

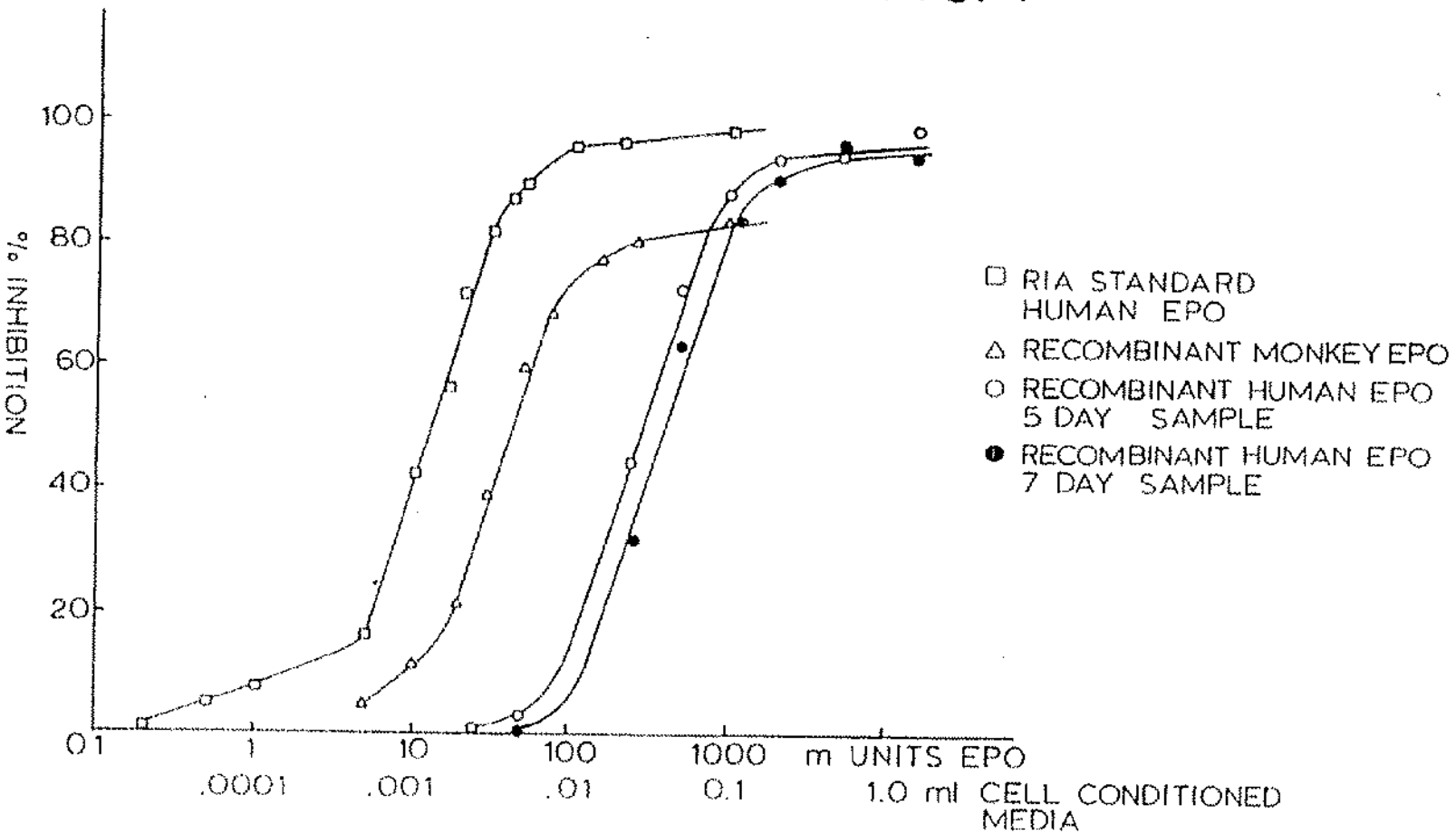
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FIG. 1



