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DNA_SEQUENCE 1.0

complete sequence

4304 Length: 5130 February 24, 1998 16:39 Type: N Check: 600 ..

1 gacGTCgcgg ccgctCTAGG CCTCCAAAAA AGCCTCCTCA CTA^{CTT}CTGG
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151 GGCGGGATGG GCGGAGTTAG GGGCGGGACT ATGGTTGCTG ACTAATTGAG
201 ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG GACTTTCCAC
251 ACCTGGTTGC TGA^{CTA}AATTG AGATGCATGC TTTGCATACT TCTGCCTGCT
301 GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT
351 TAATTCCCGG GGATCGATCC Ggtcgacaat attggctatt ggccattgca
401 tacgttgat ctatatcata atatgtacat ttatattggc tcatgtccaa
451 tatgaccgcc atgttgacat tgattattga ctagttatta atagtaatca
501 attacggggt cattagtcca tagcccatat atggagtcc gcgttacata
551 acttacggta aatggcccgc ctogtgaccg cccaacgacc cccgcccatt
601 gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc
651 attgacgtca atgggtggag tatttacggt aaactgcca cttggcagta
701 catcaagtgt atcatatgcc aagtccggcc ccctattgac gtcaatgacg
751 gtaaatggcc cgctggcat tatgcccagt acatgacctt acgggacttt
801 cctactggc agtacatcta cgtattagtc atcgctatta ccatggtgat
851 gcggttttg cagtacacca atgggcgtgg atagcggttt gactcacggg
901 gattccaag tctccacccc attgacgtca atgggagttt gttttggcac

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951 caaaatcaac gggactttcc aaaatgtcgt aataacccccg ccccggtgac
1001 gcaaattgggc ggtaggcgtg tacggtagga ggtctatata agcagagctc
1051 gtttagtgaa ccgtcagatc gcctggagac gccatccacg ctgttttgac
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1451 tctgtatttt tacaggatgg ggtcccattt attatttaca aattcacata
1501 tacaacaacg ccgtcccccg tgcccgcagt tttattaaa catagcgtgg
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1951 ccagacataa tagctgacag actaacagac tgttccttcc catgggtctt

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2201 CTCCATGGAG AAACCCAGat ctacgtatga tcaGCCTCGA CTGTGCCTTC
2251 TAGttgccag ccatctgttg tttgccctc ccccgcttcc tcctgacct
2301 tggaaggtgc cactcccact gtcctttct AATAAAatga ggaaattgca
2351 tcgcattgtc tgagtaggtg tcattctatt ctgggggggtg ggggtggggca
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2601 TCGCCTTCTA TCGCCTTCTT GACGAGTTCT TctgaGCGGG ACTCTGGGGT
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2801 CCCACCCCAA CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT
2851 AGCATCACAA ATTTACAAA TAAAGCATT TTTTCACTGC ATTCTAGTTG
2901 TGGTTTGTCC AAACCTCATCA ATGTATCTTA TCATGTCTgg atcgcggccg
2951 cgaTCCcGTC gagagcttGG CGTAATCATG GTCATAGCTG TTTCTGTGT
3001 GAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGAGC CGGAAGCATA

