2140

6443 GGAATCTCTCTGGGATCACCATTTCATCTTACACCTGATCAAGAAGAAAAACCCTTTACA 6502

2141 G I S L G S P F H L T P D Q E E K P F T 2160

6503 AGTAATAAAGGCCACGAATTCTAAAACCAGGGGAGAAAAGTACATTGGAAACTAAAAAG 6562

2161 S N K G P R I L K P G E K S T L E T K K 2180

6563 ATAGAATCTGAAAGTAAAGGAATCAAAGGAGGAAAAAAGTTTATAAAAGTTTGATTACT 6622

2181 I E S E S K G I K G G K K V Y K S L I T 2200

Amended *Figure 7R*

6623 GGAAAAGTTCGATCTAATTCAGAAATTTAGGCCAAATGAAACAGCCCCTTCAAGCAAAC 6682

2201 G K V R S N S E I S G Q M K Q P L Q A N 2220

6683 ATGCCTTCAATCTCTCGAGGCAGGACAATGATTCATATTCAGGAGTTCGAAATAGCTCC 6742

2221 M P S I S R G R T M I H I P G V R N S S 2240

6743 TCAAGTACAAGTCCTGTTTCTAAAAAAGGCCACCCCTTAAGACTCCAGCCTCCAAAAGC 6802

2241 S S T S P V S K K G P P L K T P A S K S 2260

6803 CCTAGTGAAGGTCAAACAGCCACCACTTCTCCTAGAGGAGCCAAGCCATCTGTGAAATCA 6862

2261 P S E G Q T A T T S P R G A K P S V K S 2280

6863 GAATTAAGCCCTGTTGCCAGGCAGACATCCCAAATAGGTGGGTCAAGTAAAGCACCTTCT 6922

2281 E L S P V A R Q T S Q I G G S S K A P S 2300

6923 AGATCAGGATCTAGAGATTCGACCCCTTCAAGACCTGCCAGCAACCATTAAGTAGACCT 6982

2301 R S G S R D S T P S R P A Q Q P L S R P 2320

6983 ATACAGTCTCCTGGCCGAAACTCAATTTCCCCTGGTAGAAATGGAATAAGTCCTCCTAAC 7042

Amended *Figure 7S*

2321 I Q S P G R N S I S P G R N G I S P P N 2340

7043 AAATTATCTCAACTTCCAAGGACATCATCCCCTAGTACTGCTTCAACTAAGTCCTCAGGT 7102

2341 K L S Q L P R T S S P S T A S T K S S G 2360

7103 TCTGGAAAATGTCATATACATCTCCAGGTAGACAGATGAGCCAACAGAACCTTACCAA 7162

2361 S G K M S Y T S P G R Q M S Q Q N L T K 2380

7163 CAAACAGGTTTATCCAAGAATGCCAGTAGTATTCCAAGAAGTGAGTCTGCCTCAAAGGA 7222

2381 Q T G L S K N A S S I P R S E S A S K G 2400

7223 CTAAATCAGATGAATAATGGTAATGGAGCCAATAAAAAGGTAGAACTTTCTAGAATGTCT 7282

2401 L N Q M N N G N G A N K K V E L S R M S 2420

7283 TCAACTAAATCAAGTGGAAGTGAATCTGATAGATCAGAAAGACCTGTATTAGTACGCCAG 7342

2421 S T K S S G S E S D R S E R P V L V R Q 2440

7343 TCAACTTTCATCAAAGAAGCTCCAAGCCCAACCTTAAGAAGAAAATTGGAGGAATCTGCT 7402

2441 S T F I K E A P S P T L R R K L E E S A 2460

Amended *Figure 7T*

7403 TCATTTGAATCTCTTTCTCCATCATCTAGACCAGCTTCTCCCCTAGGTCCCAGGCACAA 7462

2461 S F E S L S P S S R P A S P T R S Q A Q 2480

7463 ACTCCAGTTTTAAGTCCTTCCCTCCTGATATGTCTCTATCCACACATTCGTCTGTTTCAG 7522

2481 T P V L S P S L P D M S L S T H S S V Q 2500

7523 GCTGGTGGATGGCGAAAACCTCCCACCTAATCTCAGTCCCCTATAGAGTATAATGATGGA 7582

2501 A G G W R K L P P N L S P T I E Y N D G 2520

7583 AGACCAGCAAAGCGCCATGATATTGCACGGTCTCATTCTGAAAGTCCTTCTAGACTTCCA 7642

2521 R P A K R H D I A R S H S E S P S R L P 2540

7643 ATCAATAGGTCAGGAACCTGGAAACGTGAGCACAGCAAACATTCATCATCCCTTCCTCGA 7702

2541 I N R S G T W K R E H S K H S S S L P R 2560

7703 GTAAGCACTTGGAGAAGAAGTGGAAAGTTCATCTTCAATTCTTTCTGCTTCATCAGAATCC 7762

2561 V S T W R R T G S S S S I L S A S S E S 2580

7763 AGTGAAAAGCAAAAAGTGAGGATGAAAACATGTGAACTCTATTTTCAGGAACCAAACAA 7822

Amended *Figure 7U*

2581 S E K A K S E D E K H V N S I S G T K Q 2600

7823 AGTAAAGAAAACCAAGTATCCGCAAAGGAACATGGAGAAAATAAAAAGAAAATGAATTT 7882

2601 S K E N Q V S A K G T W R K I K E N E F 2620

7883 TCTCCCACAAATAGTACTTCTCAGACCGTTTCCTCAGGTGCTACAAATGGTGCTGAATCA 7942

2621 S P T N S T S Q T V S S G A T N G A E S 2640

7943 AAGACTCTAATTTATCAAATGGCACCTGCTGTTTCTAAAACAGAGGATGTTTGGGTGAGA 8002

2641 K T L I Y Q M A P A V S K T E D V W V R 2660

8003 ATGAGGACTGTCCCATTAACAATCCTAGATCTGGAAGATCTCCCACAGGTAATACTCCC 8062

2661 I E D C P I N N P R S G R S P T G N T P 2680

8063 CCGGTGATTGACAGTGTTTCAGAAAAGGCAAATCCAAACATTAAAGATTCAAAGATAAT 8122

2681 P V I D S V S E K A N P N I K D S K D N 2700

8123 CAGGCAAACAAAATGTGGGTAATGGCAGTGTTCCCATGCGTACCGTGGGTTTGGAAAAT 8182

2701 Q A K Q N V G N G S V P M R T V G L E N 2720

Amended *Figure 7V*

8183 CGCCTGAACTCCTTTATTTCAGGTGGATGCCCTGACCAAAAAGGAACTGAGATAAAACCA 8242

2721 R L N S F I Q V D A P D Q K G T E I K P 2740

8243 GGACAAAATAATCCTGTCCCTGTATCAGAGACTAATGAAAGTTCTATAGTGGAACGTACC 8302

2741 G Q N N P V P V S E T N E S S I V E R T 2760

8303 CCATTCAGTTCTAGCAGCTCAAGCAAACACAGTTCACCTAGTGGGACTGTTGCTGCCAGA 8362

2761 P F S S S S S S K H S S P S G T V A A R 2780

8363 GTGACTCCTTTTAATTACAACCCAAGCCCTAGGAAAAGCAGCGCAGATAGCACTTCAGCT 8422

2781 V T P F N Y N P S P R K S S A D S T S A 2800

8423 CGGCCATCTCAGATCCCAACTCCAGTGAATAACAACACAAAGAAGCGAGATTCCAAAACCT 8482

2801 R P S Q I P T P V N N N T K K R D S K T 2820

8483 GACAGCACAGAATCCAGTGGAAACCCAAAGTCCTAAGCGCCATTCTGGGTCTTACCTTGTG 8542

2821 D S T E S S G T Q S P K R H S G S Y L V 2840

8543 ACATCTGTTTAA 8554

Amended *Figure 7W*

2841 T S V *

2844

FIG. 8A

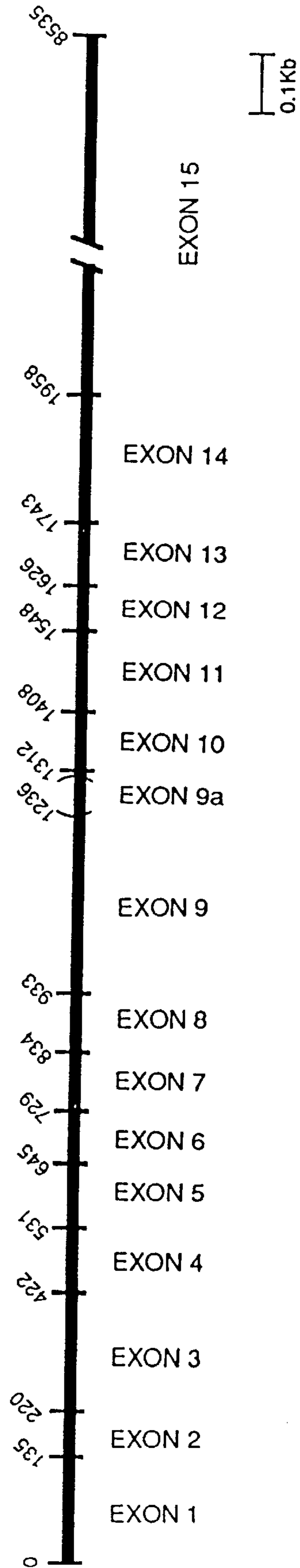


FIG. 8B-1

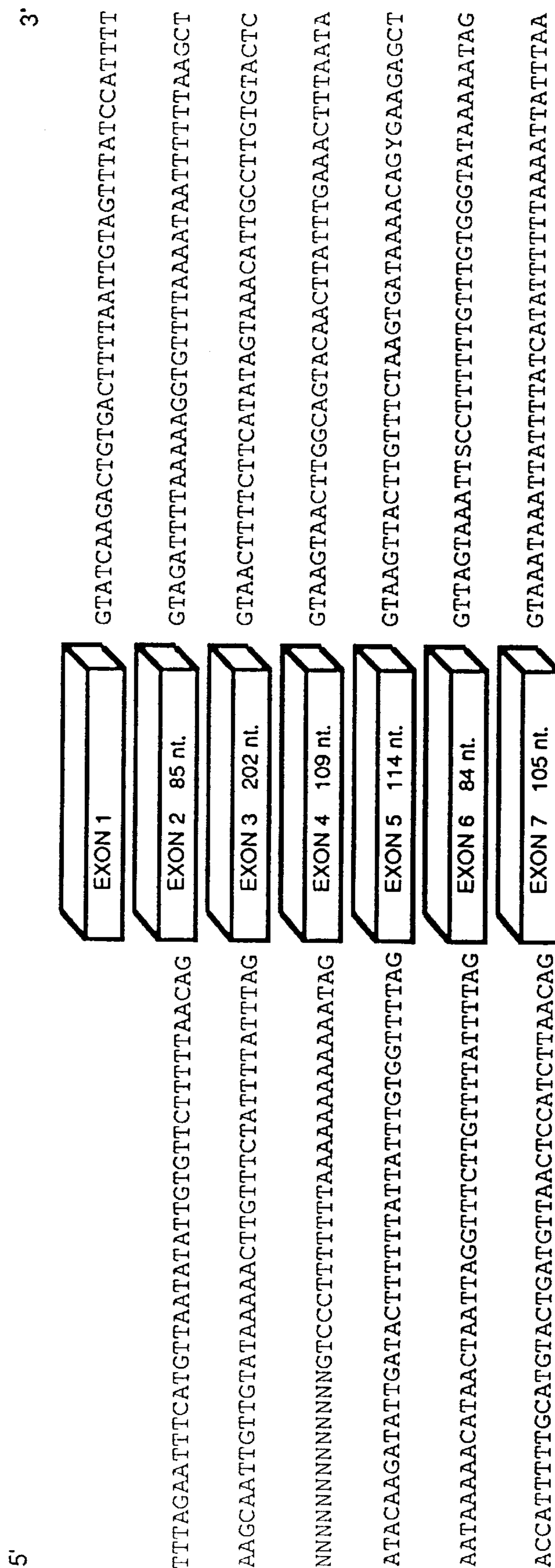


FIG. 8B-2



APC GENE AND NUCLEIC ACID PROBES DERIVED THEREFROM

Matter enclosed in heavy brackets [] appears in the original patent but forms no part of this reissue specification; matter printed in italics indicates the additions made by reissue.

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TECHNICAL AREA OF THE INVENTION

The invention relates to the area of cancer diagnostics and therapeutics. More particularly, the invention relates to detection of the germline and somatic alterations of wild-type APC genes. In addition, it relates to therapeutic intervention to restore the function of APC (adenomatous polyposis coli) gene product.

BACKGROUND OF THE INVENTION

According to the model of Knudson for tumorigenesis (Cancer Research, Vol. 45, p. 1482, 1985), there are tumor suppressor genes in all normal cells which, when they become non-functional due to mutation, cause neoplastic development. Evidence for this model has been found in the cases of retinoblastoma and colorectal tumors. The implicated suppressor genes in those tumors, RB (retinoblastoma), p53 (protein having a molecular weight of 53 kDa), Dcc (deleted in colorectal cancer) and MCC (mutated in colorectal cancer) were found to be deleted or altered in many cases of the tumors studied. (Hansen and Cavenee, Cancer Research, Vol. 47, pp. 5518-5527 (1987); Baker et al., Science, Vol. 244, p. 217 (1989); Fearon et al., Science, Vol. 247, p. 49 (1990); Kinzler et al. Science Vol. 251, p. 1366 (1991).)

In order to fully understand the pathogenesis of tumors, it will be necessary to identify the other suppressor genes that play a role in the tumorigenesis process. Prominent among these is the one(s) presumptively located at 5q21. Cytogenetic (Herrera et al., Am J. Med. Genet., Vol. 25, p. 473 (1986) and linkage (Leppert et al., Science, Vol. 238, p. 1411 (1987); Bodmer et al., Nature, Vol. 328, p. 614 (1987)) studies have shown that this chromosome region harbors the gene responsible for familial adenomatous polyposis (FAP) and Gardner's Syndrome (GS). FAP is an autosomal-dominant, inherited disease in which affected individuals develop hundreds to thousands of adenomatous polyps, some of which progress to malignancy. GS is a variant of FAP in which desmoid tumors, osteomas and other soft tissue tumors occur together with multiple adenomas of the colon and rectum. A less severe form of polyposis has been identified in which only a few (2-40) polyps develop. This condition also is familial and is linked to the same chromosomal markers as FAP and GS (Leppert et al., New England Journal of Medicine, Vol. 322, pp. 904-908, 1990.) Additionally, this chromosomal region is often deleted from the adenomas (Vogelstein et al., N. Engl. J. Med., Vol. 319, p. 525 (1988)) and carcinomas (Vogelstein et al., N. Engl. J. Med., Vol. 319, p. 525 (1988); Solomon et al., Nature, Vol. 328, p. 616 (1987); Sasaki et al., Cancer Research, Vol. 49, p. 4402 (1989); Delattre et al., Lancet, Vol. 2, p. 353 (1989); and Ashton-Rickardt et al., Oncogene, Vol. 4, p. 1169 (1989)) of patients without FAP (sporadic tumors). Thus, a putative suppressor gene on chromosome 5q21 appears to

play a role in the early stages of colorectal neoplasia in both sporadic and familial tumors.

Although the MCC gene has been identified on 5q21 as a candidate suppressor gene, it does not appear to be altered in FAP or GS patients. Thus there is a need in the art for investigations of this chromosomal region to identify genes and to determine if any of such genes are associated with FAP and/or GS and the process of tumorigenesis.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide a method for diagnosing and prognosing a neoplastic tissue of a human.

It is another object of the invention to provide a method of detecting genetic predisposition to cancer.

It is another object of the invention to provide a method of supplying wild-type APC gene function to a cell which has lost said gene function.

It is yet another object of the invention to provide a kit for determination of the nucleotide sequence of APC alleles by the polymerase chain reaction.

It is still another object of the invention to provide nucleic acid probes for detection of mutations in the human APC gene.

It is still another object of the invention to provide a cDNA molecule encoding the APC gene product.

It is yet another object of the invention to provide a preparation of the human APC protein.

It is another object of the invention to provide a method of screening for genetic predisposition to cancer.

It is an object of the invention to provide methods of testing therapeutic agents for the ability to suppress neoplasia.

It is still another object of the invention to provide animals carrying mutant APC alleles.

These and other objects of the invention are provided by one or more of the embodiments which are described below. In one embodiment of the present invention a method of diagnosing or prognosing a neoplastic tissue of a human is provided comprising: detecting somatic alteration of wild-type APC genes or their expression products in a sporadic colorectal cancer tissue, said alteration indicating neoplasia of the tissue.

In yet another embodiment a method is provided of detecting genetic predisposition to cancer in a human including familial adenomatous polyposis (FAP) and Gardner's Syndrome (GS), comprising: isolating a human sample selected from the group consisting of blood and fetal tissue; detecting alteration of wild-type APC gene coding sequences or their expression products from the sample, said alteration indicating genetic predisposition to cancer.

In another embodiment of the present invention a method is provided for supplying wild-type APC gene function to a cell which has lost said gene function by virtue of a mutation in the APC gene, comprising: introducing a wild-type APC gene into a cell which has lost said gene function such that said wild-type gene is expressed in the cell.

In another embodiment a method of supplying wild-type APC gene function to a cell is provided comprising: introducing a portion of a wild-type APC gene into a cell which has lost said gene function such that said portion is expressed in the cell, said portion encoding a part of the APC protein which is required for non-neoplastic growth of said cell. APC protein can also be applied to cells or administered

to animals to remediate for mutant APC genes. Synthetic peptides or drugs can also be used to mimic APC function in cells which have altered APC expression.

In yet another embodiment a pair of single stranded primers is provided for determination of the nucleotide sequence of the APC gene by polymerase chain reaction. The sequence of said pair of single stranded DNA primers is derived from chromosome 5q band 21, said pair of primers allowing synthesis of APC gene coding sequences.

In still another embodiment of the invention a nucleic acid probe is provided which is complementary to human wild-type APC gene coding sequences and which can form mismatches with mutant APC genes, thereby allowing their detection by enzymatic or chemical cleavage or by shifts in electrophoretic mobility.

In another embodiment of the invention a method is provided for detecting the presence of a neoplastic tissue in a human. The method comprises isolating a body sample from a human; detecting in said sample alteration of a wild-type APC gene sequence or wild-type APC expression product, said alteration indicating the presence of a neoplastic tissue in the human.

In still another embodiment a cDNA molecule is provided which comprises the coding sequence of the APC gene.

In even another embodiment a preparation of the human APC protein is provided which is substantially free of other human proteins. The amino acid sequence of the protein is shown in [FIG. 3 or 7] FIGS. 3A-3C or 7A-7W (SEQ ID NOS: 7 and 2).

In yet another embodiment of the invention a method is provided for screening for genetic predisposition to cancer, including familial adenomatous polyposis (FAP) and Gardner's Syndrome (GS), in a human. The method comprises: detecting among kindred persons the presence of a DNA polymorphism which is linked to a mutant APC allele in an individual having a genetic predisposition to cancer, said kindred being genetically related to the individual, the presence of said polymorphism suggesting a predisposition to cancer.

In another embodiment of the invention a method of testing therapeutic agents for the ability to suppress a neoplastically transformed phenotype is provided. The method comprises: applying a test substance to a cultured epithelial cell which carries a mutation in an APC allele; and determining whether said test substance suppresses the neoplastically transformed phenotype of the cell.

In another embodiment of the invention a method of testing therapeutic agents for the ability to suppress a neoplastically transformed phenotype is provided. The method comprises: administering a test substance to an animal which carries a mutant APC allele; and determining whether said test substance prevents or suppresses the growth of tumors.

In still other embodiments of the invention transgenic animals are provided. The animals carry a mutant APC allele from a second animal species or have been genetically engineered to contain an insertion mutation which disrupts an APC allele.

The present invention provides the art with the information that the APC gene, a heretofore unknown gene is, in fact, a target of mutational alterations on chromosome 5q21 and that these alterations are associated with the process of tumorigenesis. This information allows highly specific assays to be performed to assess the neoplastic status of a particular tissue or the predisposition to cancer of an indi-

vidual. This invention has applicability to Familial Adenomatous Polyposis, sporadic colorectal cancers, Gardner's Syndrome, as well as the less severe familial polyposis discussed above.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1A shows an overview of yeast artificial chromosome (YAC) contigs (contiguous stretches of sequence). Genetic distances between selected RFLP markers from within the contigs are shown in centiMorgans.

[FIG. 1B shows] FIGS. 1B-1I, and -1II show a detailed map of the three central contigs. The position of the six identified genes from within the FAP region is shown; the 5' and 3' ends of the transcripts from these genes have in general not yet been isolated, as indicated by the string of dots surrounding the bars denoting the genes positions. Selected restriction endonuclease recognition sites are indicated. B, BssH2; S, SstII; M, MluI; N, NruI.

FIG. 2 shows the sequence of TB1 (SEQ ID NO: 5) and TB2 (SEQ ID NO: 6) genes. The cDNA sequence of the TB1 gene was determined from the analysis of 11 cDNA clones derived from normal colon and liver, as described in the text. A total of 2314 bp were contained within the overlapping cDNA clones, defining an ORF of 424 amino acids beginning at nucleotide 1. Only the predicted amino acids from the ORF are shown. The carboxy-terminal end of the ORF has apparently been identified, but the 5' end of the TB1 transcript has not yet been precisely determined.

The cDNA sequence of the TB2 gene was determined from the YS-39 clone derived as described in the text. This clone consisted of 2300 bp and defined an ORF of 185 amino acids beginning at nucleotide 1. Only the predicted amino acids are shown. The carboxy terminal end of the ORF has apparently been identified, but the 5' end of the TB2 transcript has not been precisely determined.

[FIG. 3 shows] FIGS. 3A-3C (collectively, FIG. 3) show the sequence of the APC gene product (SEQ ID NO: 7). The cDNA sequence was determined through the analysis of 87 cDNA clones derived from normal colon, liver, and brain. A total of 8973 bp were contained within overlapping cDNA clones, defining an ORF of [2842] 2843 amino acids. In frame stop codons surrounded this ORF, as described in the text, suggesting that the entire APC gene product was represented in the ORF illustrated. Only the predicted amino acids are shown.

FIG. 4 shows the local similarity between human APC (SEQ ID NO: 2) and ral2 (SEQ ID NO: 8) of yeast. Local similarity among the APC (SEQ ID NO: 2) and MCC genes (SEQ ID NO: 10) and the m3 muscarinic acetylcholine receptor (SEQ ID NO: 9) is shown. The region of the mAChR shown corresponds to that responsible for coupling the receptor to G proteins. The connecting lines indicate identities; dots indicate related amino acids residues.

FIG. 5 shows the genomic map of the 1200 kb NotI fragment at the FAP locus. The NotI fragment is shown as a bold line. Relevant parts of the deletion chromosomes from patients 3214 and 3824 are shown as stippled lines. Probes used to characterize the NotI fragment and the deletions, and three YACs from which subclones were obtained, are shown below the restriction map. The chimeric end of YAC 183H12 is indicated by a dotted line. The orientation and approximate position of MCC are indicated above the map.

FIG. 6 shows the DNA sequence (SEQ ID NO: 3) and predicted amino acid sequence of DP1 (TB2) (SEQ ID NO: 4). The nucleotide numbering begins at the most 5' nucle-

otide isolated. A proposed initiation methionine (base 77) is indicated in bold type. The entire coding sequence is presented.

