

APPENDICES

Appendix I

Solutions and Reagents for DNA Extraction

Preparation of 1X Red Blood Cell (RBC) Lysis Buffer

Ammonium chloride	8.260 g
Potassium bicarbonate	1.000 g
EDTA powder	0.037 g
ddH ₂ O	1000 ml

All the above-mentioned ingredients were weighed and dissolved in 1000 ml ddH₂O by stirring with magnetic stirrer on the hot plate to mix well. The solution was then sterilized by autoclaving at 121°C for 15 min prior long term storage at 4°C or to be kept at room temperature for six months.

Preparation of 1X Tris-EDTA (TE) Buffer

1M Tris-HCl, pH 7.5	5.0 ml
0.5M EDTA, pH 8.0	1.0 ml
ddH ₂ O	500.0 ml

Tris-HCl and EDTA mixed together by dissolving in 500 ml ddH₂O.

Appendix II

Solutions and Reagents for Agarose Gel Electrophoresis

Preparation of 5X Tris-Borate EDTA (TBE) Buffer

Tris-base	54.0 g
0.5 M EDTA powder	3.7 g
Boric acid	27.5 g

Firstly, molecular biology grade Tris-base and EDTA were weighed out and dissolved in 500 ml double-distilled water before adding boric acid gradually. The volume was made up to 1000 ml using a graduated measuring cylinder.

Preparation of Ethidium Bromide (10 mg/ ml)

Ethidium bromide	0.2 g
Deionized water	20.0 ml

The solution was then stored at room temperature in a dark container and diluted to 1.0 $\mu\text{g}/\text{ml}$ with distilled water before use.

Appendix III

DNA Purification Protocol

1. 5 volumes of Buffer PB was added to 1 volume of the PCR sample and mixed. Before use, ethanol (96 - 100%) was added to Buffer PE.
2. A QIAquick spin column was placed in a 2.0 ml collection tube provided by the manufacturer.
3. To bind DNA, the sample was discarded to the QIAquick column and centrifuged for 1 min at 14,000 rpm.
4. The flow-through was discarded. QIAquick column was placed back into the same tube.
5. To wash, 0.75 ml Buffer PE was added to the QIAquick column and centrifuged for 1 min.
6. The flow-through was discarded and the QIAquick column was placed back in the same tube. The column was centrifuged for additional 1 min.
7. QIAquick column was placed in a clean 1.5 ml microcentrifuge tube.
8. To elute DNA, 50 – 100 µl Buffer EB (10 mM Tris-Cl, pH 8.5) or dH₂O was added to the centre of the QIAquick membrane, the column was let to stand for 1 min and then centrifuged for 1 min.
9. Labelled microcentrifuge tubes were sent for sequencing or kept for long time in -80°C freezer.

Appendix IV

Primer Map

LOCUS HUMRETBLAS 180388 bp DNA linear PRI 21-OCT-2008
DEFINITION Human retinoblastoma susceptibility gene exons 1-27,
complete cds.
ACCESSION L11910
VERSION L11910.1 GI:292420
KEYWORDS nuclear protein; recessive oncogene; retinoblastoma gene;
retinoblastoma protein; retinoblastoma susceptibility
tumor supressor gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates;
Haplorrhini; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Friend,S.H., Bernards,R., Rogelj,S., Weinberg,R.A.,
Rapaport,J.M.,Albert,D.M. and Dryja,T.P.
TITLE A human DNA segment with properties of the gene that
predisposes to retinoblastoma and osteosarcoma
JOURNAL Nature 323 (6089), 643-646 (1986)
PUBMED 2877398
REFERENCE 2 (sites)
AUTHORS Friend,S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F.,
Bogenmann,E., Li,F.P. and Weinberg,R.A.
TITLE Deletions of a DNA sequence in retinoblastomas and
mesenchymal tumors: organization of the sequence and its
encoded protein
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
PUBMED 3480530
REFERENCE 3 (sites)
AUTHORS Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and
Lee,E.Y.
TITLE Human retinoblastoma susceptibility gene: cloning,
identification and sequence
JOURNAL Science 235 (4794), 1394-1399 (1987)
PUBMED 3823889
REFERENCE 4 (sites)
AUTHORS McGee,T.L., Yandell,D.W. and Dryja,T.P.
TITLE Structure and partial genomic sequence of the human
retinoblastoma susceptibility gene
JOURNAL Gene 80 (1), 119-128 (1989)
PUBMED 2701949
REFERENCE 5 (sites)
AUTHORS Sakai,T., Ohtani,N., McGee,T.L., Robbins,P.D. and
Dryja,T.P.
TITLE Oncogenic germ-line mutations in Sp1 and ATF sites in the
human retinoblastoma gene
JOURNAL Nature 353 (6339), 83-86 (1991)
PUBMED 1881452
REFERENCE 6 (bases 1 to 180388)
AUTHORS Toguchida,J., McGee,T.L., Paterson,J.C., Eagle,J.R.,
Tucker,S., Yandell,D.W. and Dryja,T.P.
TITLE Complete genomic sequence of the human retinoblastoma
susceptibility gene
JOURNAL Genomics 17 (3), 535-543 (1993)
PUBMED 7902321