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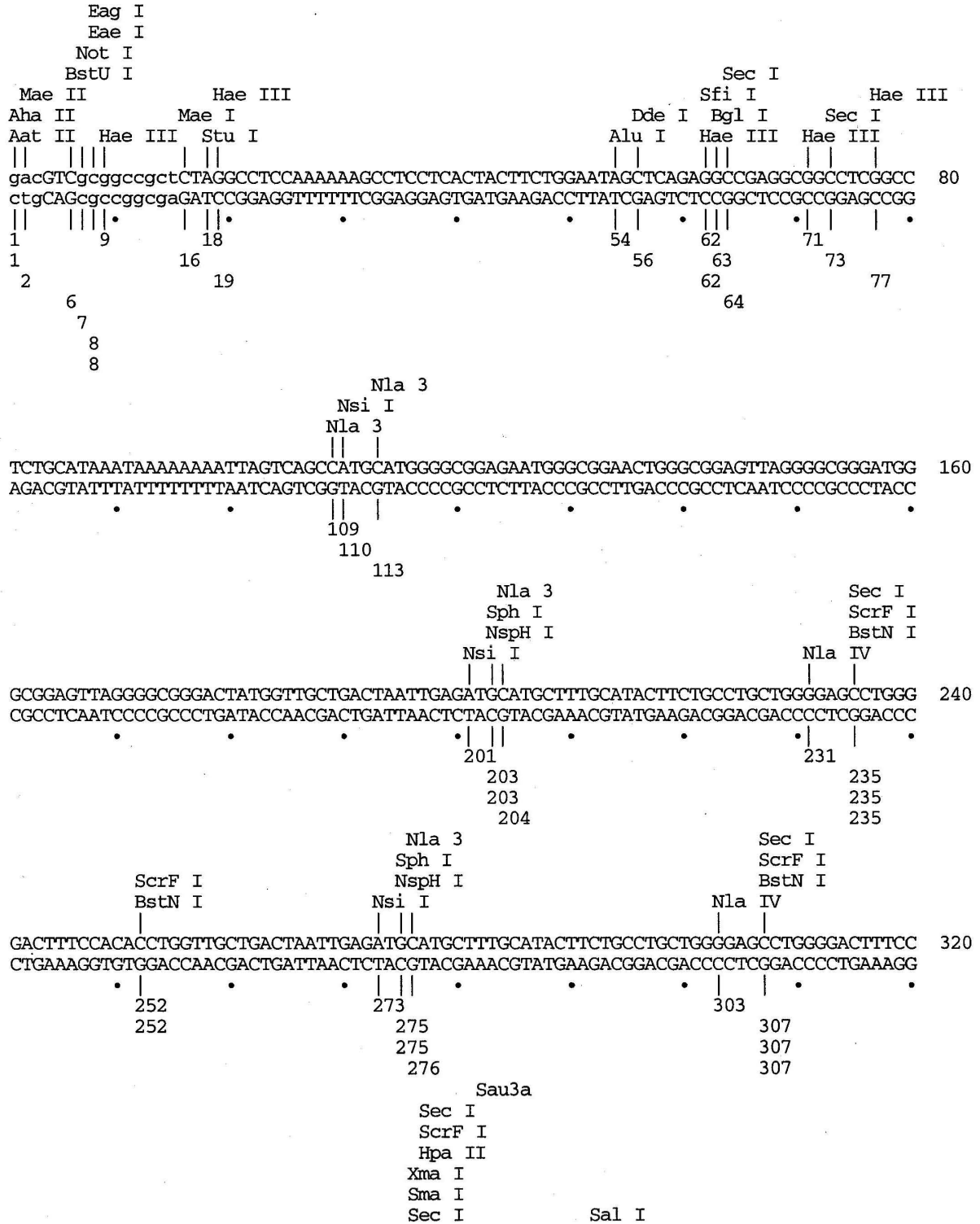
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3101 GTTGCGCTCA CTGCCCGCTT TCCAGTCGGG AACCTGTCTG TGCCAGCTGC
3151 ATTAATGAAT CGGCCAACGC GCGGGGAGAG GCGGTTTGCG TATTGGGCGC
3201 TCTTCCGCTT CCTCGCTCAC TGA CTGCTG CGCTCGGTCTG TCCGGCTGCG
3251 GCGAGCGGTA TCAGCTCACT CAAAGGCGGT AATACGGTTA TCCACAGAAT
3301 CAGGGGATAA CGCAGGAAAG AACATGTGAG CAAAAGGCCA GCAAAGGCC
3351 AGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTCCATA GGCTCCGCCC
3401 CCCTGACGAG CATCACAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC
3451 CGACAGGACT ATAAAGATAC CAGGCGTTTC CCCCTGGAAG CTCCCTCGTG
3501 CGCTCTCCTG TTCCGACCCT GCCGCTTACC GGATACCTGT CCGCCTTTCT
3551 CCCTTCGGGA AGCGTGGCGC TTTCTCAATG CTCACGCTGT AGGTATCTCA
3601 GTTCGGTGTA GGTCGTTCTGC TCCAAGCTGG GCTGTGTGCA CGAACCCCCC
3651 GTTCAGCCCG ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA
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3751 TTAGCAGAGC GAGGTATGTA GGCGGTGCTA CAGAGTTCTT GAAGTGGTGG
3801 CCTAACTACG GCTACACTAG AAGGACAGTA TTTGGTATCT GCGCTCTGCT
3851 GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG TAGCTCTTGA TCCGGCAAAC
3901 AAACCACCGC TGGTAGCGGT GGTTTTTTTG TTTGCAAGCA GCAGATTACG
3951 CGCAGAAAAA AAGGATCTCA AGAAGATCCT TTGATCTTTT CTACGGGGTC
4001 TGACGCTCAG TGGAACGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT
4051 TATCAAAAAG GATCTTCACC TAGATCCTTT TAAATTA AAA ATGAAGTTTT