[FIG. 7 shows] FIGS. 7A–7W (collectively, FIG. 7) show the cDNA (SEQ ID NO: 1) and predicted amino acid sequence of DP2.5 (APC) (SEQ ID NO: 2). The nucleotide numbering begins at the proposed initiation methionine. The nucleotides and amino acids of the alternatively spliced exon (exon 9; nucleotide positions [934–1236] 957–1259) are presented in lower case letters. At the 3' end, a poly(A) addition signal occurs at 9530, and one cDNA clone has a poly(A) at 9563. Other cDNA clones extend beyond 9563, however, and their consensus sequence is included here.

FIG. 8 shows the arrangement of exons in DP2.5 (APC) (A) FIG. 8A. Exon 9 corresponds to nucleotides 933–1312; exon 9a corresponds to nucleotides 1236–1312. The stop codon in the cDNA is at nucleotide 8535. (B) FIG. 8B Partial intronic sequence surrounding each exon is shown (SEQ ID NOS: 11–38). 5'intron sequences of exons 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, and 15 are shown in SEQ ID NOS: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, respectively, 3'intron sequences of exons 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, and 14 are shown in SEQ ID NOS: 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, respectively.

DETAILED DESCRIPTION

It is a discovery of the present invention that mutational events associated with tumorigenesis occur in a previously unknown gene on chromosome 5q named here the APC (Adenomamus Polyposis Coli) gene. Although it was previously known that deletion of alleles on chromosome 5q were common in certain types of cancers, it was not known that a target gene of these deletions was the APC gene. Further it was not known that other types of mutational events in the APC gene are also associated with cancers. The mutations of the APC gene can involve gross rearrangements, such as insertions and deletions. Point mutations have also been observed.

According to the diagnostic and prognostic method of the present invention, alteration of the wild-type APC gene is detected. "Alteration of a wild-type gene" according to the present invention encompasses all forms of mutations—including deletions. The alteration may be due to either rearrangements such as insertions, inversions, and deletions, or to point mutations. Deletions may be of the entire gene or only a portion of the gene. Somatic mutations are those which occur only in certain tissues, e.g., in the tumor tissue, and are not inherited in the germline. Germline mutations can be found in any of a body's tissues. If only a single allele is somatically mutated, an early neoplastic state is indicated. However, if both alleles are mutated then a late neoplastic state is indicated. The finding of APC mutations thus provides both diagnostic and prognostic information. An APC allele which is not deleted (e.g., that on the sister chromosome to a chromosome carrying an APC deletion) can be screened for other mutations, such as insertions, small deletions, and point mutations. It is believed that many mutations found in tumor tissues will be those leading to decreased expression of the APC gene product. However, mutations leading to non-functional gene products would also lead to a cancerous state. Point mutational events may occur in regulatory regions, such as in the promoter of the gene, leading to loss or diminution of expression of the mRNA. Point mutations may also abolish proper RNA processing, leading to loss of expression of the APC gene product.

In order to detect the alteration of the wild-type APC gene in a tissue, it is helpful to isolate the tissue free from surrounding normal tissues. Means for enriching a tissue preparation for tumor cells are known in the art. For example, the tissue may be isolated from paraffin or cryostat sections. Cancer cells may also be separated from normal cells by flow cytometry. These as well as other techniques for separating tumor from normal cells are well known in the art. If the tumor tissue is highly contaminated with normal cells detection of mutations is more difficult.

Detection of point mutations may be accomplished by molecular cloning of the APC allele (or alleles) and sequencing that allele(s) using techniques well known in the art. Alternatively, the polymerase chain reaction (PCR) can be used to amplify gene sequences directly from a genomic DNA preparation from the tumor tissue. The DNA sequence of the amplified sequences can then be determined. The polymerase chain reaction itself is well known in the art. See, e.g., Saiki et al., Science, Vol. 239, p. 487, 1988; U.S. Pat. No. 4,683,203; and U.S. Pat. No. 4,683,195. Specific primers which can be used in order to amplify the gene will be discussed in more detail below. The ligase chain reaction, which is known in the art, can also be used to amplify APC sequences. See Wu et al., Genomics, Vol. 4, pp. 560–569 (1989). In addition, a technique known as allele specific PCR can be used. (See Ruano and Kidd, Nucleic Acids Research, Vol. 17, p. 8392, 1989.) According to this technique, primers are used which hybridize at their 3' ends to a particular APC mutation. If the particular APC mutation is not present, an amplification product is not observed. Amplification Refractory Mutation System (ALUMS) can also be used as disclosed in European Patent Application Publication No. 0332435 and in Newton et al., Nucleic Acids Research, Vol. 17, p.7, 1989. Insertions and deletions of genes can also be detected by cloning, sequencing and amplification. In addition, restriction fragment length polymorphism (RFLP) probes for the gene or surrounding marker genes can be used to score alteration of an allele or an insertion in a polymorphic fragment. Such a method is particularly useful for screening among kindred persons of an affected individual for the presence of the APC mutation found in that individual. Single stranded conformation polymorphism (SSCP) analysis can also be used to detect base change variants of an allele. (Orita et al., Proc. Natl. Acad. Sci. USA Vol. 86, pp. 2766–2770, 1989, and Genomics, Vol. 5, pp. 874–879, 1989.) Other techniques for detecting insertions and deletions as are known in the art can be used.

Alteration of wild-type genes can also be detected on the basis of the alteration of a wild-type expression product of the gene. Such expression products include both the APC mRNA as well as the APC protein product. The sequences of these products are shown in [FIGS. 3 and 7] FIGS. 3A–3C and 7A–7W. Point mutations may be detected by amplifying and sequencing the mRNA or via molecular cloning of cDNA made from the mRNA. The sequence of the cloned cDNA can be determined using DNA sequencing techniques which are well known in the art. The cDNA can also be sequenced via the polymerase chain reaction (PCR) which will be discussed in more detail below.

Mismatches, according to the present invention are hybridized nucleic acid duplexes which are not 100% homologous. The lack of total homology may be due to deletions, insertions, inversions, substitutions or frameshift mutations. Mismatch detection can be used to detect point mutations in the gene or its mRNA product. While these techniques are less sensitive than sequencing, they are simpler to perform on a large number of tumor samples. An

example of a mismatch cleavage technique is the RNase protection method, which is described in detail in Winter et al., Proc. Natl. Acad. Sci. USA, Vol. 82, p. 7575, 1985 and Meyers et al., Science, Vol. 230, p. 1242, 1985. In the practice of the present invention the method involves the use of a labeled riboprobe which is complementary to the human wild-type AIsC gene coding sequence. The riboprobe and either mRNA or DNA isolated from the tumor tissue are annealed (hybridized) together and subsequently digested with the enzyme RNase A which is able to detect some mismatches in a duplex RNA structure. If a mismatch is detected by RNase A, it cleaves at the site of the mismatch. Thus, when the annealed RNA preparation is separated on an electrophoretic gel matrix, if a mismatch has been detected and cleaved by RNase A, an RNA product will be seen which is smaller than the full-length duplex RNA for the riboprobe and the mRNA or DNA. The riboprobe need not be the full length of the ArC mRNA or gene but can be a segment of either. If the riboprobe comprises only a segment of the ArC mRNA or gene it will be desirable to use a number of these probes to screen the whole mRNA sequence for mismatches.

In similar fashion, DNA probes can be used to detect mismatches, through enzymatic or chemical cleavage. See, e.g., Cotton et al., Proc. Natl. Acad. Sci. USA, Vol. 85, 4397, 1988; and Shenk et al., Proc. Natl. Acad. Sci. USA, Vol. 72, p. 989, 1975. Alternatively, mismatches can be detected by shifts in the electrophoretic mobility of mismatched duplexes relative to matched duplexes. See, e.g., Cariello, Human Genetics, Vol. 42, p. 726, 1988. With either riboprobes or DNA probes, the cellular mRNA or DNA which might contain a mutation can be amplified using PCR (see below) before hybridization. Changes in DNA of the ArC gene can also be detected using Southern hybridization, especially if the changes are gross rearrangements, such as deletions and insertions.

DNA sequences of the APC gene which have been amplified by use of polymerase chain reaction may also be screened using allele-specific probes. These probes are nucleic acid oligomers, each of which contains a region of the APC gene sequence harboring a known mutation. For example, one oligomer may be about 30 nucleotides in length, corresponding to a portion of the APC gene sequence. By use of a battery of such allele-specific probes, PCR amplification products can be screened to identify the presence of a previously identified mutation in the APC gene. Hybridization of allele-specific probes with amplified APC sequences can be performed, for example, on a nylon filter. Hybridization to a particular probe under stringent hybridization conditions indicates the presence of the same mutation in the tumor tissue as in the allele-specific probe.

Alteration of APC mRNA expression can be detected by any technique known in the art. These include Northern blot analysis, PCR amplification and RNase protection. Diminished mRNA expression indicates an alteration of the wild-type APC gene.

Alteration of wild-type APC genes can also be detected by screening for alteration of wild-type APC protein. For example, monoclonal antibodies immunoreactive with APC can be used to screen a tissue. Lack of cognate antigen would indicate an APC mutation. Antibodies specific for products of mutant alleles could also be used to detect mutant APC gene product. Such immunological assays can be done in any convenient format known in the art. These include Western blots, immunohistochemical assays and ELISA assays. Any means for detecting an altered APC protein can be used to detect alteration of wild-type APC

genes. Functional assays can be used, such as protein binding determinations. For example, it is believed that APC protein oligomerizes to itself and/or MCC protein or binds to a G protein. Thus, an assay for the ability to bind to wild type APC or MCC protein or that G protein can be employed. In addition, assays can be used which detect APC biochemical function. It is believed that APC is involved in phospholipid metabolism. Thus, assaying the enzymatic products of the involved phospholipid metabolic pathway can be used to determine APC activity. Finding a mutant APC gene product indicates alteration of a wild-type APC gene.

Mutant APC genes or gene products can also be detected in other human body samples, such as, serum, stool, urine and sputum. The same techniques discussed above for detection of mutant APC genes or gene products in tissues can be applied to other body samples. Cancer cells are sloughed off from tumors and appear in such body samples. In addition, the APC gene product itself may be secreted into the extracellular space and found in these body samples even in the absence of cancer cells. By screening such body samples, a simple early diagnosis can be achieved for many types of cancers. In addition, the progress of chemotherapy or radiotherapy can be monitored more easily by testing such body samples for mutant APC genes or gene products.

The methods of diagnosis of the present invention are applicable to any tumor in which APC has a role in tumorigenesis. Deletions of chromosome arm 5q have been observed in tumors of lung, breast, colon, rectum, bladder, liver, sarcomas, stomach and prostate, as well as in leukemias and lymphomas. Thus these are likely to be tumors in which APC has a role. The diagnostic method of the present invention is useful for clinicians so that they can decide upon an appropriate course of treatment. For example, a tumor displaying alteration of both APC alleles might suggest a more aggressive therapeutic regimen than a tumor displaying alteration of only one APC allele.

The primer pairs of the present invention are useful for determination of the nucleotide sequence of a particular APC allele using the polymerase chain reaction. The pairs of single stranded DNA primers can be annealed to sequences within or surrounding the APC gene on chromosome 5q in order to prime amplifying DNA synthesis of the APC gene itself. A complete set of these primers allows synthesis of all of the nucleotides of the APC gene coding sequences, i.e., the exons. The set of primers preferably allows synthesis of both intron and exon sequences. Allele specific primers can also be used. Such primers anneal only to particular APC mutant alleles, and thus will only amplify a product in the presence of the mutant allele as a template.

In order to facilitate subsequent cloning of amplified sequences, primers may have restriction enzyme site sequences appended to their 5' ends. Thus, all nucleotides of the primers are derived from APC sequences or sequences adjacent to APC except the few nucleotides necessary to form a restriction enzyme site. Such enzymes and sites are well known in the art. The primers themselves can be synthesized using techniques which are well known in the art. Generally, the primers can be made using oligonucleotide synthesizing machines which are commercially available. Given the sequence of the APC open reading frame shown in [FIG. 7] FIGS. 7A-7W (SEQ ID NO: 1), design of particular primers is well within the skill of the art.

The nucleic acid probes provided by the present invention are useful for a number of purposes. They can be used in Southern hybridization to genomic DNA and in the RNase

protection method for detecting point mutations already discussed above. The probes can be used to detect PCR amplification products. They may also be used to detect mismatches with the APC gene or mRNA using other techniques. Mismatches can be detected using either enzymes (e.g., S1 nuclease), chemicals (e.g., hydroxylamine or osmium tetroxide and piperidine), or changes in electrophoretic mobility of mismatched hybrids as compared to totally matched hybrids. These techniques are known in the art. See, Cotton, supra, Shenk, supra, Myers, supra, Winter, supra, and Novack et al., Proc. Natl. Acad. Sci. USA, Vol. 83, p. 586, 1986. Generally, the probes are complementary to APC gene coding sequences, although probes to certain introns are also contemplated. An entire battery of nucleic acid probes is used to compose a kit for detecting alteration of wild-type APC genes. The kit allows for hybridization to the entire APC gene. The probes may overlap with each other or be contiguous.

If a riboprobe is used to detect mismatches with mRNA, it is complementary to the mRNA of the human wild-type APC gene. The riboprobe thus is an anti-sense probe in that it does not code for the APC protein because it is of the opposite polarity to the sense strand. The riboprobe generally will be labeled with a radioactive, colorimetric, or fluorometric material, which can be accomplished by any means known in the art. If the riboprobe is used to detect mismatches with DNA it can be of either polarity, sense or anti-sense. Similarly, DNA probes also may be used to detect mismatches.

Nucleic acid probes may also be complementary to mutant alleles of the APC gene. These are useful to detect similar mutations in other patients on the basis of hybridization rather than mismatches. These are discussed above and referred to as allele-specific probes. As mentioned above, the APC probes can also be used in Southern hybridizations to genomic DNA to detect gross chromosomal changes such as deletions and insertions. The probes can also be used to select cDNA clones of APC genes from tumor and normal tissues. In addition, the probes can be used to detect APC mRNA in tissues to determine if expression is diminished as a result of alteration of wild-type APC genes. Provided with the APC coding sequence shown in [FIG. 7] FIGS. 7A-7W (SEQ ID NO:1), design of particular probes is well within the skill of the ordinary artisan.

According to the present invention a method is also provided of supplying wild-type APC function to a cell which carries mutant APC alleles. Supplying such function should suppress neoplastic growth of the recipient cells. The wild-type APC gene or a part of the gene may be introduced into the cell in a vector such that the gene remains extrachromosomal. In such a situation the gene will be expressed by the cell from the extrachromosomal location. If a gene portion is introduced and expressed in a cell carrying a mutant APC allele, the gene portion should encode a part of the APC protein which is required for non-neoplastic growth of the cell. More preferred is the situation where the wild-type APC gene or a part of it is introduced into the mutant cell in such a way that it recombines with the endogenous mutant APC gene present in the cell. Such recombination requires a double recombination event which results in the correction of the APC gene mutation. Vectors for introduction of genes both for recombination and for extrachromosomal maintenance are known in the art and any suitable vector may be used. Methods for introducing DNA into cells such as electroporation, calcium phosphate co-precipitation and viral transduction are known in the art and the choice of method is within the competence of the routineer. Cells

transformed with the wild-type APC gene can be used as model systems to study cancer remission and drug treatments which promote such remission.

Similarly, cells and animals which carry a mutant APC allele can be used as model systems to study and test for substances which have potential as therapeutic agents. The cells are typically cultured epithelial cells. These may be isolated from individuals with APC mutations, either somatic or germline. Alternatively, the cell line can be engineered to carry the mutation in the APC allele. After a test substance is applied to the cells, the neoplastically transformed phenotype of the cell will be determined. Any trait of neoplastically transformed cells can be assessed, including anchorage-independent growth, tumorigenicity in nude mice, invasiveness of cells, and growth factor dependence. Assays for each of these traits are known in the art.

Animals for testing therapeutic agents can be selected after mutagenesis of whole animals or after treatment of germline cells or zygotes. Such treatments include insertion of mutant APC alleles, usually from a second animal species, as well as insertion of disrupted homologous genes. Alternatively, the endogenous APC gene(s) of the animals may be disrupted by insertion or deletion mutation. After test substances have been administered to the animals, the growth of tumors must be assessed. If the test substance prevents or suppresses the growth of tumors, then the test substance is a candidate therapeutic agent for the treatment of FAP and/or sporadic cancers.

Polypeptides which have APC activity can be supplied to cells which carry mutant or missing APC alleles. The sequence of the APC protein is disclosed in [FIG. 3 or 7 (SEQ ID NO:7 or 1)] FIGS. 3A-3C and 7A-7W (SEQ ID NOS: 2 or 7). [These two sequences differ slightly and appear to indicate the existence of two different forms of the APC protein.] Protein can be produced by expression of the cDNA sequence in bacteria, for example, using known expression vectors. Alternatively, APC can be extracted from APC-producing mammalian cells such as brain cells. In addition, the techniques of synthetic chemistry can be employed to synthesize APC protein. Any of such techniques can provide the preparation of the present invention which comprises the APC protein. The preparation is substantially free of other human proteins. This is most readily accomplished by synthesis in a microorganism or in vitro.

Active APC molecules can be introduced into cells by microinjection or by use of liposomes, for example. Alternatively, some such active molecules may be taken up by cells, actively or by diffusion. Extracellular application of APC gene product may be sufficient to affect tumor growth. Supply of molecules with APC activity should lead to a partial reversal of the neoplastic state. Other molecules with APC activity may also be used to effect such a reversal, for example peptides, drugs, or organic compounds.

The present invention also provides a preparation of antibodies immunoreactive with a human APC protein. The antibodies may be polyclonal or monoclonal and may be raised against native APC protein, APC fusion proteins, or mutant APC proteins. The antibodies should be immunoreactive with APC epitopes, preferably epitopes not present on other human proteins. In a preferred embodiment of the invention the antibodies will immunoprecipitate APC proteins from solution as well as react with APC protein on Western or immunoblots of polyacrylamide gels. In another preferred embodiment, the antibodies will detect APC proteins in paraffin or frozen tissue sections, using immunocytochemical techniques. Techniques for raising and purifying

antibodies are well known in the art and any such techniques may be chosen to achieve the preparation of the invention.

Predisposition to cancers as in FAP and GS can be ascertained by testing any tissue of a human for mutations of the APC gene. For example, a person who has inherited a germline APC mutation would be prone to develop cancers. This can be determined by testing DNA from any tissue of the person's body. Most simply, blood can be drawn and DNA extracted from the cells of the blood. In addition, prenatal diagnosis can be accomplished by testing fetal cells, placental cells, or amniotic fluid for mutations of the APC gene. Alteration of a wild-type APC allele, whether for example, by point mutation or by deletion, can be detected by any of the means discussed above.

Molecules of cDNA according to the present invention are intron-free, APC gene coding molecules. They can be made by reverse transcriptase using the APC mRNA as a template. These molecules can be propagated in vectors and cell lines as is known in the art. Such molecules have the sequence shown in SEQ ID NO: 7. The cDNA can also be made using the techniques of synthetic chemistry given the sequence disclosed herein.

A short region of homology has been identified between APC and the human m3 muscarinic acetylcholine receptor (mAChR). This homology was largely confined to 29 residues in which 6 out of 7 amino acids (EL(GorA)GLQA) were identical (See FIG. 4 (SEQ ID NO: 9)). Initially, it was not known whether this homology was significant, because many other proteins had higher levels of global homology (though few had six out of seven contiguous amino acids in common). However, a study on the sequence elements controlling G protein activation by mAChR subtypes (Lechleiter et al., EMBO J., p. 4381 (1990)) has shown that a 21 amino acid region from the m3 mAChR completely mediated G protein specificity when substituted for the 21 amino acids of m2 mAChR at the analogous protein position. These 21 residues overlap the 19 amino acid homology between APC and m3 mAChR.

This connection between APC and the G protein activating region of mAChR is intriguing in light of previous investigations relating G proteins to cancer. For example, the RAS oncogenes, which are often mutated in colorectal cancers (Vogelstein, et al., N. Engl. J. Med., Vol. 319, p. 525 (1988); Bos et al., Nature Vol. 327, p. 293 (1987)), are members of the G protein family (Bourne, et al., Nature, Vol. 348, p. 125 (1990)) as is an in vitro transformation suppressor (Noda et al., Proc. Natl. Acad. Sci. USA, Vol. 86, p. 162 (1989)) and genes mutated in hormone producing tumors (Candis et al., Nature, Vol. 340, p. 692 (1989); Lyons et al., Science, Vol. 249, p. 655 (1990)). Additionally, the gene responsible for neurofibromatosis (presumably a tumor suppressor gene) has been shown to activate the GTPase activity of RAS (Xu et al., Cell, Vol. 63, p. 835 (1990); Martin et al., Cell, Vol. 63, p. 843 (1990); Ballester et al., Cell, Vol. 63, p. 851 (1990)). Another interesting link between G proteins and colon cancer involves the drug sulindae. This agent has been shown to inhibit the growth of benign colon tumors in patients with FAP, presumably by virtue of its activity as a cyclooxygenase inhibitor (Waddell et al., J. Surg. Oncology 24(1), 83 (1983); Waddell, et al., Am. J. Surg., 157(1), 175 (1989); Charneau et al., Gastroenterologie Clinique at Biologique 14(2), 153 (1990)). Cyclooxygenase is required to convert arachidonic acid to prostaglandins and other biologically active molecules. G proteins are known to regulate phospholipase A2 activity, which generates arachidonic acid from phospholipids (Role et al., Proc. Natl. Acad. Sci. USA, Vol. 84, p. 3623 (1987); Kurachi

et al., Nature, Vol. 337, 12 555 (1989)). Therefore we propose that wild-type APC protein functions by interacting with a G protein and is involved in phospholipid metabolism.

The following are provided for exemplification purposes only and are not intended to limit the scope of the invention which has been described in broad terms above.

EXAMPLE 1

This example demonstrates the isolation of a 5.5 Mb region of human DNA linked to the FAP locus. Six genes are identified in this region, all of which are expressed in normal colon cells and in colorectal, lung, and bladder tumors.

The cosmid markers YN5.64 and YN5.48 have previously been shown to delimit an 8 cM region containing the locus for FAP (Nakamura et al., Am. J. Hum. Genet. Vol. 43, p. 638 (1988)). Further linkage and pulse-field gel electrophoresis (PFGE) analysis with additional markers has shown that the FAP locus is contained within a 4 cM region bordered by cosmids EF5.44 and L5.99. In order to isolate clones representing a significant portion of this locus, a yeast artificial chromosome (YAC) library was screened with various 5q21 markers. Twenty-one YAC clones, distributed within six contigs and including 5.5 Mb from the region between YN5.64 and YN5.48, were obtained (FIG. 1A).

Three contigs encompassing approximately 4 Mb were contained within the central portion of this region. The YAC's constituting these contigs, together with the markers used for their isolation and orientations, are shown in FIG. 1. These YAC contigs were obtained in the following way. To initiate each contig, the sequence of a genomic marker cloned from chromosome 5q21 was determined and used to design primers for PCR. PCR was then carried out on pools of YAC clones distributed in microtiter trays as previously described (Anand et al., Nucleic Acids Research, Vol. 18, p. 1951 (1980)). Individual YAC clones from the positive pools were identified by further PCR or hybridization based assays, and the YAC sizes were determined by PFGE.