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The Sequence Manipulation Suite: Primer Show

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Exon
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Exon
2

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45781 tttctattttgtttaatag**GATATCTACTGAAATAAATCTGCATGGTGCTAAAAGTTTC**

**Primer 14
(Reverse)
shows
non-
specificity)**

**Primer 14
(Reverse)
shows
non-
specificity)**

**Exon
3**

**Exon
4**

**Exon
5**

**Exon
6**

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116008 GATCTACGTTCTAATAAAAACCTAGTACTATTTTGTAGAAAGTCTGACTAAGATATCTGTCC
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64501 **5' 10R**

Exon
7

Exon
8

Exon
9

Exon
10

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65221 **GAGACAACA**
65221 atctatcttctatcctatctattattgagttatcattttatgatgattttatgagacaaca
115168 tagataaaagataggtatagataataactcaatagtaaaatataactaaaatactctgttgt
65281 **GAAGCATTATAC 3' 11F**
65281 gaagcattatactgcttttttgatgcataaagcacaattgtaaattttcagtatgtgaa
115108 cttcgtaatatgacgaaaaaactacgtatcttctgtgtttaacattttaaagtcatacactt
65341 tgacttcacttattgttatttag**TTTTGAAACACAGAGAACCACGAAAAAGTAACTT**
115048 actgaagtgaataacaataaatcAAAACCTTTGTGTCTCTTGTGGTGCTTTTTTCATTGGAA
65401 **GATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAG**gtatgaattttcctacttt
114988 CTACTTCTCCACTTACATTAAGGAGGTGTGTGAGGTCAATCatactttaaaggatgaa
65461 **ACCGAAATATCACAAAGT 5' 11R**
65461 taattatattataaattttgttattcatggctttatagtgtttcagatttgttcacgtttc
114928 attaataataatattaaacaataagtagcgaatatacacaagtctaaacaagtgcgaag
.....

Exon
11

70201 **ATTGCTTAACACATTTTC 3' 12F**
70201 cttcattgcttaacacatttttctatctttttatcccctctag**GACTGTTATGAACACTATC**
110188 gaagtaacgaattgtgtaaaaggataaaaataggggagatcCTGACAATACTTGTGATAG
70261 **CAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCC**
110128 GTTGTTAATTACTACTAAAATTTAAGTCGTTCACTAGTTGGAAGTCTTTTAGACTAAAGG
70321 **AACATTATAGAACCGTTT 5' 12R**
70321 **TATTTTAAAC**gtaagccatatatgaaacattatttattgtaatatcttgcaagaaactt
110068 ATAAAATTGcattcggatataactttgtaataaataacattatagaaccgtttctttgaa
.....

Exon
12

73681 **ATCCTCGACATTGATTTCTG 3'**
73681 ttatggagcagaaaatattaattctgattacacagtatcctcgcacattgatttctgtttt
106708 aatacctcgtctttttataattaagactaatgtgtcataggagctgtaactaaagacaaaa
73741 **13F**
73741 tacctcctaag**AAGTGCACAGTGAATCCAAAAGAAAAGTATACTGAAAAGAGTGAAGGAT**
106648 atggaggatttctTGACGTGTCACTTAGGTTTTCTTTCATATGACTTTTCTCACTTCCTA
73801 **ATAGGATACATCTTTAAAGAGAAAATTTGCTAAAGCTGTGGACAGGGTTGTGTGCGAAAT**
106588 TATCCTATGTAGAAAATTTCTCTTTAAACGATTTTCGACACCCTGTCCCAACACAGCTTTAA
73861 **GTAACATTAAGCACCATGAT 5' 13R**
73861 **GGATCACAG**gtaacttgaattcattgtaattcgtggtactatagagtaataatattaaaa
106528 CCTAGTGTcattgaacttaagtaacattaagcaccatgatatactcattattataatttt
.....