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FIG. 2

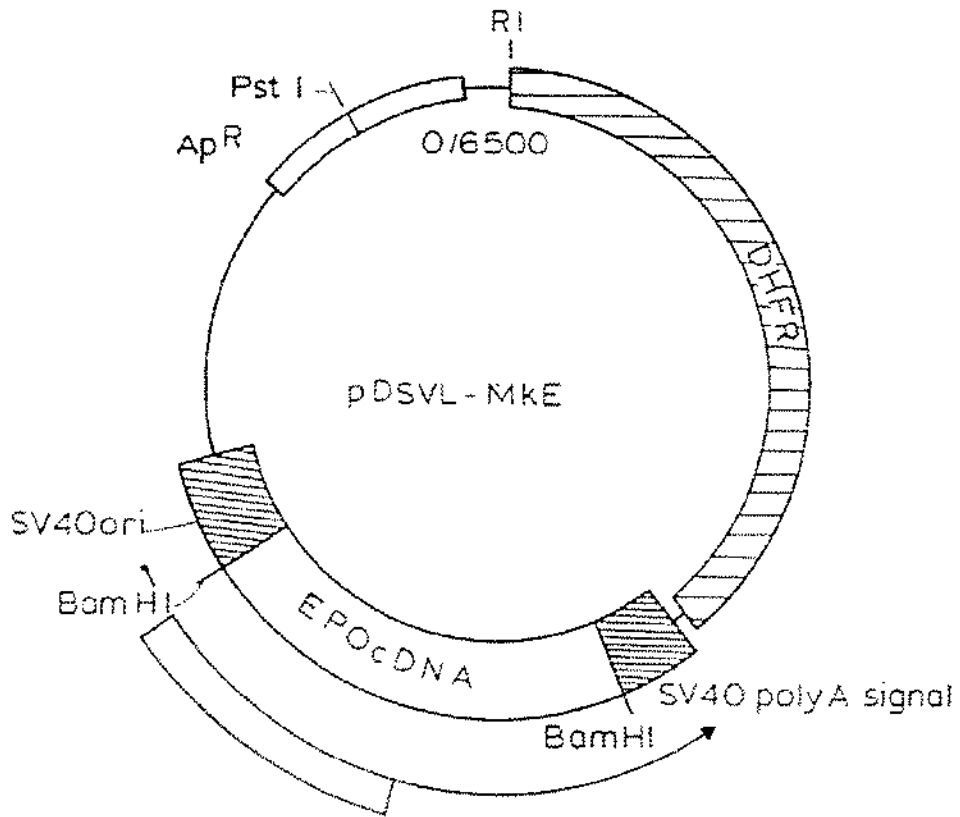
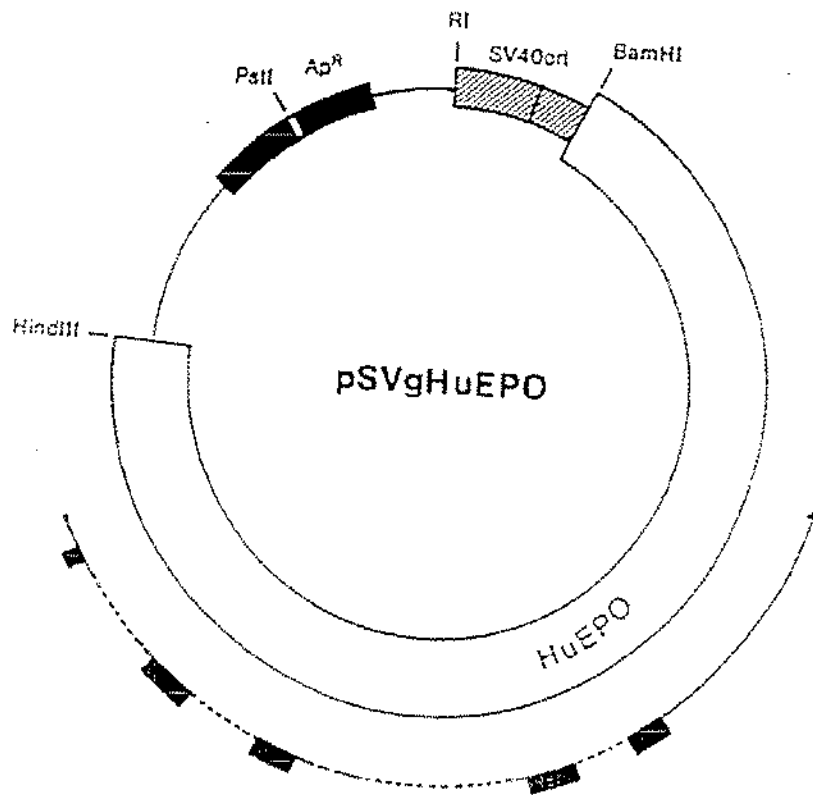