To extend the areas covered by the original YAC clones, "chromosomal walking" was performed. For this purpose, YAC termini were isolated by a PCR based method and sequenced (Riley et al., Nucleic Acids Research, Vol. 18, p. 2887 (1990)). PCR primers based on these sequences were then used to rescreen the YAC library. For example, the sequence from an intron of the FER gene (Hao et al., Mol. Cell. Biol., Vol. 9, p. 1587 (1989)) was used to design PCR primers for isolation of the 28EC1 and 5EH8 YACs. The termini of the 28EC1 YAC were sequenced to derive markers RHE28 and LHE28, respectively. The sequences of these two markers were then used to isolate YAC clones 15CH12 (from RHE28) and 40CF1 and 29EF1 (from LHE28). These five YAC's formed a config encompassing 1200 kb (contig 1, FIG. 1B).

Similarly, contig 2 was initiated using cosmid N5.66 sequences, and contig 3 was initiated using sequences both from the MCC gene and from cosmid EF5.44. A walk in the telomeric direction from YAC 14FH1 and a walk in the opposite direction from YAC 39GG3 allowed connection of the initial contig 3 clones through YAC 37HG4 (FIG. 1B). YAC37HG4 was deposited at the National Collection of Industrial and Marine Bacteria (NCIMB), P.O. Box 31, 23 St. Machar Drive, Aberdeen AB2 1RY, Scotland, under Accession No. 4035A, FB3 on Dec. 17, 1990.

Multipoint linkage analysis with the various markers used to define the contigs, combined with PFGE analysis, showed that contigs 1 and 2 were centromeric to contig 3. These

contigs were used as tools to orient and/or identify genes which might be responsible for FAP. Six genes were found to lie within this cluster of YAC's, as follows:

Contig #1: FER - The FER gene was discovered through its homology to the vital oncogene ABL (Hao et al., supra). It has an intrinsic tyrosine kinase activity, and in situ hybridization with an FER probe showed that the gene was located at 5q11-23 (Morris et al., Cytogenet. Cell. Genet., Vol. 53, p. 4, (1990)). Because of the potential role of this oncogene-related gene in neoplasia, we decided to evaluate it further with regards to the FAP locus. A human genomic clone from FER was isolated (MF 2.3) and used to define a restriction fragment length polymorphism (RFLP), and the RFLP in turn used to map FER by linkage analysis using a panel of three generation families. This showed that FER was very tightly linked to previously defined polymorphic markers for the FAP locus. The genetic mapping of FER was complemented by physical mapping using the YAC clones derived from FER sequences (FIG. 1B). Analysis of YAC contig 1 showed that FER was within 600 kb of cosmid marker M5.28, which maps to within 1.5 Mb of cosmid L5.99 by PFGE of human germline DNA. Thus, the YAC mapping results were consistent with the FER linkage data and PFGE analyses.

Contig 2:TB1 - TB1 was identified through a cross-hybridization approach. Exons of genes are often evolutionarily conserved while introns and intergenic regions are much less conserved. Thus, if a human probe cross-hybridizes strongly to the DNA from non-primate species, there is a reasonable chance that it contains exon sequences. Subclones of the cosraids shown in FIG. 1 were used to screen Southern blots containing rodent DNA samples. A subclone of cosmid N5.66 (p 5.66-4) was shown to strongly hybridize to rodent DNA, and this clone was used to screen cDNA libraries derived from normal adult colon and fetal liver. The ends of the initial cDNA clones obtained in this screen were then used to extend the cDNA sequence. Eventually, 11 cDNA clones were isolated, covering 2314 bp. The gene detected by these clones was named TB1. Sequence analysis of the overlapping clones revealed an open reading frame (ORF) that extended for 1302 bp starting from the most 5' sequence data obtained (FIG. 2A). If this entire open reading frame were translated, it would encode 434 amino acids (SEQ ID NO: 5). The product of this gene was not globally homologous to any other sequence in the current database but showed two significant local similarities to a family of ADP, ATP carrier/translocator proteins and mitochondrial brown fat uncoupling proteins which are widely distributed from yeast to mammals. These conserved regions of TB1 (underlined in FIG. 2A) may define a predictive motif for this sequence family. In addition, TB1 appeared to contain a signal peptide (or mitochondrial targeting sequence) as well as at least 7 transmembrane domains.

Contig 3: MCC, TB2, SRP and APC - The MCC gene was also discovered through a cross-hybridization approach, as described previously (Kinzler et al., Science Vol. 251, p. 1366 (1991)). The MCC gene was considered a candidate for causing FAP by virtue of its tight genetic linkage to FAP susceptibility and its somatic mutation in sporadic colorectal carcinomas. However, mapping experiments suggested that the coding region of MCC was approximately 50 kb proximal to the centromeric end of a 200 kb deletion found in an FAP patient. MCC cDNA probes detected a 10 kb mRNA transcript on Northern blot analysis of which 4151 bp, including the entire open reading frame, have been cloned. Although the 3' non-translated portion or an alternatively

spliced form of MCC might have extended into this deletion, it was possible that the deletion did not affect the MCC gene product. We therefore used MCC sequences to initiate a YAC contig, and subsequently used the YAC clones to identify genes 50 to 250 kb distal to MCC that might be contained within the deletion.

In a first approach, the insert from YAC24ED6 (FIG. 1B) was radiolabelled and hybridized to a cDNA library from normal colon. One of the cDNA clones (YS39) identified in this manner detected a 3.1 kb mRNA transcript when used as a probe for Northern blot hybridization. Sequence analysis of the YS39 clone revealed that it encompassed 2283 nucleotides and contained an ORF that extended for 555 bp from the most 5' sequence data obtained. If all of this ORF were translated, it would encode 185 amino acids (SEQ ID NO: 6) (FIG. 2B). The gene detected by YS39 was named TB2. Searches of nucleotide and protein databases revealed that the TB2 gene was not identical to any previously reported sequences nor were there any striking similarities.

Another clone (YS11) identified through the YAC 24ED6 screen appeared to contain portions of two distinct genes. Sequences from one end of YS11 were identical to at least 180 bp of the signal recognition particle protein SRP19 (Lingelbach et al. Nucleic Acids Research, Vol. 16, p. 9431 (1988)). A second ORF, from the opposite end of clone YS11, proved to be identical to 78 bp of a novel gene which was independently identified through a second YAC-based approach. For the latter, DNA from yeast cells containing YAC 14FH1 (FIG. 1B) was digested with EcoRI and subcloned into a plasmid vector. Plasmids that contained human DNA fragments were selected by colony hybridization using total human DNA as a probe. These clones were then used to search for cross-hybridizing sequences as described above for TB1, and the cross-hybridizing clones were subsequently used to screen cDNA libraries. One of the cDNA clones discovered in this way (FH38) contained a long ORF (2496 bp), 78 bp of which were identical to the above-noted sequences in YS11. The ends of the FH38 cDNA clone were then used to initiate cDNA walking to extend the sequence. Eventually, 85 cDNA clones were isolated from normal colon, brain and liver cDNA libraries and found to encompass 8973 nucleotides of contiguous transcript. The gene corresponding to this transcript was named APC. When used as probes for Northern blot analysis, APC cDNA clones hybridized to a single transcript of approximately 9.5 kb, suggesting that the great majority of the gene product was represented in the cDNA clones obtained. Sequences from the 5' end of the APC gene were found in YAC 37HG4 but not in YAC 14FH1. However, the 3' end of the APC gene was found in 14FH1 as well as 37HG4. Analogously, the 5' end of the MCC coding region was found in YAC clones 19AA9 and 26GC3 but not 24ED6 or 14FH1, while the 3' end displayed the opposite pattern. Thus, MCC and APC transcription units pointed in opposite directions, with the direction of transcription going from centromeric to telomeric in the case of MCC, and telomeric to centromeric in the case of APC. PFGE analysis of YAC DNA digested with various restriction endonucleases showed that TB2 and SRP were between MCC and APC, and that the 3' ends of the coding regions of MCC and APC were separated by approximately 150 kb (FIG. 1B).

Sequence analysis of the APC cDNA clones revealed an open reading frame of 8,535 nucleotides. The 5' end of the ORF contained a methionine codon (codon 1) that was preceded by an in-frame stop codon 9 bp upstream, and the 3' end was followed by several in-frame stop codons. The protein produced by initiation at codon 1 would contain

[2,842] 2843 amino acids [(FIG. 3)] FIGS. 3A-3C (SEQ ID NO: 7). The results of database searching with the APC gene product were quite complex due to the presence of large segments with locally biased amino acid compositions. In spite of this, APC could be roughly divided into two domains. The N-terminal 25% of the protein had a high content of leucine residues (12%) and showed local sequence similarities to myosins, various intermediate filament proteins (e.g., desmin, vimentin, neurofilaments) and *Drosophila* armadillo/human plakoglobin. The latter protein is a component of adhesive junctions (desmosomes) joining epithelial cells (Franke et al., Proc. Natl. Acad. Sci. U.S.A., Vol. 86, p. 4027 (1989); Perlet et al., Cell, Vol. 63, p. 1167 (1990)) The C-terminal 75% of APC (residues 731- 2832) is 17% serine by composition with serine residues more or less uniformly distributed. This large domain also contains local concentrations of charged (mostly acidic) and proline residues. There was no indication of potential signal peptides, transmembrane regions, or nuclear targeting signals in APC, suggesting a cytoplasmic localization.

To detect short similarities to APC, a database search was performed using the PAM-40 matrix (Altschul. J. Mol. Bio., Vol. 219, p. 555 (1991)). Potentially interesting matches to several proteins were found. The most suggestive of these involved the *ral2* gene product of yeast, which is implicated in the regulation of ras activity (Fukui et al., Mol. Cell. Biol., Vol. 9, p. 5617 (1989)). Little is known about how *ral2* might interact with ras but it is interesting to note the positively-charged character of this region in the context of the negatively-charged GAP interaction region of ras. A specific electrostatic interaction between ras and GAP-related proteins has been proposed.

Because of the proximity of the MCC and APC genes, and the fact that both are implicated in colorectal tumorigenesis, we searched for similarities between the two predicted proteins. Bourne has previously noted that MCC has the potential to form alpha helical coiled coils (Nature, Vol. 351, p. 188 (1991)). Lupas and colleagues have recently developed a program for predicting coiled coil potential from primary sequence data (Science, Vol. 252, p. 1162 (1991)) and we have used their program to analyze both MCC and APC. Analysis of MCC indicated a discontinuous pattern of coiled-coil domains separated by putative "hinge" or "spacer" regions similar to those seen in laminin and other intermediate filament proteins. Analysis of the APC sequence revealed two regions in the N-terminal domain which had strong coiled coil-forming potential, and these regions corresponded to those that showed local similarities with myosin and IF proteins on database searching. In addition, one other putative coiled coil region was identified in the central region of APC. The potential for both APC and MCC to form coiled coils is interesting in that such structures often mediate homo- and hetero-oligomerization.

Finally, it had previously been noted that MCC shared a short similarity with the region of the m3 muscarinic acetylcholine receptor (mAChR) known to regulate specificity of G-protein coupling. The APC gene also contained a local similarity to the region of the m3 mAChR (SEQ ID NO: 9) that overlapped with the MCC similarity (SEQ ID NO: 10) (FIG. 4B). Although the similarities to *ral2* (SEQ ID NO: 8) (FIG. 4A) and m3 mAChR (SEQ ID NO: 9) (FIG. 4B) were not statistically significant, they were intriguing in light of previous observations relating G-proteins to neoplasia.

Each of the six genes described above was expressed in normal colon mucosa, as indicated by their representation in colon cDNA libraries. To study expression of the genes in neoplastic colorectal epithelium, we employed reverse

transcription-polymerase chain reaction (PCR) assays. Primers based on the sequences of FER, TB1, TB2, MCC, and APC were each used to design primers for PCR performed with cDNA templates. Each of these genes was found to be expressed in normal colon, in each of ten cell lines derived from colorectal cancers, and in tumor cell lines derived from lung and bladder tumors. The ten colorectal cancer cell lines included eight from patients with sporadic CRC and two from patients with FAP.

EXAMPLE 2

This example demonstrates a genetic analysis of the role of the FER gene in FAP and sporadic colorectal cancers.

We considered FER as a candidate because of its proximity to the FAP locus as judged by physical and genetic criteria (see Example 1), and its homology to known tyrosine kinases with oncogenic potential. Primers were designed to PCR-amplify the complete coding sequence of FER from the RNA of two colorectal cancer cell lines derived from FAP patients. cDNA was generated from RNA and used as a template for PCR. The primers used were 5'-[AGAAGGATCCCTTGTGTCAGTGTGGA]AGAAGGATCCCTTGTGTCAGTGTGGA-3' (SEQ ID NO: 95) and 5'-GACAGGATCCTGAAGCTGAGTTTG-3' (SEQ ID NO: 96). The underlined nucleotides were altered from the true FER sequence to create BamHI sites. The cell lines used were JW and Dill, both derived from colorectal cancers of FAP patients. (C. Paraskeva, B. G. Buckle, D. Sheer, C. B. Wigley, Int. J. Cancer 34, 49 (1984); M. E. Gross et al., Cancer Res. 51, 1452 (1991)). The resultant 2554 basepair fragments were cloned and sequenced in their entirety. The PCR products were cloned in the BamHI site of Bluescript SK (Stratagene) and pools of at least 50 clones were sequenced en masse using T7 polymerase, as described in Nigro et al., Nature 342,705 (1989).

Only a single conservative amino acid change (GTG-<CTG, creating a val to leu substitution at codon 439) was observed. The region surrounding this codon was then amplified from the DNA of individuals without FAP and this substitution was found to be a common polymorphism, not specifically associated with FAP. Based on these results, we considered it unlikely (though still possible) the FER gene was responsible for FAP. To amplify the regions surrounding codon 439, the following primers were used: 5'-TCAGAAAGTGCTGAAGAG-3' (SEQ ID NO: 97) and 5'-GGAATAATTAGGTCTCCAA-3' (SEQ ID NO: 98). PCR products were digested with PstI, which yields a 50 bp fragment if codon 439 is leucine, but 26 and 24 bp fragments if it is valine. The primers used for sequencing were chosen from the FER cDNA sequence in Hao et al., supra.

EXAMPLE 3

This example demonstrates the genetic analysis of MCC, TB2, SRP and APC in FAP and sporadic colorectal tumors. Each of these genes is linked and encompassed by conrig 3 (see FIG. 1).

Several lines of evidence suggested that this conrig was of particular interest. First, at least three of the four genes in this conrig were within the deleted region identified in two FAP patients. (See Example 5 infra.) Second, allelic deletions of chromosome 5q21 in sporadic cancers appeared to be centered in this region. (Ashton-Rickardt et al., Oncogene, in press; and Miki et al., Jpn. J. Cancer Res., in press.) Some tumors exhibited loss of proximal RFLP markers (up to and potentially including the 5' end of MCC), but no loss of markers distal to MCC. Other tumors exhibited

loss of markers distal to and perhaps including the 3' end of MCC, but no loss of sequences proximal to MCC. This suggested either that different ends of MCC were affected by loss in all such cases, or alternatively, that two genes (one proximal to and perhaps including MCC, the other distal to MCC) were separate targets of deletion. Third, clones from each of the six FAP region genes were used as probes on Southern blots containing tumor DNA from patients with sporadic CRC. Only two examples of somatic changes were observed in over 200 tumors studied: a rearrangement/deletion whose centromeric end was located within the MCC gene (Kinzler et al., supra) and an 800 bp insertion within the APC gene between nucleotides 4424 and 5584. Fourth, point mutations of MCC were observed in two tumors (Kinzler et al.) supra strongly suggesting that MCC was a target of mutation in at least some sporadic colorectal cancers.

Based on these results, we attempted to search for subtle alterations of conrig 3 genes in patients with FAP. We chose to examine MCC and APC, rather than TB2 or SRP, because of the somatic mutations in MCC and APC noted above. To facilitate the identification of subtle alterations, the genomic sequences of MCC and APC exons were determined (see Table I; *SEQ ID NOS: 24-38*). These sequences were used to design primers for PCR analysis of constitutional DNA from FAP patients.

We first amplified eight exons and surrounding introns of the MCC gene in affected individuals from 90 different FAP kindreds. The PCR products were analyzed by a ribonuclease (RNase) protein assay. In brief, the PCR products were hybridized to in vitro transcribed RNA probes representing the normal genomic sequences. The hybrids were digested with RNase A, which can cleave at single base pair mismatches within DNA-RNA hybrids, and the cleavage products were visualized following denaturing gel electrophoresis. Two separate RNase protection analyses were performed for each exon, one with the sense and one with the antisense strand. Under these conditions, approximately 40% of all mismatches are detectable. Although some amino acid variants of MCC were observed in FAP patients, all such variants were found in a small percentage of normal individuals. These variants were thus unlikely to be responsible for the inheritance of FAP.

We next examined three exons of the APC gene. The three exons examined included those containing nt 822-930, 931-1309, and the first 300 nt of the most distal exon (nt 1956-2256). PCR and RNase protection analysis were performed as described in Kinzler et al. supra, using the primers underlined in Table I (*SEQ ID NO: 24-38*). The primers for nt 1956-2256 were 5'-GCAAATCCTAAGAGAGAACAA-3' (*SEQ ID NO: 99*) and 5'-GATGGCAAGCTTGAGCCAG-3' (*SEQ ID NO: 100*).

In 90 kindreds, the RNase protection method was used to screen for mutations and in an additional 13 kindreds, the PCR products were cloned and sequenced to search for mutations not detectable by RNase protection. PCR products were cloned into a Bluescript vector modified as described in T. A. Holton and M. W. Graham, *Nucleic Acids Res.* 19, 1156 (1991). A minimum of 100 clones were pooled and sequenced. Five variants were detected among the 103 kindreds analyzed. Cloning and subsequent DNA sequencing of the PCR product of patient P21 indicated a C to T transition in codon 413 that resulted in a change from arginine to cysteine. This amino acid variant was not observed in any of 200 DNA samples from individuals without FAP. Cloning and sequencing of the PCR product from patients P24 and P34, who demonstrated the same

abnormal RNase protection pattern indicated that both had a C to T transition at codon 301 that resulted in a change from arginine (CGA) to a stop codon (TGA). This change was not present in 200 individuals without FAP. As this point mutation resulted in the predicted loss of the recognition site for the enzyme Taq I, appropriate PCR products could be digested with Taq I to detect the mutation. This allowed us to determine that the stop codon co-segregated with disease phenotype in members of the family of P24. The inheritance of this change in affected members of the pedigree provides additional evidence for the importance of the mutation.

Cloning and sequencing of the PCR product from FAP patient P93 indicated a C to G transversion at codon 279, also resulting in a stop codon (change from TCA to TGA). This mutation was not present in 200 individuals without FAP. Finally, one additional mutation resulting in a serine (TCA) to stop codon (TGA) at codon 712 was detected in a single patient with FAP (patient P60).

The five germline mutations identified are summarized in Table IIA, as well as four others discussed in Example 9. In addition to these germline mutations, we identified several somatic mutations of MCC and APC in sporadic CRC's. Seventeen MCC exons were examined in 90 sporadic colorectal cancers by RNase protection analysis. In each case where an abnormal RNase protection pattern was observed, the corresponding PCR products were cloned and sequenced. This led to the identification of six point mutations (two described previously) (Kinzler et al., supra), each of which was not found in the germline of these patients (Table IIB). Four of the mutations resulted in amino acid substitutions and two resulted in the alteration of splice site consensus elements. Mutations at analogous splice site positions in other genes have been shown to alter RNA processing in vivo and in vitro.

Three exons of APC were also evaluated in sporadic tumors. Sixty tumors were screened by RNase protection, and an additional 98 tumors were evaluated by sequencing. The exons examined included nt 822-930, 931-1309, and 1406-1545 (Table I). A total of three mutations were identified, each of which proved to be somatic. Tumor T27 contained a somatic mutation of C GA (arginine) to TGA (stop codon) at codon 33. Tumor T135 contained a GT to GC change at a splice donor site. Tumor T34 contained a 5 bp insertion (CAGCC between codons 288 and 289) resulting in a stop at codon 291 due to a frameshift.

We serendipitously discovered one additional somatic mutation in a colorectal cancer. During our attempt to define the sequences and splice patterns of the MCC and APC gene products in colorectal epithelial cells, we cloned cDNA from the colorectal cancer cell line SW480. The amino acid sequence of the MCC gene from SW480 was identical to that previously found in clones from human brain. The sequence of APC in SW480 cells, however, differed significantly, in that a transition at codon 1338 resulted in a change from glutamine (CAG) to a stop codon (TAG). To determine if this mutation was somatic, we recovered DNA from archival paraffin blocks of the original surgical specimen (T201) from which the tumor cell line was derived 28 years ago.

DNA was purified from paraffin sections as described in S. E. Goelz, S. R. Hamilton, and B. Vogelstein. *Biochem. Biophys. Res. Comm.* 130, 118 (1985). PCR was performed using the primers 5'-GTTCCAGCAGTGTCACAG-3' (*SEQ ID NO: 101*) and 5'-GGGAGATTTTCGCTCCTGA-3' (*SEQ ID NO: 102*). A PCR product containing codon 1338 was amplified from the archival DNA and used to show that the

stop codon represented a somatic mutation present in the original primary tumor and in cell lines derived from the primary and metastatic tumor sites, but not from normal tissue of the patient.

The ten point mutations in the MCC and APC genes so far discovered in sporadic CRCs are summarized in Table IIB. Analysis of the number of mutant and wild-type PCR clones obtained from each of these tumors showed that in eight of the ten cases, the wild-type sequence was present in approximately equal proportions to the mutant. This was confirmed by RFLP analysis using flanking markers from chromosome 5q which demonstrated that only two of the ten tumors (T135 and T201) exhibited an allelic deletion on chromosome 5q. These results are consistent with previous observations showing that 20–40% of sporadic colorectal tumors had allelic deletions of chromosome 5q. Moreover, these data suggest that mutations of 5q21 genes are not limited to those colorectal tumors which contain allelic deletions of this chromosome.

EXAMPLE 4

This example characterizes small, nested deletions in DNA from two unrelated FAP patients.

DNA from 40 FAP patients was screened with cosmids that had been mapped into a region near the APC locus to identify small deletions or rearrangements. Two of these cosmids, L5.71 and L5.79, hybridized with a 1200 kb NotI fragment in DNAs from most of the FAP patients screened.

The DNA of one FAP patient, 3214, showed only a 940 kb NotI fragment instead of the expected 1200 kb fragment. DNA was analyzed from four other members of the patient's immediate family; the 940 kb fragment was present in her affected mother (4711), but not in the other, unaffected family members. The mother also carried a normal 1200 kb NotI fragment that was transmitted to her two unaffected offspring. These observations indicated that the mutant polyposis allele is on the same chromosome as the 940 kb NotI fragment. A simple interpretation is that APC patients 3214 and 4711 each carry a 260 kb deletion within the APC locus.

If a deletion were present, then other enzymes might also be expected to produce fragments with altered mobilities. Hybridization of L5.79 to NruI-digested DNAs from both affected members of the family revealed a novel NruI fragment of 1300 kb, in addition to the normal 1200 kb NruI fragment. Furthermore, MluI fragments in patients 3214 and 4711 also showed an increase in size consistent with the deletion of an MluI site. The two chromosome 5 homologs of patient 3214 were segregated in somatic cell hybrid lines; HHW1155 (deletion hybrid) carried the abnormal homolog and HHW1159 (normal hybrid) carried the normal homolog.