Exon
13

76381 **TGATTTTCTAAAATAGCAGGCTC 3' 14F**
76381 tgattttctaaaatagcaggctcttattttttctttttgtttgtttgtag**CGATACAAACT**
104008 actaaaagattttatcgtccgagaataaaaagaaaaacaaacaaacatcGCTATGTTTGA
76441 **TGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCA**gtaagttaaaaaa
103948 ACCTCAAGCGAACATAATGGCTCATTACCTTAGGTACGAATTTAGTcattcaatttttgt
76501 atataaaaaaatttcagcgggcccgggctcagcctgcaatcctcagcactttgggag
103888 tatatttttttaagtcggcccgcgccaccgagtgccgagcgttagggctgtaaacctc
76561 **CACTTT**
76561 gccgaggtgggcagatcaggaggtcaaggcatcaagatcatcctggccaaaatggtgaaa
103828 cggctccaccctcctagtcctccagttccgtagttctagtaggaccggttttaccacttt
76621 **GGGACAGAGATGATTTT 5' 14R**
76621 cctgtctctactaaaagtaaaaaattagctgggctggtggtgtagacctgtagtccc
103768 gggacagagatgattttcatgtttttaaactgcaccgcaccaccacatctggacatcaggg
76681 agctacttggcaggctgaggcaggagaatcccttgaaccacggaggtggaggttgcagtg
103708 tcgatgaaccgctccgactccgctccttagggaacttgggtgctccaccctccaacgtcac
76741 agccaagattgtgccatttcacccagcctggcaacagagcaagacaccatcaaaaaaa
103648 tcggttctaacacggtaaaagtgggctgggacggttctcgttctgtggttagattttttt
.....

Exon
14

76801 **AATGCTGACACAAAATAAGGTTTTC 3' 15F**
76801 aaaaaaaaaaaaaaaaaaattcaatgctgcacaaaataaggtttcaattaaacaacttct
103588 ttttttttttttttttttaagttacgactgtgtttattccaaagttaatttgttgaaga
76861 ttttttttttttaaatatctgtttcag**GAAGAAGAACGATTATCCATTCAAAAATTTTAG**
103528 aaaaaaaaaaaatattatagacaaagtcCTTCTTCTTGCTAATAGGTAAGTTTAAATC
76921 gtaaatttttactttttagtaaaaaattttttctttttatagaagtaagtattttataa
103468 catttaaaaaatgaaaatcatttttttaaaaaaagaaaaatcttctcattcataaaaatatt
76981 tcttttttttttctcttttag**CAAACTTCTGAATGACAACATTTTTCATATGCTTTATTG**
103408 agaaaaaaaaaaggaaatcGTTTGAAGACTTACTGTTGTAAAAAGTATACAGAAAATAAC
.....

Exon
15

77041 **CGGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCA**gtaagttaaattttcataaataa
103348 CGCACGCGAGAACTCCAACATTACCGGTGTATATCGTcattcaattttaaagattttatt
77101 acacttttgttcaattttaaagttaaataatgtgggtgtgtttcttttggtcgggggagagggat
103288 tgtgaaaacaagttaaatttcaattttacaccacacaaaagaaaccgccctctcccta
77161 **CCTCTTCCTTACGAATAAAATCTAG 5' 16R**
77161 agtgtgaggttaaggagaaggaatgcttatttttagatcactatatactgaagaatgtaat
103228 tcacactccaatttcttcttcttacgaataaaatctagtgatataatgacttcttacatta