FIG. 3



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FIG. 4

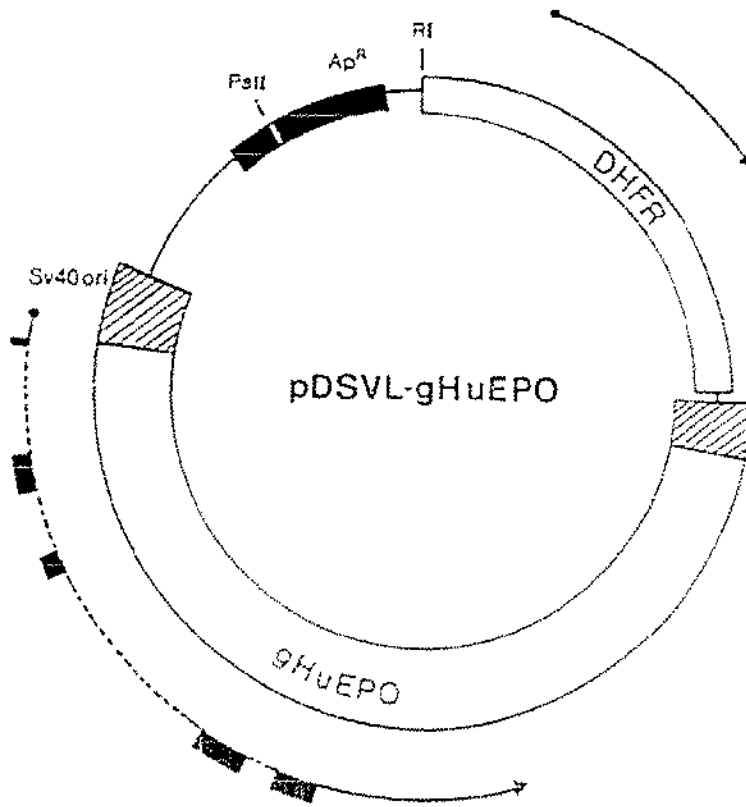


FIG.5B

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                    50
Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
GAC ACC AAA GTT AAC TTC TAT GCC TGG AAG AGG ATG GAG GTC GGG

                    60
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu
CAG CAG GCT GTA GAA GTC TGG CAG GGC CTG GCC CTG CTC TCA GAA

                    80
Ala Val Leu Arg Gly Gln Ala Val Leu Ala Asn Ser Ser Gln Pro
GCT GTC CTG CGG GGC CAG GCC GTG TTG GCC AAC TCT TCC CAG CCT
                    *

                    90
Phe Glu Pro Leu Gln Leu His Met Asp Lys Ala Ile Ser Gly Leu
TTC GAG CCC CTG CAG CTG CAC ATG GAT AAA GCC ATC AGT GGC CTT

                    110
Arg Ser Ile Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Glu Ala
CGC AGC ATC ACC ACT CTG CTT CGG GCG CTG GGA GCC CAG GAA GCC