Because patient 3214 showed only a 940 kb NotI fragment, she had not inherited the 1200 kb fragment present in the unaffected father's DNA. This observation suggests that he must be heterozygous for, and have transmitted, either a deletion of the L5.79 probe region or a variant NotI fragment too large to resolve on the gel system. As expected, the hybrid cell line HHW1159, which carries the paternal homolog, revealed no resolved NotI fragment when probed with L5.79. However, probing of HHW1159 DNA with L5.79 following digestion with other enzymes did reveal restriction fragments, demonstrating the presence of DNA homologous to the probe. The father is, therefore, interpreted as heterozygous for a polymorphism at the NotI site, with one chromosome 5 having a 1200 kb NotI fragment and the other having a fragment too large to resolve consistently on the gel. The latter was transmitted to patient 3214.

When double digests were used to order restriction sites within the 1200 kb NotI fragment, L5.71 and L5.79 were both found to lie on a 550 kb NotI-NruI fragment and, therefore, on the same side of an NruI site in the 1200 kb NotI fragment. To obtain genomic representation of sequences present over the entire 1200 kb NotI fragment, we constructed a library of small-fragment inserts enriched for sequences from this fragment. DNA from the somatic cell hybrid HHW141, which contains about 40% of chromosome 5, was digested with NotI and electrophoresed under pulsed-field gel (PFG) conditions; EcoRI fragments from the 1200 kb region of this gel were cloned into a phage vector. Probe Map30 was isolated from this library. In normal individuals probe Map30 hybridizes to the 1200 kb NotI fragment and to a 200 kb NruI fragment. This latter hybridization places Map30 distal, with respect to the locations of L5.71 and L5.79, to the NruI site of the 550 kb NotI-NruI fragment.

Because Map30 hybridized to the abnormal, 1300 kb NruI fragment of patient 3214, the locus defined by Map30 lies outside the hypothesized deletion. Furthermore, in normal chromosomes Map30 identified a 200 kb NruI fragment and L5.79 identified a 1200 kb NruI fragment; the hypothesized deletion must, therefore, be removing an NruI site, or sites, lying between Map30 and L5.79, and these two probes must flank the hypothesized deletion. A restriction map of the genomic region, showing placement of these probes is shown in FIG. 5.

A NotI digest of DNA from another FAP patient, 3824, was probed with L5.79. In addition to the 1200 kb normal NotI fragment, a fragment of approximately 1100 kb was observed, consistent with the presence of a 100 kb deletion in one chromosome 5. In this case, however, digestion with NruI and MluI did not reveal abnormal bands, indicating that if a deletion were present, its boundaries must lie distal to the NruI and MluI sites of the fragments identified by L5.79. Consistent with this expectation, hybridization of Map30 to DNA from patient 3824 identified a 760 kb MluI fragment in addition to the expected 860 kb fragment, supporting the interpretation of a 100 kb deletion in this patient. The two chromosome 5 homologs of patient 3824 were segregated in somatic cell hybrid lines; HHW1291 was found to carry only the abnormal homolog and HHW1290 only the normal homolog.

That the 860 kb MluI fragment identified by Map30 is distinct from the 830 kb MluI fragment identified previously by L5.79 was demonstrated by hybridization of Map30 and L5.79 to a NotI-MluI double digest of DNA from the hybrid cell (HHW1159) containing the nondeleted chromosome 5 homolog of patient 3214. As previously indicated, this hybrid is interpreted as missing one of the NotI sites that define the 1200 kb fragment. A 620 kb NotI-MluI fragment was seen with probe L5.79, and an 860 kb fragment was seen with Map30. Therefore, the 830 kb MluI fragment recognized by probe L5.79 must contain a NotI site in HHW1159 DNA; because the 860 kb MluI fragment remains intact, it does not carry this NotI site and must be distinct from the 830 kb MluI fragment.

EXAMPLE 5

This example demonstrates the isolation of human sequences which span the region deleted in the two unrelated FAP patients characterized in Example 4.

A strong prediction of the hypothesis that patients 3214 and 3824 carry deletions is that some sequences present on normal chromosome 5 homologs would be missing from the hypothesized deletion homologs. Therefore, to develop ger-

tomit probes that might confirm the deletions, as well as to identify genes from the region, YAC clones from a conrig seeded by cosmid L5.79 were localized from a library containing seven haploid human genome equivalents (Albertsen et al., Proc. Natl. Acad. Sci. U.S.A., Vol. 87, pp. 4256–4260 (1990)) with respect to the hypothesized deletions. Three clones, YACs 57B8, 310D8, and 183H12, were found to overlap the deleted region.

Importantly, one end of YAC 57B8 (clone AT57) was found to lie within the patient 3214 deletion. Inverse polymerase chain reaction (PCR) defined the end sequences of the insert of YAC 57B8. PCR primers based on one of these end sequences repeatedly failed to amplify DNA from the somatic cell hybrid (HHW1155) carrying the deleted homolog of patient 3214, but did amplify a product of the expected size from the somatic cell hybrid (HHW1159) carrying the normal chromosome 5 homolog. This result supported the interpretation that the abnormal restriction fragments found in the DNA of patient 3214 result from a deletion.

Additional support for the hypothesis of deletion in DNA from patient 3214 came from subcloned fragments of YAC 183H12, which spans the region in question. Y11, an EcoRI fragment cloned from YAC 183H12, hybridized to the normal, 1200 kb NotI fragment of patient 4711, but failed to hybridize to the abnormal, 940 kb NotI fragment of 4711 or to DNA from deletion cell line HHW1155. This result confirmed the deletion in patient 3214.

Two additional EcoRI fragments from YAC 183H12, Y10 and Y14, were localized within the patient 3214 deletion by their failure to hybridize to DNA from HHW1155. Probe Y10 hybridizes to a 150 kb NruI fragment in normal chromosome 5 homologs. Because the 3214 deletion creates the 1300 kb NruI fragment seen with the probes L5.79 and Map30 that flank the deletion, these NruI sites and the 150 kb NruI fragment lying between must be deleted in patient 3214. Furthermore, probe Y10 hybridizes to the same 620 kb NotI-MluI fragment seen with probe L5.79 in normal DNA, indicating its location as L5.79-proximal to the deleted MluI site and placing it between the MluI site and the L5.79-proximal NruI site. The MluI site must, therefore, lie between the NruI sites that define the 150 kb NruI fragment (see FIG. 5).

Probe Y11 also hybridized to the 150 kb NruI fragment in the normal chromosome 5 homolog, but failed to hybridize to the 620 kb NotI-MluI fragment, placing it L5.79-distal to the MluI site, but proximal to the second NruI site. Hybridization to the same (860 kb) MluI fragment as Map30 confirmed the localization of probe Y11 L5.79-distal to the MluI site.

Probe Y14 was shown to be L5.79-distal to both deleted NruI sites by virtue of its hybridization to the same 200 kb NruI fragment of the normal chromosome 5 seen with Map30. Therefore, the order of these EcoRI fragments derived from YAC 183H12 and deleted in patient 3214, with respect to L5.79 and Map30, is L5.79-Y10-Y11-Y14-Map30.

The 100 kb deletion of patient 3824 was confirmed by the failure of aberrant restriction fragments in this DNA to hybridize with probe Y11, combined with positive hybridizations to probes Y10 and/or Y14. Y10 and Y14 each hybridized to the 1100 kb NotI fragment of patient 3824 as well as to the normal 1200 kb NotI fragment, but Y11 hybridized to the 1200 kb fragment only. In the MluI digest, probe Y14 hybridized to the 860 kb and 760 kb fragments of patient 3824 DNA, but probe Y11 hybridized only to the

860 kb fragment. We conclude that the basis for the alteration in fragment size in DNA from patient 3824 is, indeed, a deletion. Furthermore, because probes Y10 and Y14 are missing from the deleted 3214 chromosome, but present on the deleted 3824 chromosome, and they have been shown to flank probe Y11, the deletion in patient 3824 must be nested within the patient 3214 deletion.

Probes Y10, Y11, Y14 and Map30 each hybridized to YAC 310D8, indicating that this YAC spanned the patient 3824 deletion and at a minimum, most of the 3214 deletion. The YAC characterizations, therefore, confirmed the presence of deletions in the patients and provided physical representation of the deleted region.

EXAMPLE 6

This example demonstrates that the MCC coding sequence maps outside of the region deleted in the two FAP patients characterized in Example 4.

An intriguing FAP candidate gene, MCC, recently was ascertained with cosmid L5.71 and was shown to have undergone mutation in colon carcinomas (Kinzler et al., supra). It was therefore of interest to map this gene with respect to the deletions in FAP patients. Hybridization of MCC probes with an overlapping series of YAC clones extending in either direction from L5.71 showed that the 3' end of MCC must be oriented toward the region of the two FAP deletions.

Therefore, two 3' cDNA clones from MCC were mapped with respect to the deletions: clone 1CI (bp 2378–4181) and clone 7 (bp 2890–3560). Clone 1CI contains sequences from the C-terminal end of the open reading frame, which stops at nucleotide 2708, as well as 3' untranslated sequence. Clone 7 contains sequence that is entirely 3' to the open reading frame. Importantly, the entire 3' untranslated sequence contained in the cDNA clones consists of a single 2.5 kb exon. These two clones were hybridized to DNAs from the YACs spanning the FAP region. Clone 7 fails to hybridize to YAC 310D8, although it does hybridize to YACs 183H12 and 5738; the same result was obtained with the cDNA 1CI. Furthermore, these probes did show hybridization to DNAs from both hybrid cell lines (HHW1159 and HHW1155) and the lymphoblastoid cell line from patient 3214, confirming their locations outside the deleted region. Additional mapping experiments suggested that the 3' end of the MCC cDNA clone contig is likely to be located more than 45 kb from the deletion of patient 3214 and, therefore, more than 100 kb from the deletion of patient 3824.

EXAMPLE 7

This example identifies three genes within the deleted region of chromosome 5 in the two unrelated FAP patients characterized in Example 4.

Genomic clones were used to screen cDNA libraries in three separate experiments. One screening was done with a phage clone derived from YAC 310D8 known to span the 260 kb deletion of patient 3214. A large-insert phage library was constructed from this YAC; screening with Y11 identified λ 205, which mapped within both deletions. When clone λ 205 was used to probe a random-, plus oligo(dT)-, primed fetal brain cDNA library (approximately 300,000 phage), six cDNA clones were isolated and each of them mapped entirely within both deletions. Sequence analysis of these six clones formed a single cDNA contig, but did not reveal an extended open reading frame. One of the six cDNAs was used to isolate more cDNA clones, some of which crossed the L5.71-proximal breakpoint of the 3824

deletion, as indicated by hybridization to both chromosome of this patient. These clones also contained an open reading frame, indicating a transcriptional orientation proximal to distal with respect to L5.71. This gene was named DP1 (deleted in polyposis 1). This gene is identical to TB2 described above.

cDNA walks yielded a cDNA conrig of 3.0–3.5 kb, and included two clones containing terminal poly(A) sequences. This size corresponds to the 3.5 kb band seen by Northern analysis. Sequencing of the first 3163 bp of the cDNA conrig revealed an open reading frame extending from the first base to nucleotide 631, followed by a 2.5 kb 3' untranslated region. The sequence surrounding the methionine codon at base 77 conforms to the Kozak consensus of an initiation methionine (Kozak, 1984). Failed attempts to walk farther, coupled with the similarity of the lengths of isolated cDNA and mRNA, suggested that the NH₂-terminus of the DP1 protein had been reached. Hybridization to a combination of genomic and YAC DNAs cut with various enzymes indicated the genomic coverage of DP1 to be approximately 30 kb.

Two additional probes for the locus, YS-11 and YS-39, which had been ascertained by screening of a cDNA library with an independent YAC probe identified with MCC sequences adjacent to L5.71, were mapped into the deletion region. YS-39 was shown to be a cDNA identical in sequence to DP1. Partial characterization of YS-11 had shown that 200 bp of DNA sequence at one end was identical to sequence coding for the 19 kd protein of the ribosomal signal recognition particle. SRP19 (Lingelbach et al., supra). Hybridization experiments mapped YS-11 within both deletions. The sequence of this clone, however, was found to be complex. Although 454 bp of the 1032 bp sequence of YS-11 were identical to the GenBank entry for the SRP19 gene, another 578 bp appended 5' to the SRP19 sequence was found to consist of previously unreported sequence containing no extended open reading frames. This suggested that YS-11 was either a chimeric clone containing two independent inserts or a clone of an incompletely processed or aberrant message. If YS-11 were a conventional chimeric clone, the independent segments would not be expected to map to the same physical region. The segments resulting from anomalous processing of a continuous transcript, however, would map to a single chromosomal region.

Inverse PCR with primers specific to the two ends of YS-11, the SRP19 end and the unidentified region, verified that both sequences map within the YAC 310D8; therefore, YS-11 is most likely a clone of an immature or anomalous mRNA species. Subsequently, both ends were shown to lie with the deleted region of patient 3824, and YS-11 was used to screen for additional cDNA clones.

Of the 14 cDNA clones selected from the fetal brain library, one clone, V5, was of particular interest in that it contained an open reading frame throughout, although it included only a short identity to the first 78 5' bases of the YS-11 sequence. Following the 78 bp of identical sequence, the two cDNA sequences diverged at an AG. Furthermore, divergence from genomic sequence was also seen after these 78 bp, suggesting the presence of a splice junction, and supporting the view that YS-11 represents an irregular message.

Starting with V5, successive 5' and 3' walks were performed; the resulting cDNA contig consisted of more than 100 clones, which defined a new transcript, DP2. Clones walking in the 5' direction crossed the 3824 deletion break-

point farthest from L5.71; since its 3' end is closer to this cosmid than its 5' end, the transcriptional orientation of DP2 is opposite to that of MCC and DP1.

The third screening approach relied on hybridization with a 120 kb MluI fragment from YAC 57B8. This fragment hybridizes with probe Y11 and completely spans the 100 kb deletion in patient 3824. The fragment was purified on two preparative PFGs, labeled, and used to screen a fetal brain cDNA library. A number of cDNA clones previously identified in the development of the DP1 and DP2 contigs were reascertained. However, 19 new cDNA clones mapped into the patient 3824 deletion. Analysis indicated that these 19 formed a new contig, DP3, containing a large open reading frame.

A clone from the 5' end of this new cDNA contig hybridized to the same EcoRI fragment as the 3' end of DP2. Subsequently, the DP2 and DP3 contigs were connected by a single 5' walking step from DP3, to form the single contig DP2.5. The complete nucleotide sequence of DP2.5 is shown in FIG. 7.

The consensus cDNA sequence of DP2.5 suggests that the entire coding sequence of DP2.5 has been obtained and is 8532 bp long. The most 5' ATG codon occurs two codons from an in-frame stop and conforms to the Kozak initiation consensus (Kozak, Nucl. Acids. Res., Vol. 12, p. 857–872 1984). The 3' open reading frame breaks down over the final 1.8 kb, giving multiple stops in all frames. A poly(A) sequence was found in one clone approximately 1 kb into the 3' untranslated region, associated with a polyadenylation signal 33 bp upstream (position 9530). The open reading frame is almost identical to that identified as APC above.

An alternatively spliced exon at nucleotide 934 of the DP2.5 transcript is of potential interest. It was first discovered by noting that two classes of cDNA had been isolated. The more abundant cDNA class contains a 303 bp exon not included in the other. The presence in vivo of the two transcripts was verified by an exon connection experiment. Primers flanking the alternatively spliced exon were used to amplify, by PCR, cDNA prepared from various adult tissues. Two PCR products that differed in size by approximately 300 bases were amplified from all the tissues tested; the larger product was always more abundant than the smaller.

EXAMPLE 8

This example demonstrates the primers used to identify subtle mutations in DP1, SRP19, and DP2.5.

To obtain DNA sequence adjacent to the exons of the genes DP1, DP2.5, and SRP19, sequencing substrate was obtained by inverse PCR amplification of DNAs from two YACs, 310D8 and 183H12, that span the deletions. Ligation at low concentration cyclized the restriction enzyme-digested YAC DNAs. Oligonucleotides with sequencing tails, designed in inverse orientation at intervals along the cDNAs, primed PCR amplification from the cyclized templates. Comparison of these DNA sequences with the cDNA sequences placed exon boundaries at the divergence points. SRP19 and DP1 were each shown to have five exons. DP2.5 consisted of 15 exons. The sequences of the oligonucleotides synthesized to provide PCR amplification primers for the exons of each of these genes are listed in Table III (*SEQ ID NOS: 39–94*). With the exception of exons 1, 3, 4, 9, and 15 of DP2.5 (see below), the primer sequences were located in intron sequences flanking the exons. The 5' primer of exon 1 is complementary to the cDNA sequence, but extends just into the 5' Kozak consensus sequence for the initiator methionine, allowing a survey of the translated sequences.

The 5' primer of exon 3 is actually in the 5' coding sequences of this exon, as three separate intronic primers simply would not amplify. The 5' primer of exon 4 just overlaps the 5' end of this exon, and we thus fail to survey the 19 most 5' bases of this exon. For exon 9, two overlapping primer sets were used, such that each had one end within the exon. For exon 15, the large 3' exon of DP2.5, overlapping primer pairs were placed along the length of the exon; each pair amplified a product of 250–400 bases.

EXAMPLE 9

This example demonstrates the use of single stranded conformation polymorphism (SSCP) analysis as described by Orita et al. Proc. Natl. Acad. Sci. U.S.A., Vol. 86, pp. 2766–70 (1989) and Genomics, Vol. 5, pp. 874–879 (1989) as applied to DP1, SRP19 and DP2.5.

SSCP analysis identifies most single- or multiple-base changes in DNA fragments up to 400 bases in length. Sequence alterations are detected as shifts in electrophoretic mobility of single-stranded DNA on nondenaturing acrylamide gels; the two complementary strands of a DNA segment usually resolve as two SSCP conformers of distinct mobilities. However, if the sample is from an individual heterozygous for a base-pair variant within the amplified segment, often three or more bands are seen. In some cases, even the sample from a homozygous individual will show multiple bands. Base-pair-change variants are identified by differences in pattern among the DNAs of the sample set.

Exons of the candidate genes were amplified by PCR from the DNAs of 61 related FAP patients and a control set of 12 normal individuals. The five exons from DP1 revealed no unique conformers in the FAP patients, although common conformers were observed with exons 2 and 3 in some individuals of both affected and control sets, indicating the presence of DNA sequence polymorphisms. Likewise, none of the five exons of SRP19 revealed unique conformers in DNA from FAP patients in the test panel.

Testing of exons 1 through 14 and primer sets A through N of exon 15 of the DP2.5 gene, however, revealed variant conformers specific to FAP patients in exons 7, 8, 10, 11, and 15. These variants were in the unrelated patients 3746, 3460, 3827, 3712, and 3751, respectively. The PCR-SSCP procedure was repeated for each of these exons in the five affected individuals and in an expanded set of 48 normal controls. The variant bands were reproducible in the FAP patients but were not observed in any of the control DNA samples. Additional variant conformers in exons 11 and 15 of the DP2.5 gene were seen; however, each of these was found in both the affected and control DNA sets. The five sets of conformers unique to the FAP patients were sequenced to determine the nucleotide changes responsible for their altered mobilities. The normal conformers from the host individuals were sequenced also. Bands were cut from the dried acrylamide gels, and the DNA was eluted. PCR amplification of these DNAs provided template for sequencing.

The sequences of the unique conformers from exons 7, 8, 10, and 11 of DP2.5 revealed dramatic mutations in the DP2.5 gene. The sequence of the new mutation creating the exon 7 conformer in patient 3746 was shown to contain a deletion of two adjacent nucleotides, at positions 730 and 731 in the cDNA sequence [(FIG. 7)] FIGS. 7A–7W (SEQ ID NO: 1). The normal sequence at this splice junction is CAGGGTCA (intronic sequence underlined), with the intron-exon boundary between the two repetitions of AG. The mutant allele in this patient has the sequence CAG-

GTCA. Although this exchange is at the 5' splice site, comparison with known consensus sequences of splice junctions would suggest that a functional splice junction is maintained. If this new splice junction were functional, the mutation would introduce a frameshift that creates a stop codon 15 nucleotides downstream. If the new splice junction were not functional, messenger processing would be significantly altered.

To confirm the 2-base deletion, the PCR product from FAP patient 3746 and a control DNA were electrophoresed on an acrylamide-urea denaturing gel, along with the products of a sequencing reaction. The sample from patient 3746 showed two bands differing in size by 2 nucleotides, with the larger band identical in mobility to the control sample; this result was independent confirmation that patient 3746 is heterozygous for a 2 bp deletion.

The unique conformer found in exon 8 of patient 3460 was found to carry a C-T transition, at position 904 in the cDNA sequence of DP2.5 (shown in FIG. 7), which replaced the normal sequence of CGA with TGA. This point mutation, when read in frame, results in a stop codon replacing the normal arginine codon. This single-base change had occurred within the context of a CG dimer, a potential hot spot for mutation (Barker et al., 1984).

The conformer unique to FAP patient 3827 in exon 10 was found to contain a deletion of one nucleotide (1367, 1368, or 1369) when compared to the normal sequence found in the other bands on the SSCP gel. This deletion, occurring within a set of three T's, changed the sequence from CTTTCA to CTTCA; this 1 base frameshift creates a downstream stop within 30 bases. The PCR product amplified from this patient's DNA also was electrophoresed on an acrylamide-urea denaturing along with the PCR product from a control DNA and products from a sequencing reaction. The patient's PCR product showed two bands differing by 1 bp in length, with the larger identical in mobility to the PCR product from the normal DNA; this result confirmed the presence of a 1 bp deletion in patient 3827.

Sequence analysis of the variant conformer of exon 11 from patient 3712 revealed the substitution of a T by a G at position 1500, changing the normal tyrosine codon to a stop codon.

The pair of conformers observed in exon 15 of the DP2.5 gene for FAP patient 3751 also was sequenced. These conformers were found to carry a nucleotide substitution of C to G at position 5253, the third base of a valine codon. No amino acid change resulted from this substitution, suggesting that this conformer reflects a genetically silent polymorphism.

The observation of distinct inactivating mutations in the DP2.5 gene in four unrelated patients strongly suggested that DP2.5 is the gene involved in FAP. These mutations are summarized in Table IIA.

EXAMPLE 10

This example demonstrates that the mutations identified in the DP2.5 (APC) gene segregate with the FAP phenotype.

Patient 3746, described above as carrying an APC allele with a frameshift mutation, is an affected offspring of two normal parents. Colonoscopy revealed no polyps in either parent nor among the patient's three siblings.

DNA samples from both parents, from the patient's wife, and from their three children were examined. SSCP analysis of DNA from both of the patient's parents displayed the normal pattern of conformers for exon 7, as did DNA from

the patients's wife and one of his offspring. The two other children, however, displayed the same new conformers as their affected father. Testing of the patient and his parents with highly polymorphic VNTR (variable number of tandem repeat) markers showed a 99.98% likelihood that they are his biological parents.

These observations confirmed that this novel conformer, known to reflect a 2 bp deletion mutation in the DP2.5 gene, appeared spontaneously with FAP in this pedigree and was transmitted to two of the children of the affected individual.

EXAMPLE 11

This example demonstrates polymorphisms in the APC gene which appear to be unrelated to disease (FAP).

Sequencing of variant conformers found among controls as well as individuals with APC has revealed the following polymorphisms in the APC gene: first, in exon 11, at position 1458, a substitution of T to C creating an *RsaI* restriction site but no amino acid change; and second, in exon 15, at positions 5037 and 5271, substitutions of A to G and G to T, respectively, neither resulting in amino acid substitutions. These nucleotide polymorphisms in the APC gene sequence may be useful for diagnostic purposes.

EXAMPLE 12

This example shows the structure of the APC gene.

The structure of the APC gene is schematically shown in FIG. 8, with flanking intron sequences indicated (*SEQ ID NOS: 11-38*).