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4101 AAATCAATCT AAAGTATATA TGAGTAACT TGGTCTGACA GttaCCAATG
4151 CTTAATCAGT GAGGCACCTA TCTCAGCGAT CTGTCTATTT CGTTCATCCA
4201 TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA
4251 CCATCTGGCC CCAGTGCTGC AATGATACCG CGAGACCCAC GCTCACCGGC
4301 TCCAGATTTA TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA
4351 GTGGTCCTGC AACTTTATCC GCCTCCATCC AGTCTATTAA TTGTTGCCGG
4401 GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC
4451 CATTGCTACA GGCATCGTGG TGTCACGCTC GTCGTTTGGT ATGGCTTCAT
4501 TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG
4551 TGCAAAAAAG CGGTTAGCTC CTTCGGTCCT CCGATCGTTG TCAGAAGTAA
4601 GTTGGCCGCA GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC
4651 TTA CTGTCAT GCCATCCGTA AGATGCTTTT CTGTGACTGG TGAGTACTCA
4701 ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC
4751 GGCGTCAATA CGGGATAATA CCGCGCCACA TAGCAGA ACT TAAAAGTGC
4801 TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG
4851 CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGCACCCA ACTGATCTTC
4901 AGCATCTTTT ACTTTCACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC
4951 AAAATGCCGC AAAAAAGGGA ATAAGGGCGA CACGGAAATG TTGAATACTc
5001 atACTCTTCC TTTTCAATA TTATTGAAGC ATTTATCAGG GTTATTGTCT
5051 CATGAGCGGA TACATATTTG AATGTATTTA GAAAAATAAA CAAATAGGGG
5101 TTCCGCGCAC ATTTCCCCGA AAAGTGCCAC

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Positions of Restriction Endonucleases sites (unique sites underlined)



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                ScrF I      Hpa II  Ssp I
                Mse I  Bcn I   Sau3a  Taq I      Hae III
                Ase I  Bcn I   Taq I   HinC II     Eae I
                Xmn I  Ava I   Cla I   Acc I      Bal I
    ACACCCTAACTGACACACATTCCACAGAATTAATTCCCGGGGATCGATCCGgtcgacaatattggctattggccattgca 400
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                347      356      363      372      390
                349      356      364      372      390
                350      357      366      373      391
                356      369      378
                356      372
                356
                357
                357
                357
                362
    Mae II      Rsa I      Nla 3      HinC II      Spe I
    |          |          |          |          |
    tacgttgatctatatcataatatgtacatttatattggctcatgtccaatatgaccgccatggtgacattgattattga 480
    atgcaacatagatatagttatacatgtaaatataaccgagttacaggttatactggcgggtacaactgtaactaataact
    |          |          |          |          |
    402      425      442      460      480
                463
                Mae III
                BstU I
    Mae I  Ase I  Mse I
    |      |      |
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    |      |      |          |          |
    481      488      540      543
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                Mae II
                Aha II
                Aat II
    Sau96 I  Hae III  Mae III
    |      |      |
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    ttaccggggcgagcactggcgggttgcgtggggcgggtaactgcagttatactgcatacaagggtatcattgcggttat
    |      |      |          |          |          |
    564      574      601      614      629
    564
                602
                Mae II
                Aha II
                Aat II
                Bgl I      Rsa I      Nde I
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    ccctgaaaggtaactgcagttaccacctcataaatgccatttgacgggtgaaccgtcatgtagttcacatagtatacgg
    |      |      |          |          |          |
    654      686      698      713
    654
    655
                ScrF I
                BstN I
    Sau96 I  Nla IV  Mae II
    |      |      |
    aagtccggccccctattgacgtcaatgacggtaaatggccccgcctggcattatgccagttacatgaccttacgggacttt 800
    Hpa II  Aha II  Sau96 I  Nla 3
    |      |      |          |
    Hae III  Aat II  Hae III      Rsa I
    |      |          |          |
    