Exon
16

78001 **CAAAAAATACCTAGCTCAAG 3' 17F**
78001 ttgtctgataataacttccaaaaaaatcacctagctcaagggttaattttcataaatag
102388 aacagactattattgaagggtttttttatggatcgagttcccaattataaagtattttatca
78061 tacttttttttttcaatttttag**GAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTG**
102328 atgaaaaaaaaaagtaaaaatcCTTCATGTAGAGTCTTAGAACTAAGACCTTGTCTAAAC
78121 **TCTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTACAAAGTGATC**
102268 AGAAAGGGTACCTAAGACTTACACGAATTAATTTTCGGAACTAAAAATGTTTCACTAG
78181 **GAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAAATGATAAAACATTTAGAACGA**
102208 CTTTTCAAATAGTTTTCGTCTTCCGTTGAACTGTTCTCTTTACTATTTTGTAAATCTTGCT
78241 **TGTGAACATCGAATCATGGAATCCCTTGATGGCTCTCA**gtaagtagctaaataattgaa
102148 AACTTGTAGCTTAGTACCTTAGGGAACGTACCGAGAGTcattcatcgatttattaactt
78301 **CAATCACTCTCCACAAAGAAATG**
78301 gaaattcattcatgtgcatatggctaacaattattgttagtgagaggtgttttcttaaca
102088 ctttaagtaagtacacgtataccgattgtttaataacaatcactctccacaaagaattgt
78361 **5' 17R**
78361 aatctacctcaagaacaaatagggaaatttaataatgaataatgattttcagtctatagccca
102028 ttagatggagttcttggtttatcccttaaattacttattacaataaagtcagatatcgggt

Exon
17

149941 **AATTATGCTTACTAATGTGG 3' 18F**
149941 gtacctgggaaaattatgcttactaatgtgggttttaatttcatcatgtttcatatag**GAT**
30448 catggacccttttaatacgaatgattacaccaaataaagtagtacaaagtatatcCTA
150001 **TCACCTTTATTTGATCTTATTAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTT**
30388 AGTGGAAATAAACTAGAATAATTTGTAGTTTCTCTGGCTCTTCTGTTGACTAGTGGAA
150061 **AGACTGTCTTGTCTCTTAATCTTCTCTCCAGAATAATCAGACTGCAGCAGATAT**gtaa
30328 CTTAGACGAACAGGAGAATTAGAAGGAGAGGTCTTATTAGTGTGACGTCTATAcatt
150121 **CAATACAACCTGGTAAGTTTGA 5' 18R**
150121 gcaaaatataatgattatggtgaccattcaaactgcaaatagattttaagcataagtgcaat
30268 cgttttatatacaatacaactggtaagtttgacgtttatctaaaattcgtattcacgtta

Exon
18

153121 **AACTTGAAAT**
153121 tatctgggtgtacaaccttgaagtgtatgtataatctgtgattccttagccaacttgaat
27268 atagaccacatggttgaacttcacatacatattagacactaagaatcggttgaacttta
153181 **GAAGACTTTTCC 3' 19F**
153181 gaagacttttctttaaataatctag**GTATCTTTCTCTGTAAGATCTCCAAAGAAAAA**
27208 cttctgaaaaggaaatttatatagatcCATAGAAAGAGGACATTCTAGAGGTTTCTTTTT
153241 **AGGTTCAAACACTACGCGTGTAAATTTCTACTGCAAAATGCAGAGACACAAGCAACCTCAGCCTT**
27148 TCCAAGTTGATGCGCACATTTAAGATGACGTTTACGTCTCTGTGTTGTTGGAGTCGGAA
153301 **CCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAG**gttagta
27088 GGTCTGGGTCTTCGGTAACTTTAGATGGAGAGAAAAGTGACAAAAATTTTTTTCaatcat
153361 **CTCGTACCTGAGACTTTGAT 5' 19R**
153361 gatgattattttcaagagcatggactctgaaactaggctgaggttcaaatcatgttt
27028 ctactaataaaagttctcgtactgagactttgatccgactgacccaagtttagtaciaa

Exon
19

156661 **GACTAATTTTTCTTATTCCAC 3' 20F**
156661 gtaaaaatgactaatttttcttattcccacag**TGTATCGGCTAGCCTATCTCCGGCTAAA**
23728 ctttttactgattaaaaagaataaggggtgtcACATAGCCGATCGGATAGAGGCCGATTT
156721 **TACACTTTGTGAACGCCTTCTGTCTGAGCACCAGAATTAGAACATATCATCTGGACCCT**
23668 ATGTGAAACACTTGCAGGAGACAGACTCGTGGGTCTTAATCTTGTATAGTAGACCTGGGA
156781 **TTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTGGACCAA**gt
23608 AAAGGTCGTGTGGGACGTCTTACTACACTTGAGTACTCTGTCCGTAAACCTGGTTca
156841 **CGTGAAGTGAAGAGAGAG 5' 20R**
156841 aagaaaatcaagcacttcaccttctcctcctcctacttacttgtaactgatttctttct
23548 ttcttttagttcgtgaagtggagagaggggatgaatgaacaattgactaaagaaaga