The continuity of the very large (6.5 kb), most 3' exon in DP2.5 was shown in two ways. First, inverse PCR with primers spanning the entire length of this exon revealed no divergence of the cDNA sequence from the genomic sequence. Second, PCR amplification with converging primers placed at intervals along the exon generated products of the same size whether amplified from the originally isolated cDNA, cDNA from various tissues, or genomic template. Two forms of exon 9 were found in DP2.5: one is the complete exon; and the other, labeled exon 9A, is the result of a splice into the interior of the exon that deletes bases 934 to 1236 in the mRNA and removes 101 amino acids from the predicted protein (see [FIG. 7] *SEQ ID NOS: 1 & 2*).

EXAMPLE 13

This example demonstrates the mapping of the FAP deletions with respect to the APC exons.

Somatic cell hybrids carrying the segregated chromosomes 5 from the 100 kb (HHW1291) and 260 kb (HHW1155) deletion patients were used to determine the distribution of the APC genes exons across the deletions. DNAs from these cell lines were used as template, along with genomic DNA from a normal control, for PCR-based amplification of the APC exons.

PCR analysis of the hybrids from the 260 kb deletion of patient 3214 showed that all but one (exon 1) of the APC exons are removed by this deletion. PCR analysis of the somatic cell hybrid HHW1291, carrying the chromosome 5 homolog with the 100 kb deletion from patient 3824, revealed that exons 1 through 9 are present but exons 10 through 15 are missing. This result placed the deletion breakpoint either between exons 9 and 10 or within exon 10.

EXAMPLE 14

This example demonstrates the expression of alternately spliced APC messenger in normal tissues and in cancer cell lines.

Tissues that express the APC gene were identified by PCR amplification of cDNA made to mRNA with primers located within adjacent APC exons. In addition, PCR primers that flank the alternatively spliced exon 9 were chosen so that the expression pattern of both splice forms could be assessed. All tissue types tested (brain, lung, aorta, spleen, heart, kidney, liver, stomach, placenta, and colonic mucosa) and cultured cell lines (lymphoblasts, HL60, and ehorioeareinoma) expressed both splice forms of the APC gene. We note, however, that expression by lymphocytes normally residing in some tissues, including colon, prevents unequivocal assessment of expression. The large mRNA, containing the complete exon 9 rather than only exon 9A, appears to be the more abundant message.

Northern analysis of poly(A)-selected RNA from lymphoblasts revealed a single band of approximately 10 kb, consistent with the size of the sequenced cDNA.

EXAMPLE 15

This example discusses structural features of the APC protein predicted from the sequence.

The cDNA consensus sequence of APC predicts that the longer, more abundant form of the message codes for a [2842 or 28444] 2843 amino acid peptide with a mass of 311.8 kd. This predicted APC peptide was compared with the current data bases of protein and DNA sequences using both Intelligenetics and GCG software packages. No genes with a high degree of amino acid sequence similarity were found. Although many short (approximately 20 amino acid) regions of sequence similarity were uncovered, none was sufficiently strong to reveal which, if any, might represent functional homology. Interestingly, multiple similarities to myosins and keratins did appear. The APC gene also was scanned for sequence motifs of known function; although multiple glycosylation, phosphorylation, and myristoylation sites were seen, their significance is uncertain.

Analysis of the APC peptide sequence did identify features important in considering potential protein structure. Hydropathy plots (Kyte and Doolittle, *J. Mol. Biol.* Vol. 157, pp. 105-132 (1982)) indicate that the APC protein is notably hydrophilic. No hydrophobic domains suggesting a signal peptide or a membrane-spanning domain were found. Analysis of the first 1000 residues indicates that α -helical rods may form (Cohen and Parry, *Trends Biochem. Sci.* Vol. 77, pp. 245-248 (1986); there is a scarcity of proline residues and, there are a number of regions containing heptad repeats (apolar-X-X-apolar-X-X-X). Interestingly, in exon 9A, the deleted form of exon 9, two heptad repeat regions are reconnected in the proper heptad repeat frame, deleting the intervening peptide region. After the first 1000 residues, the high proline content of the remainder of the peptide suggests a compact rather than a rod-like structure.

The most prominent feature of the second 1000 residues is a 20 amino acid repeat that is iterated seven times with semiregular spacing (Table 4). The intervening sequences between the seven repeat regions contained 114, 116, 151, 205, 107, and 58 amino acids, respectively. Finally, residues 2200-24000 contain a 200 amino acid basic domain.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 102

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8532 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
 (B) CLONE: DP2.5(APC)

(viii) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCTGCAG	CTTCATATGA	TCAGTTGTTA	AAGCAAGTTG	AGGCACTGAA	GATGGAGAAC	60
TCAAATCTTC	GACAAGAGCT	AGAAGATAAT	TCCAATCATC	TTACAAAAC	GGAAACTGAG	120
GCATCTAATA	TGAAGGAAGT	ACTTAAACAA	CTACAAGGAA	GTATTGAAGA	TGAAGCTATG	180
GCTTCTTCTG	GACAGATTGA	TTTATTAGAG	CGTCTTAAAG	AGCTTAACTT	AGATAGCAGT	240
AATTTCCCTG	GAGTAAAAC	GCGGTCAAAA	ATGTCCCTCC	GTTCTTATGG	AAGCCGGGAA	300
GGATCTGTAT	CAAGCCGTTT	TGGAGAGTGC	AGTCCTGTTC	CTATGGGTTC	ATTTCCAAGA	360
AGAGGGTTTG	TAAATGGAAG	CAGAGAAAGT	ACTGGATATT	TAGAAGAACT	TGAGAAAGAG	420
AGGTCATTGC	TTCTTGCTGA	TCTTGACAAA	GAAGAAAAGG	AAAAAGACTG	GTATTACGCT	480
CAACTTCAGA	ATCTCACTAA	AAGAATAGAT	AGTCTTCCTT	TAAGTAAAA	TTTTTCCTTA	540
CAAACAGATA	TGACCAGAAG	GCAATTGGAA	TATGAAGCAA	GGCAAATCAG	AGTTGCGATG	600
GAAGAACAAC	TAGGTACCTG	CCAGGATATG	GAAAAACGAG	CACAGCGAAG	AATAGCCAGA	660
ATTCAGCAAA	TCGAAAAGGA	CATACTTCGT	ATACGACAGC	TTTTACAGTC	CCAAGCAACA	720
GAAGCAGAGA	GGTCATCTCA	GAACAAGCAT	GAAACCGGCT	CACATGATGC	TGAGCGGCAG	780
AATGAAGGTC	AAGGAGTGGG	AGAAATCAAC	ATGGCAACTT	CTGGTAATGG	TCAGGGTTCA	840
ACTACACGAA	TGGACCATGA	AACAGCCAGT	GTTTTGAGTT	CTAGTAGCAC	ACACTCTGCA	900
CCTCGAAGGC	TGACAAGTCA	TCTGGGAACC	AAGGTGGAAA	TGGTGTATTC	ATTGTTGTCA	960
ATGCTTGGTA	CTCATGATAA	GGATGATATG	TCGCGAACTT	TGCTAGCTAT	GTCTAGCTCC	1020
CAAGACAGCT	GTATATCCAT	GCGACAGTCT	GGATGTCTTC	CTCTCCTCAT	CCAGCTTTTA	1080
CATGGCAATG	ACAAAGACTC	TGTATTGTTG	GGAAATTCCC	GGGGCAGTAA	AGAGGCTCGG	1140
GCCAGGGCCA	GTGCAGCACT	CCACAACATC	ATTCACTCAC	AGCCTGATGA	CAAGAGAGGC	1200
AGGCGTGAAG	TCCGAGTCCT	TCATCTTTTG	GAACAGATAC	GCGCTTACTG	TGAAACCTGT	1260
TGGGAGTGGC	AGGAAGCTCA	TGAACCAGGC	ATGGACCAGG	ACAAAAATCC	AATGCCAGCT	1320
CCTGTTGAAC	ATCAGATCTG	TCCTGCTGTG	TGTGTTCTAA	TGAAACTTTC	ATTTGATGAA	1380
GAGCATAGAC	ATGCAATGAA	TGAACTAGGG	GGACTACAGG	CCATTGCAGA	ATTATTGCAA	1440
GTGGACTGTG	AAATGTACGG	GCTTACTAAT	GACCACTACA	GTATTACACT	AAGACGATAT	1500
GCTGGAATGG	CTTTGACAAA	CTTGACTTTT	GGAGATGTAG	CCAACAAGGC	TACGCTATGC	1560
TCTATGAAAG	GCTGCATGAG	AGCACTTGTG	GCCCAACTAA	AATCTGAAAG	TGAAGACTTA	1620

-continued

CAGCAGGTTA	TTGCAAGTGT	TTGAGGAAT	TTGTCTTGGC	GAGCAGATGT	AAATAGTAAA	1680
AAGACGTTGC	GAGAAGTTGG	AAGTGTGAAA	GCATTGATGG	AATGTGCTTT	AGAAGTAAA	1740
AAGGAATCAA	CCCTCAAAAAG	CGTATTGAGT	GCCTTATGGA	ATTTGTCAGC	ACATTGCACT	1800
GAGAATAAAG	CTGATATATG	TGCTGTAGAT	GGTGCACCTG	CATTTTTGGT	TGGCACTCTT	1860
ACTTACCGGA	GCCAGACAAA	CACTTTAGCC	ATTATTGAAA	GTGGAGGTGG	GATATTACGG	1920
AATGTGTCCA	GCTTGATAGC	TACAAATGAG	GACCACAGGC	AAATCCTAAG	AGAGAACAAC	1980
TGTCTACAAA	CTTTATTACA	ACACTTAAAA	TCTCATAGTT	TGACAATAGT	CAGTAATGCA	2040
TGTGGAACCT	TGTGGAATCT	CTCAGCAAGA	AATCCTAAAG	ACCAGGAAGC	ATTATGGGAC	2100
ATGGGGGCAG	TTAGCATGCT	CAAGAACCTC	ATTCATTCAA	AGCACAAAAT	GATTGCTATG	2160
GGAAGTGCTG	CAGCTTTAAG	GAATCTCATG	GCAAATAGGC	CTGCGAAGTA	CAAGGATGCC	2220
AATATTATGT	CTCCTGGCTC	AAGCTTGCCA	TCTCTTCATG	TTAGGAAACA	AAAAGCCCTA	2280
GAAGCAGAAT	TAGATGCTCA	GCACTTATCA	GAAACTTTTG	ACAATATAGA	CAATTTAAGT	2340
CCCAAGGCAT	CTCATCGTAG	TAAGCAGAGA	CACAAGCAAA	GTCTCTATGG	TGATTATGTT	2400
TTTGACACCA	ATCGACATGA	TGATAATAGG	TCAGACAATT	TTAATACTGG	CAACATGACT	2460
GTCCTTTCAC	CATATTTGAA	TACTACAGTG	TTACCCAGCT	CCTCTTCATC	AAGAGGAAGC	2520
TTAGATAGTT	CTCGTTCTGA	AAAAGATAGA	AGTTTGGAGA	GAGAACGCGG	AATTGGTCTA	2580
GGCAACTACC	ATCCAGCAAC	AGAAAATCCA	GGAACTTCTT	CAAAGCGAGG	TTTGCAGATC	2640
TCCACCCTG	CAGCCCAGAT	TGCCAAAGTC	ATGGAAGAAG	TGTCAGCCAT	TCATACCTCT	2700
CAGGAAGACA	GAAGTTCTGG	GTCTACCACT	GAATTACATT	GTGTGACAGA	TGAGAGAAAT	2760
GCACTTAGAA	GAAGCTCTGC	TGCCATACA	CATTCAAACA	CTTACAATTT	CACTAAGTCG	2820
GAAAATTCAA	ATAGGACATG	TTCTATGCCT	TATGCCAAAT	TAGAATACAA	GAGATCTTCA	2880
AATGATAGTT	TAAATAGTGT	CAGTAGTAGT	GATGGTTATG	GTAAAAGAGG	TCAAATGAAA	2940
CCCTCGATTG	AATCCTATTC	TGAAGATGAT	GAAAGTAAGT	TTTGCAGTTA	TGGTCAATAC	3000
CCAGCCGACC	TAGCCCATAA	AATACATAGT	GCAAATCATA	TGGATGATAA	TGATGGAGAA	3060
CTAGATACAC	CAATAAATTA	TAGTCTTAAA	TATTCAGATG	AGCAGTTGAA	CTCTGGAAGG	3120
CAAAGTCCTT	CACAGAATGA	AAGATGGGCA	AGACCCAAAC	ACATAATAGA	AGATGAAATA	3180
AAACAAAGTG	AGCAAAGACA	ATCAAGGAAT	CAAAGTACAA	CTTATCCTGT	TTATACTGAG	3240
AGCACTGATG	ATAAACACCT	CAAGTTCCAA	CCACATTTTG	GACAGCAGGA	ATGTGTTTCT	3300
CCATACAGGT	CACGGGGAGC	CAATGGTTCA	GAAACAAATC	GAGTGGGTTC	TAATCATGGA	3360
ATTAATCAAA	ATGTAAGCCA	GTCTTTGTGT	CAAGAAGATG	ACTATGAAGA	TGATAAGCCT	3420
ACCAATTATA	GTGAACGTTA	CTCTGAAGAA	GAACAGCATG	AAGAAGAAGA	GAGACCAACA	3480
AATTATAGCA	TAAAATATAA	TGAAGAGAAA	CGTCATGTGG	ATCAGCCTAT	TGATTATAGT	3540
TTAAAATATG	CCACAGATAT	TCCTTCATCA	CAGAAACAGT	CATTTTCATT	CTCAAAGAGT	3600
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CCTTCATCTA	ATGCCAAGAG	GCAGAATCAG	CTCCATCCAA	GTTCTGCACA	GAGTAGAAGT	3720
GGTCAGCCTC	AAAAGGCTGC	CACTTGCAAA	GTTTCTTCTA	TTAACCAAGA	AACAATACAG	3780
ACTTATTGTG	TAGAAGATAC	TCCAATATGT	TTTTCAAGAT	GTAGTTCATT	ATCATCTTTG	3840
TCATCAGCTG	AAGATGAAAT	AGGATGTAAT	CAGACGACAC	AGGAAGCAGA	TTCTGCTAAT	3900
ACCCTGCAAA	TAGCAGAAAT	AAAAGAAAAG	ATTGGAACTA	GGTCAGCTGA	AGATCCTGTG	3960
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CCACTCATGT	TTAGCAGATG	TACTTCTGTC	AGTTCACTTG	ATAGTTTTGA	GAGTCGTTCCG	4200
ATTGCCAGCT	CCGTTTCAGAG	TGAACCATGC	AGTGGAAATGG	TAAGTGGCAT	TATAAGCCCC	4260
AGTGATCTTC	CAGATAGCCC	TGGACAAAAC	ATGCCACCAA	GCAGAAGTAA	AACACCTCCA	4320
CCACCTCCTC	AAACAGCTCA	AACCAAGCGA	GAAGTACCTA	AAAATAAAGC	ACCTACTGCT	4380
GAAAAGAGAG	AGAGTGGACC	TAAGCAAGCT	GCAGTAAATG	CTGCAGTTCA	GAGGGTCCAG	4440
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TCTTGTTTCAT	CCAGCCTGAG	TGCTCTGAGC	CTCGATGAGC	CATTTATACA	GAAAGATGTG	4560
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CAGCCTAAAG	AATCAAATGA	AAACCAAGAG	AAAGAGGCAG	AAAAAACTAT	TGATTCTGAA	4680
AAGGACCTAT	TAGATGATTC	AGATGATGAT	GATATTGAAA	TACTAGAAGA	ATGTATTATT	4740
TCTGCCATGC	CAACAAAGTC	ATCACGTAAA	GCAAAAAAGC	CAGCCCAGAC	TGCTTCAAAA	4800
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ACAATCGAAT	CCCCTCCAAA	TGAGTTAGCT	GCTGGAGAAG	GAGTTAGAGG	AGGAGCACAG	5040
TCAGGTGAAT	TTGAAAAACG	AGATACCATT	CCTACAGAAG	GCAGAAGTAC	AGATGAGGCT	5100
CAAGGAGGAA	AAACCTCATC	TGTAACCATA	CCTGAATTGG	ATGACAATAA	AGCAGAGGAA	5160
GGTGATATTC	TTGCAGAATG	CATTAATTCT	GCTATGCCCA	AAGGGAAAAG	TCACAAGCCT	5220
TTCCGTGTGA	AAAAGATAAT	GGACCAGGTC	CAGCAAGCAT	CTGCGTCGTC	TTCTGCACCC	5280
AACAAAAATC	AGTTAGATGG	TAAGAAAAAG	AAACCAACTT	CACCAGTAAA	ACCTATACCA	5340
CAAATACTG	AATATAGGAC	ACGTGTAAGA	AAAAATGCAG	ACTCAAAAAA	TAATTTAAAT	5400
GCTGAGAGAG	TTTTCTCAGA	CAACAAAGAT	TCAAAGAAAC	AGAATTTGAA	AAATAATTCC	5460
AAGGACTTCA	ATGATAAGCT	CCCAAATAAT	GAAGATAGAG	TCAGAGGAAG	TTTTGCTTTT	5520
GATTCACCTC	ATCATTACAC	GCCTATTGAA	GGAACTCCTT	ACTGTTTTTC	ACGAAATGAT	5580
TCTTTGAGTT	CTCTAGATTT	TGATGATGAT	GATGTTGACC	TTTCCAGGGA	AAAGGCTGAA	5640
TTAAGAAAGG	CAAAAGAAAA	TAAGGAATCA	GAGGCTAAAG	TTACCAGCCA	CACAGAACTA	5700
ACCTCCAACC	AACAATCAGC	TAATAAGACA	CAAGCTATTG	CAAAGCAGCC	AATAAATCGA	5760
GGTCAGCCTA	AACCCATACT	TCAGAAACAA	TCCACTTTTC	CCCAGTCATC	CAAAGACATA	5820
CCAGACAGAG	GGGCAGCAAC	TGATGAAAAAG	TTACAGAATT	TTGCTATTGA	AAATACTCCA	5880
GTTTGCTTTT	CTCATAATTC	CTCTCTGAGT	TCTCTCAGTG	ACATTGACCA	AGAAAACAAC	5940
AATAAAGAAA	ATGAACCTAT	CAAAGAGACT	GAGCCCCCTG	ACTCACAGGG	AGAACCAAGT	6000
AAACCTCAAG	CATCAGGCTA	TGCTCCTAAA	TCATTTTCATG	TTGAAGATAC	CCCAGTTTGT	6060
TTCTCAAGAA	ACAGTTCTCT	CAGTTCTCTT	AGTATTGACT	CTGAAGATGA	CCTGTTGCAG	6120
GAATGTATAA	GCTCCGCAAT	GCCAAAAAAG	AAAAAGCCTT	CAAGACTCAA	GGGTGATAAT	6180
GAAAAACATA	GTCCCAGAAA	TATGGGTGGC	ATATTAGGTG	AAGATCTGAC	ACTTGATTTG	6240
AAAGATATAC	AGAGACCAGA	TTCAGAACAT	GGTCTATCCC	CTGATTCAGA	AAATTTTGAT	6300
TGGAAAGCTA	TTCAGGAAGG	TGCAAATTCC	ATAGTAAGTA	GTTTACATCA	AGCTGCTGCT	6360
GCTGCATGTT	TATCTAGACA	AGCTTCGTCT	GATTCAGATT	CCATCCTTTC	CCTGAAATCA	6420

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ATAGAATCTG	AAAGTAAAGG	AATCAAAGGA	GGAAAAAAG	TTTATAAAG	TTTGATTACT	6600
GGAAAAGTTC	GATCTAATTC	AGAAAATTTCA	GGCCAAATGA	AACAGCCCCT	TCAAGCAAAC	6660
ATGCCTTCAA	TCTCTCGAGG	CAGGACAATG	ATTCATATTC	CAGGAGTTCG	AAATAGCTCC	6720
TCAAGTACAA	GTCCTGTTTC	TAAAAAAGGC	CCACCCCTTA	AGACTCCAGC	CTCCAAAAGC	6780
CCTAGTGAAG	GTCAAACAGC	CACCACTTCT	CCTAGAGGAG	CCAAGCCATC	TGTGAAATCA	6840
GAATTAAGCC	CTGTTGCCAG	GCAGACATCC	CAAATAGGTG	GGTCAAGTAA	AGCACCTTCT	6900
AGATCAGGAT	CTAGAGATTC	GACCCCTTCA	AGACCTGCCC	AGCAACCATT	AAGTAGACCT	6960
ATACAGTCTC	CTGGCCGAAA	CTCAATTTCC	CCTGGTAGAA	ATGGAATAAG	TCCTCCTAAC	7020
AAATTATCTC	AACTTCCAAG	GACATCATCC	CCTAGTACTG	CTTCAACTAA	GTCCTCAGGT	7080
TCTGGAAAAA	TGTCATATAC	ATCTCCAGGT	AGACAGATGA	GCCAACAGAA	CCTTACCAA	7140
CAAACAGGTT	TATCCAAGAA	TGCCAGTAGT	ATTCCAAGAA	GTGAGTCTGC	CTCCAAAGGA	7200
CTAAATCAGA	TGAATAATGG	TAATGGAGCC	AATAAAAAGG	TAGAACTTTC	TAGAATGTCT	7260
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TCATTTGAAT	CTCTTTCTCC	ATCATCTAGA	CCAGCTTCTC	CCACTAGGTC	CCAGGCACAA	7440
ACTCCAGTTT	TAAGTCCTTC	CCTTCCTGAT	ATGTCTCTAT	CCACACATTC	GTCTGTTTCCAG	7500
GCTGGTGGAT	GGCGAAAAC	CCCACCTAAT	CTCAGTCCCA	CTATAGAGTA	TAATGATGGA	7560
AGACCAGCAA	AGCGCCATGA	TATTGCACGG	TCTCATTCTG	AAAGTCCTTC	TAGACTTCCA	7620
ATCAATAGGT	CAGGAACCTG	GAAACGTGAG	CACAGCAAAC	ATTCATCATC	CCTTCCTCGA	7680
GTAAGCACTT	GGAGAAGAAC	TGGAAGTTCA	TCTTCAATTC	TTTCTGCTTC	ATCAGAATCC	7740
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TCTCCCACAA	ATAGTACTTC	TCAGACCGTT	TCCTCAGGTG	CTACAAATGG	TGCTGAATCA	7920
AAGACTCTAA	TTTATCAAAT	GGCACCTGCT	GTTTCTAAAA	CAGAGGATGT	TTGGGTGAGA	7980
ATTGAGGACT	GTCCCATTA	CAATCCTAGA	TCTGGAAGAT	CTCCACAGG	TAATACTCCC	8040
CCGGTGATG	ACAGTGTTTC	AGAAAAGGCA	AATCCAAACA	TTAAAGATTC	AAAAGATAAT	8100
CAGGCAAAAC	AAAATGTGGG	TAATGGCAGT	GTTCCCATGC	GTACCGTGGG	TTTGGAAAAT	8160
CGCCTGAACT	CCTTTATTC	GGTGGATGCC	CCTGACCAA	AAGGAACTGA	GATAAAACCA	8220
GGACAAAATA	ATCCTGTCCC	TGTATCAGAG	ACTAATGAAA	GTTCTATAGT	GGAACGTACC	8280
CCATTCAGTT	CTAGCAGCTC	AAGCAAACAC	AGTTCACCTA	GTGGGACTGT	TGCTGCCAGA	8340
GTGACTCCTT	TTAATTACAA	CCCAAGCCCT	AGGAAAAGCA	GCGCAGATAG	CAC TTCAGCT	8400
CGGCCATCTC	AGATCCCAAC	TCCAGTGAAT	AACAACACAA	AGAAGCGAGA	TTCCAAAAC	8460
GACAGCACAG	AATCCAGTGG	AACCCAAAGT	CCTAAGCGCC	ATTCTGGGTC	TTACCTTGTG	8520
ACATCTGTTT	AA					8532