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 725      738      757      779
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 727      739      758
 727
 763
 763
  Nla 3
  Sty I
  Sec I
  Mae II
  SnaB I
  Nco I
  Rsa I
  Rsa I
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ggatgaaccgtcatgtagatgcataatcagtagcgcataatggtaccactacgccaaaaccgtcatgtggttaccgcacc
 812      819      841      863
 820
 841
 841
 842
  Mae II
  Aha II
  Aat II
  Nla IV
  Ban I
  Hinf I
  HinC II
  Rsa I
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 891      924      946
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 995      1020
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 1067      1078      1108
 1045      1072      1117
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 1045      1115
 1046      1115
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 1118
  ScrF I
  Hpa II
  Bcn I
  Hae III
  Eag I
  BstU I
  Sec I
  Sac II
  Bgl I
  Eae I
  Sau3a
  NspB II
  Hinf I
  BstU I
  Mae II
  Mae III
  Rsa I
  Alu I
  Sac I
  HgiA I
  Ban II
  ScrF I
  BstN I
  Sau3a
  Aha II
  Bbv II
  Nla IV
  Sau96 I
  Ava II
  ScrF I
  Hpa II
  Bcn I
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1123 1129 1133 1136 1159 1163 1180 1183 1189

1133
1133
1134
1136
1137
1139
1139
1139

Nla 3
Sph I
NspH I
Hae III
Sau96 I
Nla IV
EcoO109 I
Hinf I
Nsi I

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Dde I
Esp I
Alu I
Mae III

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PflM I
Nla 3

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|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
1374 1380

Sau96 I
Nla IV
Ava II
PpuM I
Nla IV
EcoO109 I
Hinf I

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1448 1470 1470 1470 1471 1471 1471

Ava I
Hpa II
Sau3a
Hinf I
Mae II
Nla 3
Mse I
BstY I
BstU I
Rsa I
BspM II
Ban II
Hpa II

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        BstU I
        HinP I
        Hha I
        Rsa I
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        1925 1940 1962 1990
        1926 1941 1990
        1941 1990
        1941 1991
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        1945

        Mae III
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        2003 2018 2029 2048
        2008
        2019
        ScrF I
        Hpa II
        Bcn I
        Xma I
        Sma I
        Sec I
        ScrF I
        Bcn I
        Ava I
        Mae I
        BstU I
        Mae I
        BstU I
        BstU I
        Mlu I
        Sau3a
        Bbv II
        Nhe I
        Mlu I
        Sau3a
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        2094 2105 2124 2148
        2098 2110 2124 2148
        2098 2110 2125 2149
        2098
        2098
        2098
        2098
        2099
        2099
        2099