Exon
20

160681 **CATGTAATAAAAATTCTGACTAC 3' 21F**
160681 aaacatgtaataaaaattctgactacttttacatcaatttatttactag**ATTATGATGTG**
19708 tttggtacattattttaaagactgatgaaaatgtagttaaataaatgatcTAATACTACAC

174361 TAAACATCTCCCAGGAGAGTCCAAATTTTCAGCAGAAACTGGCAGAAATGA gtaagtactt
 6028 ATTTGTAGAGGGTCCTCTCAGGTTTAAAGTCGTCTTTGACCGTCTTTACTcattcatgaa
 174421 GTGACGTTCTTCAGAAAAG 5' 2
 174421 ttttcaccttgtgtaaacgaaataaacaattgtttactgcaagaagtcttttcgttat
 5968 aaaagtggaacacatttgctttatttgtaacaaatgtgacgttcttcagaaaagcaata
 174481 6R
 174481 ataaaagaatgtataatcttccagttggcaggtttgtttatgcatttaaaatataattc
 5908 tttttcttacatattaaagaagtcaaccgtccaacaaatacgtaaattttatattaag

 176941 AATGCTGTTAACAGTTCTTC 3' 27F
 176941 gcagccacttgccaacttaccagtagcatcaatgctgtaaacagttcttcatcctttt
 3448 cgtcgggtgaacgggttgatgggtcatggtagttacgacaattgtcaagaagtaggaaaaa
 177001 ccagCTTCTACTCGAACACGAATGCAAAAAGCAGAAAATGAATGATAGCATGGATACCTCA
 3388 ggtcGAAGATGAGCTTGTGCTTACGTTTTTCGTCTTTTACTTACTATCGTACCTATGGAGT
 177061 CCTAA
 177061 AACAAAGGAAGAGAAAATGA ggatctcaggaccttggtggacactgtgtacacctctggatt
 3328 TTGTTTCCTTCTCTTTACTcctagagtcctggaaccacctgtgacacatgtggagacctaa
 177121 GTAACAGAGAGTGT 5' 27R
 177121 cattgtctctcacagatgtgactgtataactttcccaggttctgtttatggccacattta
 3268 gtaacagagagtgctactgacatattgaaagggccaagacaaataaccggtgtaaat

Exon
26

Exon
27

Appendix V

Retinoblastoma Gene Translation

The Sequence Manipulation Suite: Show Translation

Results for 2787 residue sequence "mRNA /gene="fem-2" (exons in uppercase)" starting "ATGCCGCCCA".