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2843 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu
 1 5 10 15
 Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn
 20 25 30
 His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu
 35 40 45
 Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly
 50 55 60
 Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser
 65 70 75 80
 Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr
 85 90 95
 Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro
 100 105 110
 Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg
 115 120 125
 Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu
 130 135 140
 Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala
 145 150 155 160
 Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Leu Thr Glu
 165 170 175
 Asn Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu
 180 185 190
 Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln
 195 200 205
 Asp Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile
 210 215 220
 Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr
 225 230 235 240
 Glu Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp
 245 250 255
 Ala Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala
 260 265 270
 Thr Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr
 275 280 285
 Ala Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu
 290 295 300
 Thr Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser
 305 310 315 320
 Met Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala
 325 330 335
 Met Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys
 340 345 350
 Leu Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val
 355 360 365
 Leu Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser
 370 375 380
 Ala Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly
 385 390 395 400
 Arg Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr

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405					410					415					
Cys	Glu	Thr	Cys	Trp	Glu	Trp	Gln	Glu	Ala	His	Glu	Pro	Gly	Met	Asp
			420					425					430		
Gln	Asp	Lys	Asn	Pro	Met	Pro	Ala	Pro	Val	Glu	His	Gln	Ile	Cys	Pro
		435					440					445			
Ala	Val	Cys	Val	Leu	Met	Lys	Leu	Ser	Phe	Asp	Glu	Glu	His	Arg	His
	450					455					460				
Ala	Met	Asn	Glu	Leu	Gly	Gly	Leu	Gln	Ala	Ile	Ala	Glu	Leu	Leu	Gln
465						470					475				480
Val	Asp	Cys	Glu	Met	Tyr	Gly	Leu	Thr	Asn	Asp	His	Tyr	Ser	Ile	Thr
				485					490					495	
Leu	Arg	Arg	Tyr	Ala	Gly	Met	Ala	Leu	Thr	Asn	Leu	Thr	Phe	Gly	Asp
			500					505					510		
Val	Ala	Asn	Lys	Ala	Thr	Leu	Cys	Ser	Met	Lys	Gly	Cys	Met	Arg	Ala
		515					520					525			
Leu	Val	Ala	Gln	Leu	Lys	Ser	Glu	Ser	Glu	Asp	Leu	Gln	Gln	Val	Ile
	530						535					540			
Ala	Ser	Val	Leu	Arg	Asn	Leu	Ser	Trp	Arg	Ala	Asp	Val	Asn	Ser	Lys
545						550					555				560
Lys	Thr	Leu	Arg	Glu	Val	Gly	Ser	Val	Lys	Ala	Leu	Met	Glu	Cys	Ala
				565					570					575	
Leu	Glu	Val	Lys	Lys	Glu	Ser	Thr	Leu	Lys	Ser	Val	Leu	Ser	Ala	Leu
			580					585					590		
Trp	Asn	Leu	Ser	Ala	His	Cys	Thr	Glu	Asn	Lys	Ala	Asp	Ile	Cys	Ala
		595					600					605			
Val	Asp	Gly	Ala	Leu	Ala	Phe	Leu	Val	Gly	Thr	Leu	Thr	Tyr	Arg	Ser
	610					615					620				
Gln	Thr	Asn	Thr	Leu	Ala	Ile	Ile	Glu	Ser	Gly	Gly	Gly	Ile	Leu	Arg
625						630					635				640
Asn	Val	Ser	Ser	Leu	Ile	Ala	Thr	Asn	Glu	Asp	His	Arg	Gln	Ile	Leu
				645					650					655	
Arg	Glu	Asn	Asn	Cys	Leu	Gln	Thr	Leu	Leu	Gln	His	Leu	Lys	Ser	His
			660					665					670		
Ser	Leu	Thr	Ile	Val	Ser	Asn	Ala	Cys	Gly	Thr	Leu	Trp	Asn	Leu	Ser
		675					680					685			
Ala	Arg	Asn	Pro	Lys	Asp	Gln	Glu	Ala	Leu	Trp	Asp	Met	Gly	Ala	Val
	690					695					700				
Ser	Met	Leu	Lys	Asn	Leu	Ile	His	Ser	Lys	His	Lys	Met	Ile	Ala	Met
705						710					715				720
Gly	Ser	Ala	Ala	Ala	Leu	Arg	Asn	Leu	Met	Ala	Asn	Arg	Pro	Ala	Lys
				725					730					735	
Tyr	Lys	Asp	Ala	Asn	Ile	Met	Ser	Pro	Gly	Ser	Ser	Leu	Pro	Ser	Leu
			740					745					750		
His	Val	Arg	Lys	Gln	Lys	Ala	Leu	Glu	Ala	Glu	Leu	Asp	Ala	Gln	His
		755					760					765			
Leu	Ser	Glu	Thr	Phe	Asp	Asn	Ile	Asp	Asn	Leu	Ser	Pro	Lys	Ala	Ser
						775						780			
His	Arg	Ser	Lys	Gln	Arg	His	Lys	Gln	Ser	Leu	Tyr	Gly	Asp	Tyr	Val
785						790					795				800
Phe	Asp	Thr	Asn	Arg	His	Asp	Asp	Asn	Arg	Ser	Asp	Asn	Phe	Asn	Thr
				805					810					815	
Gly	Asn	Met	Thr	Val	Leu	Ser	Pro	Tyr	Leu	Asn	Thr	Thr	Val	Leu	Pro
				820				825						830	

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Ser Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys
 835 840 845

Asp Arg Ser Leu Glu Arg Gly Arg Gly Ile Gly Leu Gly Asn Tyr His
 850 855 860

Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile
 865 870 875 880

Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala
 885 890 895

Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu
 900 905 910

His Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala
 915 920 925

His Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn
 930 935 940

Arg Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser
 945 950 955 960

Asn Asp Ser Leu Asn Ser Val Ser Ser Ser Asp Gly Tyr Gly Lys Arg
 965 970 975

Gly Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser
 980 985 990

Lys Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile
 995 1000 1005

His Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro
 1010 1015 1020

Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg
 025 1030 1035 1040

Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile
 1045 1050 1055

Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser
 1060 1065 1070

Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys
 1075 1080 1085

Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser
 1090 1095 1100

Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly
 105 1110 1115 1120

Ile Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu
 1125 1130 1135

Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln
 1140 1145 1150

His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu
 1155 1160 1165

Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala
 1170 1175 1180

Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser
 185 1190 1195 1200

Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Ser Glu
 1205 1210 1215

Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His
 1220 1225 1230

Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr
 1235 1240 1245

Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val
 1250 1255 1260

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Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu
 265 1270 1275 1280
 Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala
 1285 1290 1295
 Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly
 1300 1305 1310
 Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln
 1315 1320 1325
 His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser
 1330 1335 1340
 Glu Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser
 345 1350 1355 1360
 Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr
 1365 1370 1375
 Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser
 1380 1385 1390
 Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu
 1395 1400 1405
 Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro
 1410 1415 1420
 Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro
 425 1430 1435 1440
 Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys
 1445 1450 1455
 Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val
 1460 1465 1470
 Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu
 1475 1480 1485
 Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser
 1490 1495 1500
 Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val
 505 1510 1515 1520
 Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu
 1525 1530 1535
 Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu
 1540 1545 1550
 Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp
 1555 1560 1565
 Asp Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro
 1570 1575 1580
 Thr Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys
 585 1590 1595 1600
 Leu Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys
 1605 1610 1615
 Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe
 1620 1625 1630
 Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro
 1635 1640 1645
 Ile Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser
 1650 1655 1660
 Pro Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln
 665 1670 1675 1680
 Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser

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1685					1690					1695					
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		1700					1705					1710			
Leu	Asp	Asp	Asn	Lys	Ala	Glu	Glu	Gly	Asp	Ile	Leu	Ala	Glu	Cys	Ile
		1715					1720					1725			
Asn	Ser	Ala	Met	Pro	Lys	Gly	Lys	Ser	His	Lys	Pro	Phe	Arg	Val	Lys
		1730					1735					1740			
Lys	Ile	Met	Asp	Gln	Val	Gln	Gln	Ala	Ser	Ala	Ser	Ser	Ser	Ala	Pro
		745					1750					1755			
Asn	Lys	Asn	Gln	Leu	Asp	Gly	Lys	Lys	Lys	Lys	Pro	Thr	Ser	Pro	Val
				1765								1770			
Lys	Pro	Ile	Pro	Gln	Asn	Thr	Glu	Tyr	Arg	Thr	Arg	Val	Arg	Lys	Asn
				1780					1785					1790	
Ala	Asp	Ser	Lys	Asn	Asn	Leu	Asn	Ala	Glu	Arg	Val	Phe	Ser	Asp	Asn
				1795					1800					1805	
Lys	Asp	Ser	Lys	Lys	Gln	Asn	Leu	Lys	Asn	Asn	Ser	Lys	Asp	Phe	Asn
				1810					1815					1820	
Asp	Lys	Leu	Pro	Asn	Asn	Glu	Asp	Arg	Val	Arg	Gly	Ser	Phe	Ala	Phe
				825					1830					1840	
Asp	Ser	Pro	His	His	Tyr	Thr	Pro	Ile	Glu	Gly	Thr	Pro	Tyr	Cys	Phe
				1845					1850					1855	
Ser	Arg	Asn	Asp	Ser	Leu	Ser	Ser	Leu	Asp	Phe	Asp	Asp	Asp	Asp	Val
				1860					1865					1870	
Asp	Leu	Ser	Arg	Glu	Lys	Ala	Glu	Leu	Arg	Lys	Ala	Lys	Glu	Asn	Lys
				1875					1880					1885	
Glu	Ser	Glu	Ala	Lys	Val	Thr	Ser	His	Thr	Glu	Leu	Thr	Ser	Asn	Gln
				1890					1895					1900	
Gln	Ser	Ala	Asn	Lys	Thr	Gln	Ala	Ile	Ala	Lys	Gln	Pro	Ile	Asn	Arg
				905					1910					1915	
Gly	Gln	Pro	Lys	Pro	Ile	Leu	Gln	Lys	Gln	Ser	Thr	Phe	Pro	Gln	Ser
				1925					1930					1935	
Ser	Lys	Asp	Ile	Pro	Asp	Arg	Gly	Ala	Ala	Thr	Asp	Glu	Lys	Leu	Gln
				1940					1945					1950	
Asn	Phe	Ala	Ile	Glu	Asn	Thr	Pro	Val	Cys	Phe	Ser	His	Asn	Ser	Ser
				1955					1960					1965	
Leu	Ser	Ser	Leu	Ser	Asp	Ile	Asp	Gln	Glu	Asn	Asn	Asn	Lys	Glu	Asn
				1970					1975					1980	
Glu	Pro	Ile	Lys	Glu	Thr	Glu	Pro	Pro	Asp	Ser	Gln	Gly	Glu	Pro	Ser
				985					1990					1995	
Lys	Pro	Gln	Ala	Ser	Gly	Tyr	Ala	Pro	Lys	Ser	Phe	His	Val	Glu	Asp
				2005					2010					2015	
Thr	Pro	Val	Cys	Phe	Ser	Arg	Asn	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Ile
				2020					2025					2030	
Asp	Ser	Glu	Asp	Asp	Leu	Leu	Gln	Glu	Cys	Ile	Ser	Ser	Ala	Met	Pro
				2035					2040					2045	
Lys	Lys	Lys	Lys	Pro	Ser	Arg	Leu	Lys	Gly	Asp	Asn	Glu	Lys	His	Ser
				2050					2055					2060	
Pro	Arg	Asn	Met	Gly	Gly	Ile	Leu	Gly	Glu	Asp	Leu	Thr	Leu	Asp	Leu
				065					2070					2075	
Lys	Asp	Ile	Gln	Arg	Pro	Asp	Ser	Glu	His	Gly	Leu	Ser	Pro	Asp	Ser
				2085					2090					2095	
Glu	Asn	Phe	Asp	Trp	Lys	Ala	Ile	Gln	Glu	Gly	Ala	Asn	Ser	Ile	Val
				2100					2105					2110	

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Ser Ser Leu His Gln Ala Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala
 2115 2120 2125
 Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu
 2130 2135 2140
 Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr
 145 2150 2155 2160
 Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu
 2165 2170 2175
 Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys
 2180 2185 2190
 Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu
 2195 2200 2205
 Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile
 2210 2215 2220
 Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser
 225 2230 2235 2240
 Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro
 2245 2250 2255
 Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg
 2260 2265 2270
 Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln
 2275 2280 2285
 Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser
 2290 2295 2300
 Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro
 305 2310 2315 2320
 Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile
 2325 2330 2335
 Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser
 2340 2345 2350
 Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser
 2355 2360 2365
 Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu
 2370 2375 2380
 Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly
 385 2390 2395 2400
 Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu
 2405 2410 2415
 Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser
 2420 2425 2430
 Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro
 2435 2440 2445
 Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser
 2450 2455 2460
 Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln
 465 2470 2475 2480
 Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His
 2485 2490 2495
 Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser
 2500 2505 2510
 Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile
 2515 2520 2525
 Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser
 2530 2535 2540

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Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg
 545 2550 2555 2560
 Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala
 2565 2570 2575
 Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val
 2580 2585 2590
 Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala
 2595 2600 2605
 Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn
 2610 2615 2620
 Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser
 625 2630 2635 2640
 Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp
 2645 2650 2655
 Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly
 2660 2665 2670
 Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu
 2675 2680 2685
 Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln
 2690 2695 2700
 Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn
 705 2710 2715 2720
 Arg Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr
 2725 2730 2735
 Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn
 2740 2745 2750
 Glu Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Ser
 2755 2760 2765
 Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe
 2770 2775 2780
 Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala
 785 2790 2795 2800
 Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg
 2805 2810 2815
 Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys
 2820 2825 2830
 Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val
 2835 2840

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: DP1(TB2)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GCA GTC GCC GCT CCA GTC TAT CCG GCA CTA GGA ACA GCC CCG GGN GGC	48
Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly	
1 5 10 15	
GAG ACG GTC CCC GCC ATG TCT GCG GCC ATG AGG GAG AGG TTC GAC CGG	96
Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg	
20 25 30	
TTC CTG CAC GAG AAG AAC TGC ATG ACT GAC CTT CTG GCC AAG CTC GAG	144
Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu	
35 40 45	
GCC AAA ACC GGC GTG AAC AGG AGC TTC ATC GCT CTT GGT GTC ATC GGA	192
Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly	
50 55 60	
CTG GTG GCC TTG TAC CTG GTG TTC GGT TAT GGA GCC TCT CTC CTC TGC	240
Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys	
65 70 75 80	
AAC CTG ATA GGA TTT GGC TAC CCA GCC TAC ATC TCA ATT AAA GCT ATA	288
Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile Ser Ile Lys Ala Ile	
85 90 95	
GAG AGT CCC AAC AAA GAA GAT GAT ACC CAG TGG CTG ACC TAC TGG GTA	336
Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp Leu Thr Tyr Trp Val	
100 105 110	
GTG TAT GGT GTG TTC AGC ATT GCT GAA TTC TTC TCT GAT ATC TTC CTG	384
Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu	
115 120 125	
TCA TGG TTC CCC TTC TAC TAC ATG CTG AAG TGT GGC TTC CTG TTG TGG	432
Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys Gly Phe Leu Leu Trp	
130 135 140	
TGC ATG GCC CCG AGC CCT TCT AAT GGG GCT GAA CTG CTC TAC AAG CGC	480
Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg	
145 150 155 160	
ATC ATC CGT CCT TTC TTC CTG AAG CAC GAG TCC CAG ATG GAC AGT GTG	528
Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Gln Met Asp Ser Val	
165 170 175	
GTC AAG GAC CTT AAA GAC AAG TCC AAA GAG ACT GCA GAT GCC ATC ACT	576
Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr	
180 185 190	
AAA GAA GCG AAG AAA GCT ACC GTG AAT TTA CTG GGT GAA GAA AAG AAG	624
Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys	
195 200 205	
AGC ACC TAAACCAGAC TAAACCAGAC TGGATGGAAA CTTCTGCCC TCTCTGTACC	680
Ser Thr	
210	
TTCCTACTGG AGCTTGATGT TATATTAGGG ACTGTGGTAT AATTATTTTA ATAATGTTGC	740
CTTGGAACA TTTTGTAGAT ATTAAAGATT GGAATGTGTT GTAAGTTTCT TTGCTTACTT	800
TTACTGTCTA TATATATAGG GAGCACTTTA AACTTAATGC AGTGGGCAGT GTCCACGTTT	860
TTGGAAAATG TATTTTGCCT CTGGGTAGGA AAAGATGTAT GTTGCTATCC TGCAGGAAAT	920
ATAAACTTAA AATAAAATTA TATACCCAC AGGCTGTGTA CTTTACTGGG CTCTCCCTGC	980
ACGSATTTTC TCTGTAGTTA CATTTAGGRT AATCTTTATG GTTCTACTTC CTRTAATGTA	1040
CAATTTTATA TAATTCNGRA ATGTTTTTAA TGTATTTGTG CACATGTACA TATGGAAATG	1100
TTACTGTCTG ACTACANCAT GCATCATGCT CATGGGGAGG GAGCAGGGGA AGGTTGTATG	1160
TGTCATTTAT AACTTCTGTA CAGTAAGACC ACCTGCCAAA AGCTGGAGGA ACCATTGTGC	1220
TGGTGTGGTC TACTAAATAA TACTTTAGGA AATACGTGAT TAATATGCAA GTGAACAAAG	1280
TGAGAAATGA AATCGAATGG AGATTGGCCT GGTGTTTTCC GTAGTATATG GCATATGAAT	1340
ACCAGGATAG CTTTATAAAG CAGTTAGTTA GTTAGTTACT CACTCTAGTG ATAAATCGGG	1400

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AAATTTACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAG 1460
 AGTACCCTGT AACTCTCAAT TCCCTGAAAA ACTAGTAATA CTGTCTTATC TGCTATAAAC 1520
 TTTACATATT TGTCTATTGT CAAGATGCTA CANTGGAMNC CATTCTGGT TTTATCTTCA 1580
 NAGSGGAGAN ACATGTTGAT TTAGTCTTCT TTCCCAATCT TCTTTTTTAA MCCAGTTTNA 1640
 GGMNCTTCTG RAGATTTGYC CACCTCTGAT TACATGTATG TTCTYGTTTG TATCATKAGC 1700
 AACAAATGC TAATGRCGAC ACCTAGCTCT RAGMGCAATT CTGGGAGANT GARAGGNWGT 1760
 ATARAGTMNC CCATAATCTG CTTGGCAATA GTTAAGTCAA TCTATCTTCA GTTTTTCTCT 1820
 GGCCTTTAAG GTCAAACACA AGAGGCTTCC CTAGTTTACA AGTCAGAGTC ACTTGTAGTC 1880
 CATTTAAATG CCCTCATCCG TATTCTTTGT GTTGATAAGC TGCACAKGAC TACATAGTAA 1940
 GTACAGANCA GTAAAGTTAA NNCGGATGTC TCCATTGATC TGCCAANTCG NTATAGAGAG 2000
 CAATTTGTCT GGACTAGAAA ATCTGAGTTT TACACCATAC TGTTAAGAGT CCTTTTGAAT 2060
 TAAACTAGAC TAAAACAAGT GTATAACTAA ACTAACAAGA TTAAATATCC AGCCAGTACA 2120
 GTATTTTTTA AGGCAAATAA AGATGATTAG CTCACCTTGA GNTAACAATC AGGTAAGATC 2180
 ATNACAATGT CTCATGATGT NAANAATATT AAAGATATCA ATACTAAGTG ACAGTATCAC 2240
 NNCTAATATA ATATGGATCA GAGCATTAT TTTGGGGAGG AAAACAGTGG TGATTACCGG 2300
 CTTTTTATTA AACTTAAAAC TTTGTAGAAA GCAAACAAA TTGTTCTTGG GAGAAAATCA 2360
 ACTTTTAGAT TAAAAAATT TTAAGTAWCT AGGAGTATTT AAATCCTTTT CCCATAAATA 2420
 AAAGTACAGT TTTCTTGGTG GCAGAATGAA AATCAGCAAC NTCTAGCATA TAGACTATAT 2480
 AATCAGATTG ACAGCATATA GAATATATTA TCAGACAAGA TGAGGAGGTA CAAAAGTTAC 2540
 TATTGCTCAT AATGACTTAC AGGCTAAAAN TAGNTNTAAA ATACTATATT AAATTCTGAA 2600
 TGCAATTTTT TTTTGTTCCT TTGAGACCAA AATTTAAGTT AACTGTTGCT GGCAGTCTAA 2660
 GTGTAAATGT TAACAGCAGG AGAAGTTAAG AATTGAGCAG TTCTGTTGCA TGATTTCCCA 2720
 AATGAAATAC TGCCTTGGCT AGAGTTTGAA AAATAATTG AGCCTGTGCC TGGCTAGAAA 2780
 ACAAGCGTTT ATTTGAATGT GAATAGTGTT TCAAAGGTAT GTAGTTACAG AATTCCTACC 2840
 AAACAGCTTA AATTCTTCAA GAAAGAATTC CTGCAGCAGT TATTCCCTTA CCTGAAGGCT 2900
 TCAATCATTT GGATCAACAA CTGCTACTCT CGGGAAGACT CCTCTACTCA CAGCTGAAGA 2960
 AAATGAGCAC ACCCTTCACA CTGTTATCAC CTATCCTGAA GATGTGATAC ACTGAATGGA 3020
 AATAAATAGA TGTAATAAAA ATTGAGWTCT CATTTAAAAA AAACCATGTG CCCAATGGGA 3080
 AAATGACCTC ATGTTGTGGT TTAAACAGCA ACTGCACCCA CTAGCACAGC CCATTGAGCT 3140
 ANCCTATATA TACATCTCTG TCAGTGCCCC TC 3172

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly
 1 5 10 15
 Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg
 20 25 30
 Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu

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Gln Cys Gln Val Asn Tyr His Ala Gln His Tyr His Leu Thr Pro Phe
 145 150 155 160
 Thr Val Ile Asn Ile Met Tyr Ser Phe Asn Lys Thr Gln Gly Pro Arg
 165 170 175
 Ala Leu Trp Lys Gly Met Gly Ser Thr Phe Ile Val Gln Gly Val Thr
 180 185 190
 Leu Gly Ala Glu Gly Ile Ile Ser Glu Phe Thr Pro Leu Pro Arg Glu
 195 200 205
 Val Leu His Lys Trp Ser Pro Lys Gln Ile Gly Glu His Leu Leu Leu
 210 215 220
 Lys Ser Leu Thr Tyr Val Val Ala Met Pro Phe Tyr Ser Ala Ser Leu
 225 230 235 240
 Ile Glu Thr Val Gln Ser Glu Ile Ile Arg Asp Asn Thr Gly Ile Leu
 245 250 255
 Glu Cys Val Lys Glu Gly Ile Gly Arg Val Ile Gly Met Gly Val Pro
 260 265 270
 His Ser Lys Arg Leu Leu Pro Leu Leu Ser Leu Ile Phe Pro Thr Val
 275 280 285
 Leu His Gly Val Leu His Tyr Ile Ile Ser Ser Val Ile Gln Lys Phe
 290 295 300
 Val Leu Leu Ile Leu Lys Arg Lys Thr Tyr Asn Ser His Leu Ala Glu
 305 310 315 320
 Ser Thr Ser Pro Val Gln Ser Met Leu Asp Ala Tyr Phe Pro Glu Leu
 325 330 335
 Ile Ala Asn Phe Ala Ala Ser Leu Cys Ser Asp Val Ile Leu Tyr Pro
 340 345 350
 Leu Glu Thr Val Leu His Arg Leu His Ile Gln Gly Thr Arg Thr Ile
 355 360 365
 Ile Asp Asn Thr Asp Leu Gly Tyr Glu Val Leu Pro Ile Asn Thr Gln
 370 375 380
 Tyr Glu Gly Met Arg Asp Cys Ile Asn Thr Ile Arg Gln Glu Glu Gly
 385 390 395 400
 Val Phe Gly Phe Tyr Lys Gly Phe Gly Ala Val Ile Ile Gln Tyr Thr
 405 410 415
 Leu His Ala Ala Val Leu Gln Ile Thr Lys Ile Ile Tyr Ser Thr Leu
 420 425 430
 Leu Gln