        Mae II
        Nla 3
        Sty I
        Sec I
        Nco I
        Mae II
        SnaB I
        Sau3a
        BstY I
        Bgl II
        Sau3a
        Bcl I
        Taq I
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 || . || . || . || .
 2203 2217 2228 2237
 2203 2217 2229
 2203 2218
 2204 2222
 2223 Nla IV
 ScrF I
 BstN I
 Mae I Tth111 II Sec I Ban I
 CTGTGCCCTTCTAGttgccagccatctgttgtttgccctcccccgctgccttctctgaccctggaaggtgccactcccact 2320
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 2360
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 Pvu II
 NspB II Taq I
 Nla 3 Sph I NspH I Ban II Nla IV Ban II
 Bbv II
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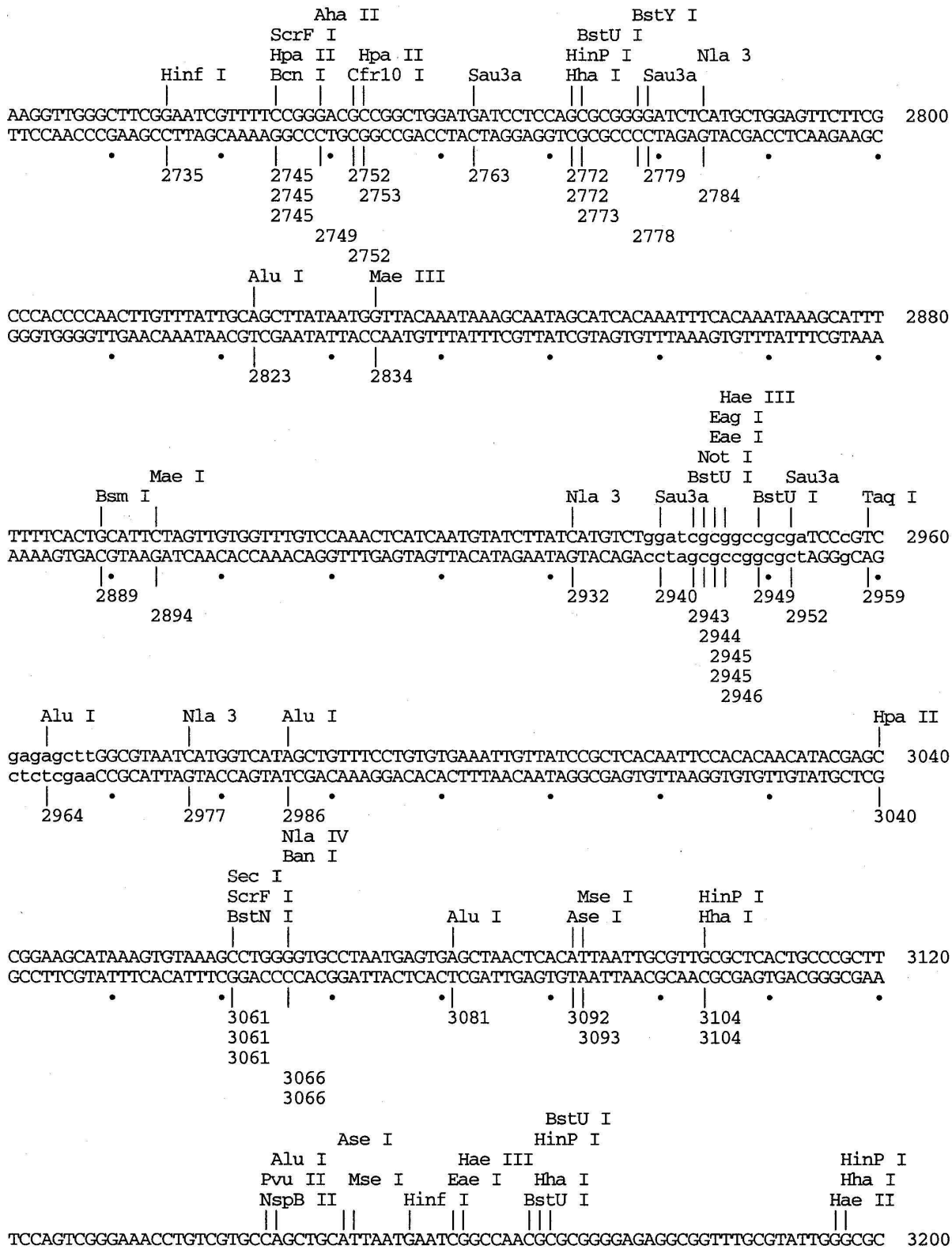
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 2469 2470
 Sau96 I
 Ava II Alu I
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 2485 2532
 2485
 HinP I
 Hinf I Hha I Dde I Hinf I
 CTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTctgaGCGGG 2640
 GAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTTCGGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGactCGCCC

 2588 2596 2596 2632 2640
 Taq I Hinf I
 BstB I Aha II BspM I Taq I
 ACTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCAGAGATTTTCGATTCCACCGCCGCTTCTATGA 2720
 TGAGACCCCAAGCTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGCGGAAGATACT

 2650 2670 2678 2696 2698
 2651 2698
 Nae I

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AGGTCAGCCCTTTGGACAGCACGGTTCGACGTAATTAAGCTTAGCCGGTTGCGCGCCCTCTCCGCCAAACGCATAACCCGCG
3144 3152 3161 3168 3196
3145 3162 3169 3197
3151 3169 3170

Hinf I Hha I Alu I
TCTTCGGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGGCGAGCGGTATCAGTCACTCAAAGGCGGT 3280
AGAAGGCGAAGGAGCGAGTGAAGTACTGAGCGACGCGAGCCAGCAAGCCGACGCGCTCGCCATAGTCGAGTGAGTTCCGCCA
3222 3230 3263
3230

Hinf I Nla 3 NspH I Hae III Hae III Nla IV ScrF I BstN I
AATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTA 3360
TTATGCCAATAGGTGTCTTAGTCCCTATTGCGTCTTTCTTTGACACTCGTTTCCGGTCGTTTTCCGGTCTTTGGCAT
3297 3322 3336 3347
3323 3349 3349 3352

BstU I Hae III Nla IV Taq I
AAAAGGCCGCGTTGCTGGCGTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGG 3440
TTTTCCGGCGCAACGACCGCAAAAAGGTATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTAGCTGCGAGTTCAGTCTCC
3365 3391 3422
3368