                    120
Ile Ser Leu Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
ATC TCC CTC CCA GAT GCG GCC TCG GCT GCT CCA CTC CGA ACC ATC

                    140
Thr Ala Asp Thr Phe Cys Lys Leu Phe Arg Val Tyr Ser Asn Phe
ACT GCT GAC ACT TTC TGC AAA CTC TTC CGA GTC TAC TCC AAT TTC

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FIG. 5C

150 Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Arg 160
 CTC CGG GGA AAG CTG AAG CTG TAC ACG GGG GAG GCC TGC AGG AGA

 165 Gly Asp Arg OP
 GGG GAC AGA TGA CCAGGTGCGTCCAGCTGGGCACATCCACCACCTCCCTCACCAACA
 CTGCCTGTGCCACACCCTCCCTCACCACTCCCGAACCCCATCGAGGGGCTCTCAGCTAAG

 CGCCAGCCTGTCCCATGGACACTCCAGTGCCAGCAATGACATCTCAGGGGCCAGAGGAAC
 TGTCAGAGCACAACCTCTGAGATCTAAGGATGTCCGAGGGCCAACTTGAGGGCCCAGAGC
 AGGAAGCATTGAGAGAGCAGCTTTAAACTCAGGAGCAGAGACAATGCAGGGAAAACACCT
 GAGCTCACTCGGCCACCTGCAAAATTTGATGCAGGACACGCTTTGGAGGCCAATTTACCTG
 TTTTGCACCTACCATCAGGGACAGGATGACTGGAGAACTTAGGTGGCAAGCTGTGACTT
 CTCAGGCCTCACGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACACTGAGAGAATATT
 TTGCAATCTGCAGCAGGAAAATTACGGACAGGTTTTGGAGGTTGGAGGGTACTTGACAG
 GTGfGTGGGAAGCAGGGCGGJAGGGGTGGAGCTGGGATGCGAGfGAGAACCCTGAAGAC
 AGGATGGGGGCTGGCCTCTGGTTCTCGTGGGGTCCAAGCTT
HindIII

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FIG.6A

ΛΛGCTTCTGGGCTTCCAGACCCAGCTACTTTGCGGAACCTCAGCAACCCAGGCATCTCTGAGTCTCCGCCCA
AGACCGGGATGCCCCCAGGGGAGGTGTCCGGGAGCCCAGCCTTTCCCAGATAGCACGCTCCGCCAGTCCC
ΛAGGGTGCACAACCGGCTGCACCTCCCCTCCCGGACCCAGGGCCCCGGGAGCAGCCCCCATGACCCACACGC
ACGTCTGCAGCAGCCCCGCTCACGCCCCGGGAGCCTCAACCCAGGCGTCCTGCCCTGCTCTGACCCCGG
GTGGCCCCCTACCCCTGGCGACCCCTCACGCACACAGCCTCTCCCCACCCCCACCCGCGCACGCACACATG
CAGATAACAGCCCCGACCCCCGGCCAGAGCCGXAGAGTCCCTGGGCCACCCCGGCCGCTCGCCTGCCGCTG
CGCCGCACCGCGCTGTCCCTCCCGGAGCCGGACCCGGGGCCACCGCGCCCCXGCTCTGCTCCGACACCGCGCCC
CTTGGACAGCCGCCCTCTCCTCTAGGCCCGTGGGGCTGGCCCTGCACCCGCCGAGCTTCCCGGGATGAGGXX
-27 -24
Met Gly Val His
CCCGGTGACCGGCGCGCCCCAAGTCGCTGAGGGACCCCGGCCAAGCGCGGAG ATG GGG GTG CAC G
GTGAGTACTCGCGGGCTGGGCGCTCCCGGCGGCCGGTTCCCTGTTTGAGCGGGATTATTAGCGCCCCGGCT