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1 M P P K T P R K T A A T A A A A A A E P
1 ATGCCGCCCAAAACCCCGAAAAACGGCCGCCACCGCCGCCGCTGCCGCCGCGGAACCC
21 P A P P P P P P P P E E D P E Q D S G P E
61 CCGGCACCGCCGCCGCCGCCCTCCTGAGGAGGCCAGAGCAGGACAGCGGCCCGGAG
41 D L P L V R L E F E E T E E P D F T A L
121 GACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTGCATTA
61 C Q K L K I P D H V R E R A W L T W E K
181 TGT CAGAAATTAAGATAACCAGATCATGTCAGAGAGAGAGCTTGGTTAACTTGGGAGAAA
81 V S S V D G V L G G Y I Q K K K E L W G
241 GTTTCATCTGTGGATGGAGTATTGGAGGTTATATTCAAAAGAAAAAGGAACCTGTGGGA
101 I C I F I A A V D L D E M S F T F T E L
301 ATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA
121 Q K N I E I S V H K F F N L L K E I D T
361 CAGAAAAACATAGAAATCAGTGTCCATAAATTCCTTAACTTACTAAAAGAAATTGATACC
141 S T K V D N A M S R L L K K Y D V L F A
421 AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTTGTTGCA
161 L F S K L E R T C E L I Y L T Q P S S S
481 CTCTTCAGCAAATTTGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGTTCG
181 I S T E I N S A L V L K V S W I T F L L
541 ATATCTACTGAAATAAATTCGCAATTGGTGCTAAAAAGTTTCTTGGATCACATTTTATTA
201 A K G E V L Q M E D D L V I S F Q L M L
601 GCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTTCATTTTCAGTTAATGCTA
221 C V L D Y F I K L S P P M L L K E P Y K
661 TGTGTCCTTGACTATTTTATTAACCTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA
241 T A V I P I N G S P R T P R R G Q N R S
721 ACAGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTGAGAACAGGAGT
261 A R I A K Q L E N D T R I I E V L C K E
781 GCACGGATAGCAAAACAAGTAAAGATAACAAGAATTATTGAAAGTTCTCTGTAAGAA
281 H E C N I D E V K N V Y F K N F I P F M
841 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATG
301 N S L G L V T S N G L P E V E N L S K R
901 AATTCTCTTGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAAATCTTTCTAAACGA
321 Y E E I Y L K N K D L D A R L F L D H D
961 TACGAAGAAATTTATCTTAAAAAATAGATCTAGATGCAAGATTATTTTGGATCATGAT
341 K T L Q T D S I D S F E T Q R T P R K S
1021 AAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACCACGAAAAAGT
361 N L D E E V N V I P P H T P V R T V M N
1081 AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC
381 T I Q Q L M M I L N S A S D Q P S E N L
1141 ACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTG
401 I S Y F N N C T V N P K E S I L K R V K
1201 ATTTCTATTTTAACTGCACAGTGAATCCAAAAGAAAGTATACTGAAAAGAGTGAAG
421 D I G Y I F K E K F A K A V G Q G C V E
1261 GATATAGGATACATCTTTAAAGAGAAATTTGCTAAAAGCTGTGGGACAGGGTGTGTGCGAA
441 I G S Q R Y K L G V R L Y Y R V M E S M
1321 ATGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATG
461 L K S E E E R L S I Q N F S K L L N D N
1381 CTTAAATCAGAAGAAGAACGATTATCCATTCAAAAATTTAGCAAACCTTCTGAATGACAAC
481 I F H M S L L A C A L E V V M A T Y S R
1441 ATTTTTTCATATGTCTTTATTGGCGTCGCTCTTGAGGTTGTAATGGCCACATATAGCAGA
501 S T S Q N L D S G T D L S F P W I L N V
1501 AGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTG
521 L N L K A F D F Y K V I E S F I K A E G
1561 CTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAAGTTTATCAAAGCAGAAGGC
541 N L T R E M I K H L E R C E H R I M E S
1621 AACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAATCC
561 L A W L S D S P L F D L I K Q S K D R E
1681 CTTGCATGGCTCTCAGATTACCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAA
581 G P T D H L E S A C P L N L P L Q N N H
1741 GGACCAACTGATCACCTTGAATCTGCTTGTCTCTTAATCTTCTCTCCAGAATAATCAC
601 T A A D M Y L S P V R S P K K K G S T T
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1801 ACTGCAGCAGATATGTATCTTTCTCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACG
621 R V N S T A N A E T Q A T S A F Q T Q K
1861 CGTGTA AATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAG
641 P L K S T S L S L F Y K K V Y R L A Y L
1921 CCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTC
661 R L N T L C E R L L S E H P E L E H I I
1981 CGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATC
681 W T L F Q H T L Q N E Y E L M R D R H L
2041 TGGACCCTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGCATTTG
701 D Q I M M C S M Y G I C K V K N I D L K
2101 GACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA
721 F K I I V T A Y K D L P H A V Q E T F K
2161 TTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTTCAGGAGACATTCAAA
741 R V L I K E E E Y D S I I V F Y N S V F
2221 CGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTC
761 M Q R L K T N I L Q Y A S T R P P T L S
2281 ATGCAGAGACTGAAAACAAATATTTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTC
781 P I P H I P R S P Y K F P S S P L R I P
2341 CCAATACCTCACATTCTCGAAGCCCTTACAAGTTTCTTAGTTCCACCCTTACGGATTCCT
801 G G N I Y I S P L K S P Y K I S E G L P
2401 GGAGGGAACATCTATATTTTCAACCCCTGAAGAGTCCATATAAAAATTTGAGAAGGTCTGCCA
821 T P T K M T P R S R I L V S I G E S F G
2461 ACACCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAATTGGTGAATCATTGGGG
841 T S E K F Q K I N Q M V C N S D R V L K
2521 ACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAA
861 R S A E G S N P P K P L K K L R F D I E
2581 AGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAA
881 G S D E A D G S K H L P G E S K F Q Q K
2641 GGATCAGATGAAGCAGATGGAAGTAAACATCTCCAGGAGAGTCCAAATTTTCAGCAGAAA
901 L A E M T S T R T R M Q K Q K M N D S M
2701 CTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAAGCAGAAAAATGAATGATAGCATG
921 D T S N K E E K *
2761 GATACCTCAAACAAGGAAGAGAAATGA