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: YS-39(TB2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Leu Arg Arg Phe Asp Arg Phe Leu His Glu Lys Asn Cys Met Thr
 1 5 10 15
 Asp Leu Leu Ala Lys Leu Glu Ala Lys Thr Gly Val Asn Arg Ser Phe

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	20		25		30														
Ile	Ala	Leu	Gly	Val	Ile	Gly	Leu	Val	Ala	Leu	Tyr	Leu	Val	Phe	Gly				
	35					40					45								
Tyr	Gly	Ala	Ser	Leu	Leu	Cys	Asn	Leu	Ile	Gly	Phe	Gly	Tyr	Pro	Ala				
	50					55					60								
Tyr	Ile	Ser	Ile	Lys	Ala	Ile	Glu	Ser	Pro	Asn	Lys	Glu	Asp	Asp	Thr				
	65				70					75					80				
Gln	Trp	Leu	Thr	Tyr	Trp	Val	Val	Tyr	Gly	Val	Phe	Ser	Ile	Ala	Glu				
				85					90					95					
Phe	Phe	Ser	Asp	Ile	Phe	Leu	Ser	Trp	Phe	Pro	Phe	Tyr	Tyr	Ile	Leu				
			100					105					110						
Lys	Cys	Gly	Phe	Leu	Leu	Trp	Cys	Met	Ala	Pro	Ser	Pro	Ser	Asn	Gly				
		115					120					125							
Ala	Glu	Leu	Leu	Tyr	Lys	Arg	Ile	Ile	Arg	Pro	Phe	Phe	Leu	Lys	His				
	130					135					140								
Glu	Ser	Gln	Met	Asp	Ser	Val	Val	Lys	Asp	Leu	Lys	Asp	Lys	Ala	Lys				
	145				150				155						160				
Glu	Thr	Ala	Asp	Ala	Ile	Thr	Lys	Glu	Ala	Lys	Lys	Ala	Thr	Val	Asn				
				165					170						175				
Leu	Leu	Gly	Glu	Glu	Lys	Lys	Ser	Thr											
			180					185											

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2843 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	Ala	Ala	Ser	Tyr	Asp	Gln	Leu	Leu	Lys	Gln	Val	Glu	Ala	Leu				
1				5				10					15						
Lys	Met	Glu	Asn	Ser	Asn	Leu	Arg	Gln	Glu	Leu	Glu	Asp	Asn	Ser	Asn				
			20					25					30						
His	Leu	Thr	Lys	Leu	Glu	Thr	Glu	Ala	Ser	Asn	Met	Lys	Glu	Val	Leu				
		35					40					45							
Lys	Gln	Leu	Gln	Gly	Ser	Ile	Glu	Asp	Glu	Ala	Met	Ala	Ser	Ser	Gly				
	50					55					60								
Gln	Ile	Asp	Leu	Leu	Glu	Arg	Leu	Lys	Glu	Leu	Asn	Leu	Asp	Ser	Ser				
	65				70				75					80					
Asn	Phe	Pro	Gly	Val	Lys	Leu	Arg	Ser	Lys	Met	Ser	Leu	Arg	Ser	Tyr				
				85					90					95					
Gly	Ser	Arg	Glu	Gly	Ser	Val	Ser	Ser	Arg	Ser	Gly	Glu	Cys	Ser	Pro				
			100					105					110						
Val	Pro	Met	Gly	Ser	Phe	Pro	Arg	Arg	Gly	Phe	Val	Asn	Gly	Ser	Arg				
		115					120					125							
Glu	Ser	Thr	Gly	Tyr	Leu	Glu	Glu	Leu	Glu	Lys	Glu	Arg	Ser	Leu	Leu				
	130					135					140								
Leu	Ala	Asp	Leu	Asp	Lys	Glu	Glu	Lys	Glu	Lys	Asp	Trp	Tyr	Tyr	Ala				
	145				150					155					160				
Gln	Leu	Gln	Asn	Leu	Thr	Lys	Arg	Ile	Asp	Ser	Leu	Pro	Leu	Thr	Glu				

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165					170					175					
Asn	Phe	Ser	Leu	Gln	Thr	Asp	Met	Thr	Arg	Arg	Gln	Leu	Glu	Tyr	Glu
			180					185					190		
Ala	Arg	Gln	Ile	Arg	Val	Ala	Met	Glu	Glu	Gln	Leu	Gly	Thr	Cys	Gln
		195					200					205			
Asp	Met	Glu	Lys	Arg	Ala	Gln	Arg	Arg	Ile	Ala	Arg	Ile	Gln	Gln	Ile
	210					215					220				
Glu	Lys	Asp	Ile	Leu	Arg	Ile	Arg	Gln	Leu	Leu	Gln	Ser	Gln	Ala	Thr
	225					230					235				240
Glu	Ala	Glu	Arg	Ser	Ser	Gln	Asn	Lys	His	Glu	Thr	Gly	Ser	His	Asp
				245					250					255	
Ala	Glu	Arg	Gln	Asn	Glu	Gly	Gln	Gly	Val	Gly	Glu	Ile	Asn	Met	Ala
			260					265					270		
Thr	Ser	Gly	Asn	Gly	Gln	Gly	Ser	Thr	Thr	Arg	Met	Asp	His	Glu	Thr
		275					280					285			
Ala	Ser	Val	Leu	Ser	Ser	Ser	Ser	Thr	His	Ser	Ala	Pro	Arg	Arg	Leu
	290						295				300				
Thr	Ser	His	Leu	Gly	Thr	Lys	Val	Glu	Met	Val	Tyr	Ser	Leu	Leu	Ser
	305					310					315				320
Met	Leu	Gly	Thr	His	Asp	Lys	Asp	Asp	Met	Ser	Arg	Thr	Leu	Leu	Ala
				325					330					335	
Met	Ser	Ser	Ser	Gln	Asp	Ser	Cys	Ile	Ser	Met	Arg	Gln	Ser	Gly	Cys
				340				345					350		
Leu	Pro	Leu	Leu	Ile	Gln	Leu	Leu	His	Gly	Asn	Asp	Lys	Asp	Ser	Val
		355					360					365			
Leu	Leu	Gly	Asn	Ser	Arg	Gly	Ser	Lys	Glu	Ala	Arg	Ala	Arg	Ala	Ser
	370					375					380				
Ala	Ala	Leu	His	Asn	Ile	Ile	His	Ser	Gln	Pro	Asp	Asp	Lys	Arg	Gly
	385					390					395				400
Arg	Arg	Glu	Ile	Arg	Val	Leu	His	Leu	Leu	Glu	Gln	Ile	Arg	Ala	Tyr
				405					410					415	
Cys	Glu	Thr	Cys	Trp	Glu	Trp	Gln	Glu	Ala	His	Glu	Pro	Gly	Met	Asp
			420					425					430		
Gln	Asp	Lys	Asn	Pro	Met	Pro	Ala	Pro	Val	Glu	His	Gln	Ile	Cys	Pro
		435					440					445			
Ala	Val	Cys	Val	Leu	Met	Lys	Leu	Ser	Phe	Asp	Glu	Glu	His	Arg	His
	450					455					460				
Ala	Met	Asn	Glu	Leu	Gly	Gly	Leu	Gln	Ala	Ile	Ala	Glu	Leu	Leu	Gln
	465					470					475				480
Val	Asp	Cys	Glu	Met	Tyr	Gly	Leu	Thr	Asn	Asp	His	Tyr	Ser	Ile	Thr
				485					490					495	
Leu	Arg	Arg	Tyr	Ala	Gly	Met	Ala	Leu	Thr	Asn	Leu	Thr	Phe	Gly	Asp
			500					505					510		
Val	Ala	Asn	Lys	Ala	Thr	Leu	Cys	Ser	Met	Lys	Gly	Cys	Met	Arg	Ala
		515					520					525			
Leu	Val	Ala	Gln	Leu	Lys	Ser	Glu	Ser	Glu	Asp	Leu	Gln	Gln	Val	Ile
	530					535					540				
Ala	Ser	Val	Leu	Arg	Asn	Leu	Ser	Trp	Arg	Ala	Asp	Val	Asn	Ser	Lys
	545					550					555				560
Lys	Thr	Leu	Arg	Glu	Val	Gly	Ser	Val	Lys	Ala	Leu	Met	Glu	Cys	Ala
				565					570					575	
Leu	Glu	Val	Lys	Lys	Glu	Ser	Thr	Leu	Lys	Ser	Val	Leu	Ser	Ala	Leu
			580					585						590	

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Trp	Asn	Leu	Ser	Ala	His	Cys	Thr	Glu	Asn	Lys	Ala	Asp	Ile	Cys	Ala
		595					600					605			
Val	Asp	Gly	Ala	Leu	Ala	Phe	Leu	Val	Gly	Thr	Leu	Thr	Tyr	Arg	Ser
	610					615					620				
Gln	Thr	Asn	Thr	Leu	Ala	Ile	Ile	Glu	Ser	Gly	Gly	Gly	Ile	Leu	Arg
625					630					635					640
Asn	Val	Ser	Ser	Leu	Ile	Ala	Thr	Asn	Glu	Asp	His	Arg	Gln	Ile	Leu
				645					650					655	
Arg	Glu	Asn	Asn	Cys	Leu	Gln	Thr	Leu	Leu	Gln	His	Leu	Lys	Ser	His
			660					665					670		
Ser	Leu	Thr	Ile	Val	Ser	Asn	Ala	Cys	Gly	Thr	Leu	Trp	Asn	Leu	Ser
		675					680					685			
Ala	Arg	Asn	Pro	Lys	Asp	Gln	Glu	Ala	Leu	Trp	Asp	Met	Gly	Ala	Val
	690					695					700				
Ser	Met	Leu	Lys	Asn	Leu	Ile	His	Ser	Lys	His	Lys	Met	Ile	Ala	Met
705					710					715					720
Gly	Ser	Ala	Ala	Ala	Leu	Arg	Asn	Leu	Met	Ala	Asn	Arg	Pro	Ala	Lys
				725					730					735	
Tyr	Lys	Asp	Ala	Asn	Ile	Met	Ser	Pro	Gly	Ser	Ser	Leu	Pro	Ser	Leu
			740					745					750		
His	Val	Arg	Lys	Gln	Lys	Ala	Leu	Glu	Ala	Glu	Leu	Asp	Ala	Gln	His
		755					760					765			
Leu	Ser	Glu	Thr	Phe	Asp	Asn	Ile	Asp	Asn	Leu	Ser	Pro	Lys	Ala	Ser
	770					775						780			
His	Arg	Ser	Lys	Gln	Arg	His	Lys	Gln	Ser	Leu	Tyr	Gly	Asp	Tyr	Val
785					790					795					800
Phe	Asp	Thr	Asn	Arg	His	Asp	Asp	Asn	Arg	Ser	Asp	Asn	Phe	Asn	Thr
				805					810					815	
Gly	Asn	Met	Thr	Val	Leu	Ser	Pro	Tyr	Leu	Asn	Thr	Thr	Val	Leu	Pro
			820					825					830		
Ser	Ser	Ser	Ser	Ser	Arg	Gly	Ser	Leu	Asp	Ser	Ser	Arg	Ser	Glu	Lys
		835					840					845			
Asp	Arg	Ser	Leu	Glu	Arg	Glu	Arg	Gly	Ile	Gly	Leu	Gly	Asn	Tyr	His
	850					855					860				
Pro	Ala	Thr	Glu	Asn	Pro	Gly	Thr	Ser	Ser	Lys	Arg	Gly	Leu	Gln	Ile
865					870					875					880
Ser	Thr	Thr	Ala	Ala	Gln	Ile	Ala	Lys	Val	Met	Glu	Glu	Val	Ser	Ala
				885					890					895	
Ile	His	Thr	Ser	Gln	Glu	Asp	Arg	Ser	Ser	Gly	Ser	Thr	Thr	Glu	Leu
			900					905						910	
His	Cys	Val	Thr	Asp	Glu	Arg	Asn	Ala	Leu	Arg	Arg	Ser	Ser	Ala	Ala
		915					920					925			
His	Thr	His	Ser	Asn	Thr	Tyr	Asn	Phe	Thr	Lys	Ser	Glu	Asn	Ser	Asn
		930				935					940				
Arg	Thr	Cys	Ser	Met	Pro	Tyr	Ala	Lys	Leu	Glu	Tyr	Lys	Arg	Ser	Ser
945					950					955					960
Asn	Asp	Ser	Leu	Asn	Ser	Val	Ser	Ser	Ser	Asp	Gly	Tyr	Gly	Lys	Arg
				965					970					975	
Gly	Gln	Met	Lys	Pro	Ser	Ile	Glu	Ser	Tyr	Ser	Glu	Asp	Asp	Glu	Ser
			980					985					990		
Lys	Phe	Cys	Ser	Tyr	Gly	Gln	Tyr	Pro	Ala	Asp	Leu	Ala	His	Lys	Ile
		995					1000					1005			
His	Ser	Ala	Asn	His	Met	Asp	Asp	Asn	Asp	Gly	Glu	Leu	Asp	Thr	Pro
						1010					1020				

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Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg
 025 1030 1035 1040
 Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile
 1045 1050 1055
 Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser
 1060 1065 1070
 Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys
 1075 1080 1085
 Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser
 1090 1095 1100
 Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly
 1105 1110 1115 1120
 Ile Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu
 1125 1130 1135
 Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln
 1140 1145 1150
 His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu
 1155 1160 1165
 Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala
 1170 1175 1180
 Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser
 1185 1190 1195 1200
 Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Ser Glu
 1205 1210 1215
 Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His
 1220 1225 1230
 Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr
 1235 1240 1245
 Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val
 1250 1255 1260
 Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu
 1265 1270 1275 1280
 Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala
 1285 1290 1295
 Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly
 1300 1305 1310
 Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln
 1315 1320 1325
 His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser
 1330 1335 1340
 Glu Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser
 1345 1350 1355 1360
 Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr
 1365 1370 1375
 Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser
 1380 1385 1390
 Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu
 1395 1400 1405
 Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro
 1410 1415 1420
 Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro
 1425 1430 1435 1440
 Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys

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1445			1450			1455									
Ala	Pro	Thr	Ala	Glu	Lys	Arg	Glu	Ser	Gly	Pro	Lys	Gln	Ala	Ala	Val
			1460					1465				1470			
Asn	Ala	Ala	Val	Gln	Arg	Val	Gln	Val	Leu	Pro	Asp	Ala	Asp	Thr	Leu
			1475				1480					1485			
Leu	His	Phe	Ala	Thr	Glu	Ser	Thr	Pro	Asp	Gly	Phe	Ser	Cys	Ser	Ser
			1490				1495				1500				
Ser	Leu	Ser	Ala	Leu	Ser	Leu	Asp	Glu	Pro	Phe	Ile	Gln	Lys	Asp	Val
					1510					1515				1520	
Glu	Leu	Arg	Ile	Met	Pro	Pro	Val	Gln	Glu	Asn	Asp	Asn	Gly	Asn	Glu
				1525						1530				1535	
Thr	Glu	Ser	Glu	Gln	Pro	Lys	Glu	Ser	Asn	Glu	Asn	Gln	Glu	Lys	Glu
			1540					1545					1550		
Ala	Glu	Lys	Thr	Ile	Asp	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Asp	Ser	Asp
			1555					1560				1565			
Asp	Asp	Asp	Ile	Glu	Ile	Leu	Glu	Glu	Cys	Ile	Ile	Ser	Ala	Met	Pro
			1570				1575				1580				
Thr	Lys	Ser	Ser	Arg	Lys	Ala	Lys	Lys	Pro	Ala	Gln	Thr	Ala	Ser	Lys
					1590						1595				1600
Leu	Pro	Pro	Pro	Val	Ala	Arg	Lys	Pro	Ser	Gln	Leu	Pro	Val	Tyr	Lys
				1605						1610				1615	
Leu	Leu	Pro	Ser	Gln	Asn	Arg	Leu	Gln	Pro	Gln	Lys	His	Val	Ser	Phe
			1620					1625					1630		
Thr	Pro	Gly	Asp	Asp	Met	Pro	Arg	Val	Tyr	Cys	Val	Glu	Gly	Thr	Pro
			1635					1640				1645			
Ile	Asn	Phe	Ser	Thr	Ala	Thr	Ser	Leu	Ser	Asp	Leu	Thr	Ile	Glu	Ser
			1650				1655				1660				
Pro	Pro	Asn	Glu	Leu	Ala	Ala	Gly	Glu	Gly	Val	Arg	Gly	Gly	Ala	Gln
					1670					1675				1680	
Ser	Gly	Glu	Phe	Glu	Lys	Arg	Asp	Thr	Ile	Pro	Thr	Glu	Gly	Arg	Ser
				1685				1690						1695	
Thr	Asp	Glu	Ala	Gln	Gly	Gly	Lys	Thr	Ser	Ser	Val	Thr	Ile	Pro	Glu
			1700					1705					1710		
Leu	Asp	Asp	Asn	Lys	Ala	Glu	Glu	Gly	Asp	Ile	Leu	Ala	Glu	Cys	Ile
			1715				1720				1725				
Asn	Ser	Ala	Met	Pro	Lys	Gly	Lys	Ser	His	Lys	Pro	Phe	Arg	Val	Lys
			1730				1735				1740				
Lys	Ile	Met	Asp	Gln	Val	Gln	Gln	Ala	Ser	Ala	Ser	Ser	Ser	Ala	Pro
					1750					1755				1760	
Asn	Lys	Asn	Gln	Leu	Asp	Gly	Lys	Lys	Lys	Lys	Pro	Thr	Ser	Pro	Val
				1765				1770						1775	
Lys	Pro	Ile	Pro	Gln	Asn	Thr	Glu	Tyr	Arg	Thr	Arg	Val	Arg	Lys	Asn
			1780					1785					1790		
Ala	Asp	Ser	Lys	Asn	Asn	Leu	Asn	Ala	Glu	Arg	Val	Phe	Ser	Asp	Asn
			1795				1800					1805			
Lys	Asp	Ser	Lys	Lys	Gln	Asn	Leu	Lys	Asn	Asn	Ser	Lys	Asp	Phe	Asn
			1810				1815				1820				
Asp	Lys	Leu	Pro	Asn	Asn	Glu	Asp	Arg	Val	Arg	Gly	Ser	Phe	Ala	Phe
				1830						1835				1840	
Asp	Ser	Pro	His	His	Tyr	Thr	Pro	Ile	Glu	Gly	Thr	Pro	Tyr	Cys	Phe
				1845				1850						1855	
Ser	Arg	Asn	Asp	Ser	Leu	Ser	Ser	Leu	Asp	Phe	Asp	Asp	Asp	Asp	Val
			1860					1865						1870	

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Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys
 1875 1880 1885

Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln
 1890 1895 1900

Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg
 905 1910 1915 1920

Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser
 1925 1930 1935

Ser Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln
 1940 1945 1950

Asn Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser
 1955 1960 1965

Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn
 1970 1975 1980

Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser
 985 1990 1995 2000

Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp
 2005 2010 2015

Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile
 2020 2025 2030

Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro
 2035 2040 2045

Lys Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser
 2050 2055 2060

Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu
 065 2070 2075 2080

Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser
 2085 2090 2095

Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val
 2100 2105 2110

Ser Ser Leu His Gln Ala Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala
 2115 2120 2125

Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu
 2130 2135 2140

Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr
 145 2150 2155 2160

Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu
 2165 2170 2175

Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys
 2180 2185 2190

Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu
 2195 2200 2205

Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile
 2210 2215 2220

Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser
 225 2230 2235 2240

Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro
 2245 2250 2255

Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg
 2260 2265 2270

Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln
 2275 2280 2285

Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser
 2290 2295 2300

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Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro
 305 2310 2315 2320

Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile
 2325 2330 2335

Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser
 2340 2345 2350

Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser
 2355 2360 2365

Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu
 2370 2375 2380

Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly
 385 2390 2395 2400

Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu
 2405 2410 2415

Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser
 2420 2425 2430

Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro
 2435 2440 2445

Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser
 2450 2455 2460

Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln
 465 2470 2475 2480

Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His
 2485 2490 2495

Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser
 2500 2505 2510

Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile
 2515 2520 2525

Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser
 2530 2535 2540

Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg
 545 2550 2555 2560

Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala
 2565 2570 2575

Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val
 2580 2585 2590

Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala
 2595 2600 2605

Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn
 2610 2615 2620

Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser
 625 2630 2635 2640

Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp
 2645 2650 2655

Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly
 2660 2665 2670

Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu
 2675 2680 2685

Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln
 2690 2695 2700

Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn
 705 2710 2715 2720

Arg Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr

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2725	2730	2735
Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn		
2740	2745	2750
Glu Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Ser		
2755	2760	2765
Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe		
2770	2775	2780
Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala		
785	2790	2795
Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg		
2805	2810	2815
Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys		
2820	2825	2830
Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val		
2835	2840	

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: ral2(yeast)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Thr Gly Ala Lys Gly Leu Gln Leu Arg Ala Leu Arg Arg Ile Ala		
1	5	10
Arg Ile Glu Gln Gly Gly Thr Ala Ile Ser Pro Thr Ser Pro Leu		
20	25	30

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: m3(mAChR)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Tyr Trp Arg Ile Tyr Lys Glu Thr Glu Lys Arg Thr Lys Glu Leu		
1	5	10
Ala Gly Leu Gln Ala Ser Gly Thr Glu Ala Glu Thr Glu		
20	25	

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

-continued

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
 (B) CLONE: MCC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Tyr Pro Asn Leu Ala Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu
 1 5 10 15

Ala Gly Leu Arg Glu Glu Asn Glu Ser Leu Thr Ala Met
 20 25

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATCAAGAC TGTGACTTTT AATTGTAGTT TATCCATTTT 40

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTAGAATTT CATGTTAATA TATTGTGTTT TTTTAAACAG 40

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTAGATTTTA AAAAGGTGTT TTAAAATAAT TTTTAAAGCT 40

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

-continued

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
 AAGCAATTGT TGTATAAAAA CTGTTTCTA TTTTATTTAG 40

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
 GTAACCTTTC TTCATATAGT AAACATTGCC TTGTGTACTC 40

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
 NNNNNNNNNN NNGTCCCTT TTTTAAAAA AAAAAAATAG 40

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
 GTAAGTAACT TGGCAGTACA ACTTATTTGA AACTTTAATA 40

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
 ATACAAGATA TTGATACTTT TTTATTATTT GTGGTTTTAG 40

-continued

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTAAGTTACT TGTTTCTAAG TGATAAAACA GYGAAGAGCT 40

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AATAAAAACA TAACTAATTA GGTTTCTTGT TTTATTTTAG 40

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTTAGTAAAT TSCCTTTTTT GTTTGTGGGT ATAAAAATAG 40

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCATTTTTG CATGTACTGA TGTTAACTCC ATCTTAACAG 40

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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-
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
GTAAATAAAT TATTTTATCA TATTTTAA AATTATTTAA 40
- (2) INFORMATION FOR SEQ ID NO:24:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
CATGATGTTA TCTGTATTTA CCTATAGTCT AAATTATACC ATCTATAATG TGCTTAATTT 60
TTAG 64
- (2) INFORMATION FOR SEQ ID NO:25:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
GTAACAGAAG ATTACAAACC CTGGTCACTA ATGCCATGAC TACTTTGCTA AG 52
- (2) INFORMATION FOR SEQ ID NO:26:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
GGATATTAAA GTCGTAATTT TGTTTCTAAA CTCATTGGC CCACAG 46
- (2) INFORMATION FOR SEQ ID NO:27:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