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FIG. 6E

130
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser
 CCA CTC CGA ACA ATC ACT GCT GAC ACT TTC CGC AAA CTC TTC CGA GTC TAC TCC
 140
 150
 Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
 AAT TTC CTC CGG GGA AAG CTG AAG CTG TAC ACA GGG GAG GCC TGC AGG ACA GGG
 160
 Asp Arg OP
 GAC AGA TGA CCAGGTGTGTCCACCTGGGCATATCCACCACCTCCCTCACCAACATTGCTTGTGCCACA
 CCCTCCCCCGCCACTCCTGAACCCCGTCGAGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACTCC
 AGTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGCAACTCTGAGATCTAAGGATGTCAC
 AGGGCCAACTTGAAGGGCCCAGAGCAGGAAGCATTGAGAGAGCAGCTTTAAACTCAGGGACAGAGCCATGC
 TGGGAAGACGCCTGAGCTCACTCGGCACCCCTGCAAAATTTGATGCCAGGACACGCTTTGGAGGCGATTTAC
 CTGTTTTTCGCACCTACCATCAGGGACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAGG
 TCTCACGGGCATGGGCCTCCCTTGGTGGCAAGAGCCCCCTTGACACCGGGGTGGTGGGAACCATGAAGAC
 AXGATXGGGGCTGGCCTCTGGCTCTCATGGGGTCCAAGTTTTGTGTATTCTCAACCTATTGACAGACTGAA
 ACACAATATGAC

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FIG. 7

-1 1
MetAla

XbaI
CTAG AAACCATGAG GGTAAATAAA TAATGGCTCC GCCGCGTCTG
TTTGGTACTC CCATTATTTT ATTACCGAGG CGGCGCAGAC

ATCTGCGACT CGAGAGTTCT GGAACGTTAC CTGCTGGAAG CTAAAGAAGC
TAGACGCTGA GCTCTCAAGA CCTTGCAATG GACGACCTTC GATTTCTTCG

TGAAAACATC ACCACTGGTT GEGCTGAACA CTGTTCTTTG AACGAAAACA
ACTTTTGTAG TGGTGACCAA CACGACTTGT GACAAGAAAC TTGCTTTTGT

TTACGGTACC AGACACCAAG GTTAACTTCT ACGCTTGGAA ACGTATGGAA
AATGCCATGG TCTGTGGTTC CAATTGAAGA TCGGAACCTT TGCATACCTT

GTTSGTCAAC AAGCAGTTGA AGTTTGGCAG GGTCTGGCAC TGCTGAGCGA
CAACCAGTTG TTCGTCAACT TCAAACCGTC CCAGACCGTG ACGACTCGCT

GGCTGTACTG CGTGGCCAGG CACTGCTGGT ARACTCCTCT CAGCCGTGGG
CCGACATGAC GCACCGGTCC GTGACGACCA TTTGAGGAGA GTCGGCACCC

AACCGCTGCA GCTGCATGTT GACAAAGCAG TATCTGGCCT GAGATCTCTG
TTGGCGACGT CGACGTACAA CTGTTTCCTC ATAGACCGGA CTCTAGAGAC

ACTACTCTGC TGGCTGCTCT GGGTGCACAG AAAGAGGCTA TCTCTCCGCC
TGATGAGACG ACGCACGAGA CCCACGTGTC TTTCTCCGAT AGAGAGGCGG

GGATGCTGCA TCTGCTGCAC CECTGCCTAC CATCACTGCT GATACCTTCC
CCTACGACGT AGACGACGTG GCGACGCTG GTAGTGACGA CTATGGAAGG

GCAAACGTGTT TCGTGTATAC TCTAACTTCC TGCCTGGTAA ACTGAAACTG
CGTTTGACAA AGCACATATG AGATTGAAGG ACGCACCATT TGACTTTGAC

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TATACTGGCG AAGCATGCCG TACTGGTGAC CGCTAATAG
ATATGACCGC TTCGTACGGC ATGACCACTG GCGATTATCA GCT

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FIG. 8

	-1	+1		
<u>HindIII</u>	<u>ArgA1a</u>			
AGCTTGGATA	AAAGAGCTCC	ACCAAGATTG	ATCTGTGACT	CGAGAGTTTT
ACCTAT	TTTCTCGAGG	TGGTTCTAAC	TAGACACTGA	GCTCTCAAAA
GGAAAGATAC	TTGTTGGAAG	CTAAGAAGC	TGAAAACATC	ACCACTGGTT
CCTTTCTATG	AACAACCTTC	GATTTCTTCG	ACTTTTGTAG	TGGTGACCAA
GTGCTGAACA	CTGTTCTTTG	AACGAAAACA	TTACGGTACC	AGACACCAAG
CACGACTTGT	GACAAGAAC	TTGCTTTTGT	AATGCCATGG	TCTGTGGTTC
GTTAACTTCT	ACGCTTGGAA	ACGTATGGAA	GTGGTCAAC	AAGCTGTTGA
CAATTGAAGA	TGCGARCCTT	TGCATACCTT	CAACCAGTTG	TTCGACAAC
AGTTTGGCAA	GGTTTGGCCT	TGTTATCTGA	AGCTGTTTTG	AGAGGTCAAG
TCAAACCGTT	CCAAACCGGA	ACAATAGACT	TCGACAAAAC	TCTCCAGTTC
CCTTGTGGT	TAACCTTCT	CAACCATGGG	AACCATTGCA	ATTGCACGTC
GGAACAACCA	ATTGAGAAGA	GTTGGTACCC	TTGGTACGCT	TAACGTGCAG
GATAAAGCCG	TCTCTGTTTT	GAGATCTTTG	ACTACTTTGT	TGAGAGCTTT
CTATTTCGGC	AGAGACCAA	CTCTAGAAAC	TGATGAAACA	ACTCTCGAAA
GGGTGCTCAA	AAGGAAGCCA	TTTCCCACC	AGACGCTGCT	TCTGCCGCTC
CCCACGAGTT	TTCTTCGGT	AAAGGGGTGG	TCTGCGACGA	AGACGGCGAG
CATTGAGAAC	CATCACTGCT	GATACCTTCA	GAAAGTTATT	CAGAGTTTAC
GTAACCTTG	GTAGTGACGA	CTATGGAAGT	CTTCAATAA	GTCTCAAATG
TCCAACCTTCT	TGAGAGGTAA	ATTGAAGTTG	TACACCGGTG	AAGCCTGTAG
AGGTTGAAGA	ACTCTCCATT	TAACTTCAAC	ATGTGGCCAC	TTCGGACATC
AACTGGTGAC	AGATAAGCCC	GACTGATAAC	AACAGTGTAG	
TTGACCACTG	TCTATTCCGG	CTGACTATTG	TTGTCACATC	
	<u>SalI</u>			
ATGTAACAAA	G			
TACATTGTTT	CAGCT			

FIG. 9

	-20	-10	+1	10	20	30	40	
Human	MGVHECPAWLWLLLSLPLGLPVLGAPPRLICDSRVLERYLLEAKEAENITGCAEHCSLNENITVPDTK							

Monkey	MGVHECPAWLWLLLSLVSLPLGLPVPGAPPRLICDSRVLERYLLEAKEAENVTMGCSEBESLNENITVPDTK							
	50	60	70	80	90	100	110	
Human	VNFYANKRMEVGQQAVEVWQGLALLBEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKE							

Monkey	VNFYAWKRMEVGQQAVEVWQGLALLBEAVLRGQAVLANSBQPFEPLQLHMDKAISGLRSITTLRALGAQ-E							
	120	130	140	150	160			
Human	AISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKCLKLYTGEACRTGDR							
	*** *****							
Monkey	AISLPDAASAAPLRTITADTFCKLFRVYSNFLRGKCLKLYTGEACRRGDR							