-continued

GTATGTTCTC TATAGTGTAC ATCGTAGTGC ATGTTTCAAA

40

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CATCATTGCT CTTCAAATAA CAAAGCATTG TGGTTTATGT TGATTTTATT TTTCAG

56

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTAAGACAAA AATGTTTTTTT AATGACATAG ACAATTACTG GTG

43

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTAGATGATT GTCTTTTCC TCTTGCCCTT TTAAATTAG

40

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTATGTTTTT ATAACATGTA TTTCTTAAGA TAGCTCAGGT ATGA

44

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs

-continued

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
- GCTTGGCTTC AAGTTGNCTT TTAAATGATC CTCTATTCTG TATTTAATTT ACAG 54
- (2) INFORMATION FOR SEQ ID NO:33:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
- GTACTATTTA GAATTCACC TGTTTTTCTT TTTTCTCTTT TTCTTTGAGG CAGGGTCTCA 60
CTCTG 65
- (2) INFORMATION FOR SEQ ID NO:34:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
- GCAACTAGTA TGATTTTATG TATAAATTAA TCTAAAATTG ATTAATTTCC AG 52
- (2) INFORMATION FOR SEQ ID NO:35:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
- GTACCTTTGA AACATTTAG TACTATAATA TGAATTTTCAT GT 42
- (2) INFORMATION FOR SEQ ID NO:36:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

-continued

-
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
 CCAACTCNAA TTAGATGACC CATATTCAGA AACTTACTAG 40
- (2) INFORMATION FOR SEQ ID NO:37:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
 GTATATATAG AGTTTTATAT TACTTTTAAA GTACAGAATT CATACTCTCA AAAA 54
- (2) INFORMATION FOR SEQ ID NO:38:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
 ATTGTGACCT TAATTTTGTG ATCTCTTGAT TTTTATTTC A G 41
- (2) INFORMATION FOR SEQ ID NO:39:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
 TCCCCGCTG CCGCTCTC 18
- (2) INFORMATION FOR SEQ ID NO:40:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
 GCAGCGCGG CTCCCGTG 18

-continued

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGAACGGCT CTCATGCTGC

20

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACGTGCGGGG AGGAATGGA

19

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGATATCTT ACCAAATGAT ATAC

24

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTATTCCTAC TTCTTCTATA CAG

23

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

-continued

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
TACCCATGCT GGCTCTTTTT C 21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
TGGGGCCATC TTGTTTCCTGA 20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
ACATTAGGCA CAAAGCTTGC AA 22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
ATCAAGCTCC AGTAAGAAGG TA 22

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
TGCGGCTCCT GGGTTGTTG 19

-continued

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCCCCTTCCT TTCTGAGGAC

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTTCTCCTG CCTCTTACTG C

21

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGACACCCC CCATTCCCTC

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCACTTAAAG CACATATATT TAGT

24

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

-continued

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:
GTATGGAAAA TAGTGAAGAA CC 22

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
TTCTTAAGTC CTGTTTTTCT TTTG 24

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
TTTAGAACCT TTTTGTGTT GTG 23

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:
CTCAGATTAT AACTAAGCC TAAC 24

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

-continued

CATGTCTCTT ACAGTAGTAC CA

22

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGGTCCAAGG GTAGCCAAGG

20

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TAAAAATGGA TAAACTACAA TTAAAAG

27

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AAATACAGAA TCATGTCTTG AAGT

24

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ACACCTAAAG ATGACAATTT GAG

23

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs

-continued

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
TAACTTAGAT AGCAGTAATT TCCC 24

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
ACAATAAACT GGAGTACACA AGG 23

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
ATAGGTCATT GCTTCTTGCT GAT 23

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
TGAATTTTAA TGGATTACCT AGGT 24

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
 CTTTTTTTGC TTTTACTGAT TAACG 25
- (2) INFORMATION FOR SEQ ID NO:68:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
 TGTAATTCAT TTTATTCCTA ATAGCTC 27
- (2) INFORMATION FOR SEQ ID NO:69:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
 GGTAGCCATA GTATGATTAT TTCT 24
- (2) INFORMATION FOR SEQ ID NO:70:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
 CTACCTATTT TTATACCCAC AAAC 24
- (2) INFORMATION FOR SEQ ID NO:71:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
 AAGAAAGCCT ACACCATTTT TGC 23
- (2) INFORMATION FOR SEQ ID NO:72:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
 GATCATTCTT AGAACCATCT TGC 23
- (2) INFORMATION FOR SEQ ID NO:73:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:
 ACCTATAGTC TAAATTATAC CATC 24
- (2) INFORMATION FOR SEQ ID NO:74:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:
 GTCATGGCAT TAGTGACCAG 20
- (2) INFORMATION FOR SEQ ID NO:75:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:
 AGTCGTAATT TTGTTTCTAA ACTC 24
- (2) INFORMATION FOR SEQ ID NO:76:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

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- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:
 TGAAGGACTC GGATTTACAG C 21
- (2) INFORMATION FOR SEQ ID NO:77:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:
 TCATTCCTC ACAGCCTGAT GAC 23
- (2) INFORMATION FOR SEQ ID NO:78:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:
 GCTTTGAAAC ATGCACTACG AT 22
- (2) INFORMATION FOR SEQ ID NO:79:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:
 AAACATCATT GCTCTTCAAA TAAC 24
- (2) INFORMATION FOR SEQ ID NO:80:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:
 TACCATGATT TAAAAATCCA CCAG 24

-continued

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GATGATTGTC TTTTTCCTCT TGC 23

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTGAGCTATC TTAAGAAATA CATG 24

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TTTTAAATGA TCCTCTATTC TGTAT 25

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACAGAGTCAG ACCCTGCCTC AAAG 24

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

-continued

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:
TTTCTATTCT TACTGCTAGC ATT 23

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:
ATACACAGGT AAGAAATTAG GA 22

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:
TAGATGACCC ATATTCTGTT TC 22

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:
CAATTAGGTC TTTTGGAGAG TA 22

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:
GTTACTGCAT ACACATTGTG AC 22

-continued

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTTTTTTGTTCCTAACATG AAG 23

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCTCCACAG GTAATACTCC C 21

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCTAGAACTG AATGGGGTAC G 21

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CAGGACAAA TAATCCTGTC CC 22

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

-continued

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATTTTCTTAG TTTCATTCTT CCTC 24

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGAAGGATCC CTTGTGCAGT GTGGA 25

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GACAGGATCC TGAAGCTGAG TTTG 24

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCAGAAAGTG CTGAAGAG 18

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

-continued

GGAATAATTA GGTCTCAA

19

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCAAATCCTA AGAGAGAACA A

21

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GATGGCAAGC TTGAGCCAG

19

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTTCCAGCAG TGTACAG

18

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGGAGATTTC GTCCTGA

18

TABLE I

APC EXONS	
EXON NUCLEOTIDES ¹	EXON BOUNDARY SEQUENCE ²
822 to 930	<u>ctgatgttatcgatttacctatagtctaaattataccatctataatgtgcttaatttttag/GGTTCA . . .</u> . . . <u>ACCAAG/gtaacagaagattacaaccctggcactaatgcatgactactttgctaag</u>
931 to 1309	<u>ggatattaaagtcgtaattttgttctaaactcattggcccacag/GTGGAA . . .</u> . . . <u>ATCCAA/gtatgttctctatagtgtacatcgtatgcatg</u>
1310 to 1405	<u>catcattgctctcaataacaagcattatggtttatggtttatgtttttttcag/TGCCAG . . .</u> . . . <u>AACTAG/gtaagacaaaaatgttttaatagacatagacaattactggtg</u>
1406 to 1545	<u>tagatgattgtcttttccctctgccttttaataatg/GGGGAC . . .</u> . . . <u>AACAAG/gtatgtttataacatgtatttcttaagatagctcggtatga</u>
1546 to 1623	<u>gcttgcttcaagttgtcttttaataatgacctctattctgtatttaattacag/GCTACG . . .</u> . . . <u>CAGCAG/gtactatttagaattcacctgttttctttcttttcttttctttgaggcagggtctcactctg</u>
1624 to 1740	<u>gcaactagtatgattttatgtataaataattctaaatgattaattgacag/GTTAAT . . .</u> . . . <u>AAAAAAG/gtacctttgaaaacattgtactataaatgaattcatgt</u>
1741 to 1955	<u>caactctaattagatgacccatattcagaactactag/GAATCA . . .</u> . . . <u>CCACAG/gtatatatagagtttatattacttttaagtacagaattcatactctcaaaa</u>
1956 to 8973	<u>tcttgattttattcag/GCAAAT . . .</u> . . . <u>GGTATTTATGCAAAAAAAAAATGTTTTTGT</u>

¹Relative to predicted translation initiation site

²Small case letters represent introns, large case letters represent exons

³The entire 3' end of the cloned APC cDNA (nt 1956-8973) appeared to be encoded in this exon, as indicated by restriction endonuclease mapping and sequencing of cloned genomic DNA. The ORF ended at 8535. The extreme 3' end of the APC transcript has not yet been indentified.

⁴The first line of sequence is (SEQ ID NO: 24); the second line of sequence is (SEQ ID NO: 25); the third line of sequence is (SEQ ID NO: 26); the fourth line of sequence is (SEQ ID NO: 27); the fifth line of sequence is (SEQ ID NO: 28); the sixth line of sequence is (SEQ ID NO: 29); the seventh line of sequence is (SEQ ID NO: 30); the eighth line of sequence is (SEQ ID NO: 31); the ninth line of sequence is (SEQ ID NO: 32); the tenth line of sequence is (SEQ ID NO: 33); the eleventh line of sequence is (SEQ ID NO: 34); the twelfth line of sequence is (SEQ ID NO: 35); the thirteenth line of sequence is (SEQ ID NO: 36); the fourteenth line of sequence is (SEQ ID NO: 37); the fifteenth line of sequence is (SEQ ID NO: 38); and the sixteenth line of sequence is (SEQ ID NO: 1).

TABLE IIA

TABLE IIB

Germline mutations of the APC gene in FAP and GS Patients						Somatic Mutations in Sporadic CRC Patients			
Pa- tient	Co- don	Nucleotide Change	Amino Acid Change	Extra- colonic Age Disease		PA- TIENT	CODON ¹	NUCLEOTIDE CHANGE	AMINO ACID CHANGE
93	279	TCA → <u>TGA</u>	Ser → Stop	39	Mandibular Osteoma	40	T35	MCC 12	GAG/gtaaga → (Splice Donor)
24	301	CGA → <u>TGA</u>	Arg → Stop	46	None	45	T16	MCC 145	vtcag/GGA → (Splice Acceptor)
34	301	CGA → <u>TGA</u>	Arg → Stop	27	Desmoid Tumor		T47	MCC 267	CGG → <u>CTG</u>
21	413	CGC → <u>TGC</u>	Arg → Cys	24	Mandibular Osteoma	50	T81	MCC 490	TCG → <u>TTG</u>
60	712	TCA → <u>TGA</u>	Ser → Stop	37	Mandibular Osteoma		T35	MCC 506	CGG → CAG
							T91	MCC 698	GCT 3 G <u>TT</u>
3746	243	CAGAG → CAG	splice- junction				T34	APC 288	CCAGT → <u>CCAGCCAGT</u>
							T27	APC 331	CGA → <u>TGA</u>
3460	301	CGA → <u>TGA</u>	Arg → stop			55	T135	APC 437	CAA/gtaa → CAA/gcaa
3827	456	CTTTCA → CTT CA	frameshift				T201	APC 1338	CAG → <u>TAG</u>
3712	500	T → <u>G</u>	Tyr → Stop			60			

*The mutated nucleotides are underlined.

For splice site mutations, the codon nearest to the mutation is listed
 The underlined nucleotides were mutant; small case letters represent introns, large case letters represent exons

TABLE III

Sequences of Primers Used for SSCP Analyses		
Exon	Primer 1	Primer 2
		<u>DP1</u>
	UP-TCCCCGCTGCCGCTCTC	RP-GCAGCGGGCGGCTCCCGTG
	UP-GTGAACGGCTCTCATGCTGC	RP-ACGTGCGGGGAGGAATGGA
	UP-ATGATATCTTACCAAATGATATAC	RP-TTATTCTACTTCTTCTATACAG
	UP-TACCCATGCTGGCTCTTTTTC	RP-TGGGGCCATCTTGTTCTTGA
	UP-ACATTAGGCACAAAGCTTGCAA	RP-ATCAAGCTCCAGTAAGAAGGTA
		<u>SRP19</u>
	UP-TGCGGCTCCTGGGTTGTTG	RP-GCCCCCTCCTTTCTGAGGAC
	UP-TTTTCTCCTGCCTCTTACTGC	RP-ATGACACCCCCATTCCCTC
	UP-CCACTTAAAGCACATATATTTAGT	RP-GTATGGAAAATAGTGAAGAACC
	UP-TTCTTAAGTCCTGTTTTCTTTTG	RP-TTTAGAACCCTTTTTTGTGTTGTG
	UP-CTCAGATTATACTAAGCCTAAC	RP-CATGTCTCTTACAGTAGTACCA
		<u>DP2.5</u>
	UP-AGGTCCAAGGGTAGCCAAGG*	RP-TAAAAATGGATAAACTACAATTAAAAG
	UP-AAATACAGAATCATGTCTTGAAGT	RP-ACACCTAAAGATGACAATTTGAG
	UP-TAACTTAGATAGCAGTAATTTCCC*	RP-ACAATAAACTGGAGTACACAAGG
	UP-ATAGGTCATTGCTTCTTGCTGAT*	RP-TGAATTTTAATGGATTACCTAGGT
	UP-CTTTTTTTGCTTTTACTGATTAACG	RP-TGTAATTCATTTTATTCTAATACCTC
	UP-GGTAGCCATAGTAGATTATTTCT	RP-CTACCTATTTTATACCCACAAAC
	UP-AAGAAAGCCTACACCAITTTTTGC	RP-GATCATTCTTAGAACCATCTTGC
	UP-ACCTTAGTCTAAATFATACCATC	RP-GTCATGGCATTACTGACCAG
	UP-AGTCGTAATTTTGTITCTAAACTC	RP-TGAAGGACTCCGATTTACCCC*
	UP-TCATTCCTCACAGCTGATGAC*	RP-GCTTTGAAACATGCACTACGAT
	UP-AAACATCATTGCTCTTCAAATAAC	RP-TACCATGATTTAAAATCCACCAG
	UP-GATGATTGTCTTTTTCTCTTGC	RP-CTGAGCTATCTTAAGAAATACATG
	UP-TTTTAAATGATCCTCTATTCTGTAT	RP-ACAGAGTCAGACCCTCCCTCAAAG
	UP-TTTCTATTCTTACTGCTAGCATT	RP-ATACACAGGTAAGAAATTAGGA
	UP-TAGATGACCCATATTCTCTTTC	RP-CAATTAGGTCTTTTTGAGAGTA
3-A	UP-GTTACTGCATACACATTGTGAC	RP-GCTTTTTGTTCGTAACATGAAG*
-B	UP-AGTACAAGGATGCCAATATTATG*	RP-ACTTCTATCTTTTTCAGAACGAG*
-C	UP-ATTGAATACTACAGTGTACCC*	RP-CTTGTATTCTAATTTGGCATAAGG*
-D	UP-CTGCCCATAACATCAAACAC*	RP-TGTTTGCGTCTTGCCCATCTT*
-E	UP-AGTCTTAAATATTAGATGAGCAG*	RP-GTTTCTCTTCAATATATTTTATGCTA*
-F	UP-AAGCCTACCAATTATAGTGAACG*	RP-AGCTGATGACAAAGATGATAATC*
-G	UP-AAGAAACAATACAGACTTATTGTG*	RP-ATGAGTGGGGTCTCCTGAAC*
-H	UPATCTCCCTCCAAAAGTGGTGC*	RP-TCCATCTGGAGTACTTTCTGTG*
-I	UP-AGTAAATGCTGCAGTTCAGAGG*	RP-CCGTGGCATATCATCCCC*
-J	UP-CCCAGACTGCTTCAAATFACC*	RP-GAGCCTCATCTGTACTTCTGC*
-K	UP-CCCTCAAATGAGTTAGCTGC*	RP-TTGTGGTATAGGTTTTACTGGTG*
-L	UP-ACCCAACAAAATCAGTTAGATG*	RP-GTGGCTGGTAACTTTAGCCTC*
-N	UP-ATGATGTTGACCTTTCCAGGG*	RP-ATTGTGTAACTTTTCATCAGTTGC*
-O	UP-AAGATGACCTGTTGCAGGAATG*	RP-GAATCAGACCAAGCTTGTCTAGAT*
-P	UP-CAATAGTAAGTAGTTTACATCAAG*	RP-AAACAGGACTTGTACTGTAGGA*
-Q	UP-CAGCCCCCTCAAGCAAACATC*	RP-GAGGACTTATTCCATTTCTACC*
-R	UP-CAGTCTCCTGGCCGAACCTC*	RP-GTTGACTGGCGTACTAATACAG*
-S	UP-TGGTAATGGAGCCAATAAAAAGG*	RP-TGGGACTTTTTCGCCATCCAC*
-T	UP-TGTCTCTATCCACACATTCGTC*	RP-ATGTTTTTCACTCCTCACTTTTTGC*
-U	UP-GGAGAAGAAGTGAAGTTCATC*	RP-TTGAATCTTAAATGTTTGGATTGC*
-V	UP-TCTCCCACAGGTAATACTCCC	RP-GCTACAAGTGAATGGGGTACG
-W	UP-CAGGACAAAATAATCCTGTCCC	RP-ATTTTCTTACTTTTCACTTTCTCCTC

All primers are read in the 5' to 3' direction. the first primer in each pair lies 5' of the exon it amplifies: the second primer lies 3' of the exon it amplifies. Primers that lie within the exon are identified by an asterisk. UP represents the -2ImI3 universal primer sequence: RP represents the MI3 reverse primer sequence. Primer 1 of DP1 exons 1, 2, 3, 4, and 5 are shown in SEQ ID NOS: 39, 41, 43, 45, and 47, respectively. Primer 2 of DP1 exons 1, 2, 3, 4, and 5 are shown in SEQ ID NOS: 40, 42, 44, 46, and 48, respectively. Primer 1 of SRP19 exons 1, 2, 3, 4, and 5 are shown in SEQ ID NOS: 49, 51, 53, 55, and 57, respectively. Primer 2 of SRP19 exons 1, 2, 3, 4, and 5 are shown in SEQ ID NOS: 50, 52, 54, 56, and 58, respectively. Primer 1 of DP2.5 exons 1, 2, 3, 4, 5, 6, 7, 8, 9, 9a, 10, 11, 12, 13, 14, and 15-A are shown in SEQ ID NOS: 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, and 89, respectively. Primer 2 of DP2.5 exons 1, 2, 3, 4, 5, 6, 7, 8, 9, 9a, 10, 11, 12, 13, 14, and 15-A are shown in SEQ ID NOS: 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, and 90, respectively. Primer 1 and primer 2 of DP2.5 exon 15-B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, and U are shown in SEQ ID NO: 1.

TABLE IV

Seven Different Versions of the 20-Amino Acid Repeat																				
Consensus:	F	.	V	E	.	T	P	.	C	F	S	R	.	S	S	L	S	S	L	S
1262:	Y	C	V	E	D	T	P	I	C	F	S	R	C	S	S	L	S	S	L	S
1376:	H	Y	V	Q	E	T	P	L	M	F	S	R	C	T	S	V	S	S	L	D
1492:	F	A	T	E	S	T	P	D	G	F	S	C	S	S	S	L	S	A	L	S
1643:	Y	C	V	E	G	T	P	I	N	F	S	T	A	T	S	L	S	D	L	T
1848:	T	P	I	E	G	T	P	Y	C	F	S	R	N	D	S	L	S	S	L	D
1953:	F	A	I	E	N	T	P	V	C	P	S	H	N	S	S	L	S	S	L	S
2013:	F	H	V	E	D	T	P	V	C	F	S	R	N	S	S	L	S	S	L	S

Numbers denote the first amino acid of each repeat. The consensus sequence at the top reflects a majority amino acid at a given position.

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We claim:

1. A cDNA molecule having the nucleotide sequence shown in SEQ ID NO: 1 or its complement.
2. An isolated DNA molecule having the nucleotide sequence shown in SEQ ID NO:1 or its complement.
3. A cDNA molecule which encodes a protein having the amino acid sequence shown in [FIG. 3 or 7 (SEQ ID NO: 7 or 2)].
4. An isolated DNA molecule which encodes a protein having the amino acid sequence shown in [FIG. 3 or 7 (SEQ ID NO: 7 or 2)].
5. A nucleic acid probe complementary to all or part of human wild-type APC gene coding sequences or the complement of said sequences such that said probe selectively hybridizes under stringent conditions to said APC gene or identifies endogenous, random modifications in said APC gene.
6. The nucleic acid probe of claim 5 which hybridizes to all or part of an exon selected from the group consisting of: (1) nucleotides 822 to 930; (2) nucleotides 931 to to 1309;

- (3) nucleotides 1406 to 1545; and (4) nucleotides 1956 to 2256 as shown in SEQ ID NO: 1.

7. A set of probes useful for detecting alteration of wild-type APC genes comprising a plurality of nucleic acid probes wherein said set is complementary to all nucleotides of the APC gene coding sequences as shown in SEQ ID NO:1 or the complement of said sequences.

8. A pair of single stranded DNA primers for determination of a nucleotide sequence of an APC gene by polymerase chain reaction, the sequence of said primers being derived from said APC gene, wherein the use of said primers in a polymerase chain reaction results in synthesis of DNA having all or part of the sequence shown in [FIG. 7 (SEQ ID NO:1)].

9. The pair of primers of claim 8 which have restriction enzyme sites at each 5' end.

10. The pair of primers of claim 8 having sequences complementary to all or part of one or more APC introns.

* * * * *

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO.: Re. 36,713

DATED: May 23, 2000

INVENTORS: Bert VOGELSTEIN, *et al.*

It is certified that an error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In [75] Inventors, "Albertson" has been replaced with --**Albertsen**--.

In [73] Assignees, "Zeneca" has been replaced with --**Zeneca Limited**--.

In [57] Abstract, line 2, "hum" has been replaced with --**human**--;

line 4, "wel" has been replaced with --**well**--;

line 5, "patents" has been replaced with --**patients**--;

line 6, "tissue" has been replaced with --**tissues**--.

Signed and Sealed this

First Day of May, 2001



NICHOLAS P. GODICI

Attest:

Attesting Officer

Acting Director of the United States Patent and Trademark Office