ScrF I BstN I Hha I Hae III Hinf I
TGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTTGGAAAGCTCCCTCGTGCGCTCTCTGTTCGACCCT 3520
ACCGCTTTGGGCTGTCTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGA
3470 3482 3489 3500
3470 3483 3500
3483

Hpa II Hinf I Hha I Hae II Dde I
GCCGCTTACCGGATACCTGTCCGCTTTTCCTTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCA 3600
CGGCGAATGGCCTATGGACAGGCGGAAAGAGGGAAAGCCCTTCGCACCGCAAAGAGTTACGAGTGCACATCCATAGAGT
3529 3566 3597
3567 3567

Alu I HgiA I Hpa I Mae III
GTTCCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGT 3680
CAAGCCACATCCAGCAAGCGAGGTTCCGACCGACACAGTGTGTTGGGGGCAAGTCGGGCTGGCGACGCGGAAATAGGCCA
3680

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        3625          3636          3662          3676
                   3636                   3667          3679
                                     3667
        Hpa II
        ScrF I
        Hinf I Bcn I                      Mae III
        |      |      |                    |
AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 3760
TTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGTCGGTGACCATTGTCCTAATCGTCTCG
        .      .      .                    .      .      .
        3693      3701                      3742
                   3701
                   3702
        Hae III                      Mae I
        |                          |
GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCT 3840
CTCCATACATCCGCCACGATGTCTCAAGAACTTCACCACCGGATGTGATGCCGATGTGATCTTCCTGTCATAAACCATAGA
        .      .      .                    .      .      .
        3799                      3817
        Hpa II
        Hha I                      Mae III      Alu I      Sau3a      Tth111 II      NspB II
        |                          |            |      |      |      |      |
GCGCTCTGCTGAAGCCAGTTACCTTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGT 3920
CGCGAGACGACTTCGGTCAATGGAAGCCTTTCTCAACCATCGAGAAGTACGAGCCGTTTGTGTTGGTGGCGACCATCGCCA
        .      .      .                    .      .      .      .      .
        3841      3858                      3882      3889      3896      3907
        3841
        3892
        Hpa II
        Hha I                      Mae III      Alu I      Sau3a      Tth111 II      NspB II
        |                          |            |      |      |      |      |
GGTTTTTTTGTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC 4000
CCAAAAAACAACGTTTCGTCGCTAATGCGCGTCTTTTTTCTCCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAG
        .      .      .                    .      .      .      .      .
        3929      3935                      3949      3963      3974      3983
        3950
        3950
        Hpa II
        Hha I                      Mae III      Alu I      Sau3a      Tth111 II      NspB II
        |                          |            |      |      |      |      |
TGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTGGTTCATGAGATTATCAAAAAGGATCTTACCTTAGATCCTTT 4080
ACTGCGAGTCACCTTGCTTTTGGAGTGCAAATCCCTAAAACCAGTACTCTAATAGTTTTTCTAGAAAGTGGATCTAGGAAA
        .      .      .                    .      .      .      .      .
        4006      4025                      4042      4060      4070      4079
        4028
        4043
        4061
        4072
        4080
        4073
        Hpa II
        Hha I                      Mae III      Alu I      Sau3a      Tth111 II      NspB II
        |                          |            |      |      |      |      |
TAAATTAAAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTtaCCAATGCTTAAATCAGT 4160
ATTTAATTTTTACTTCAAAAATTAGTTAGATTTTCATATATACTCAATTTGAACCAGACTGTCaatGGTTACGAATTAGTCA
        .      .      .                    .      .      .      .      .
        4085      4098                      4141      4152
        4099
        Hpa II
        Hha I                      Mae III      Alu I      Sau3a      Tth111 II      NspB II
        |                          |            |      |      |      |      |
GAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCGTCGTGTAGATAAATACGATACG 4240
CTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGC
        .      .      .                    .      .      .      .      .
        4163      4172                      4210
    
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4163 4178
Sau96 I Nla IV Hpa II Nla IV
Nla IV Hae III BstU I Cfr10 I
Hae III
GGAGGGCTTACCATCTGGCCCCAGTGCATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAA 4320
CCTCCCGAATGGTAGACCGGGTACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGCTCTAAATAGTCGTTATT
4257 4279 4295 4296 4298
4257 4296
4257 4298
HinP I
Hae III Hha I Sau96 I Mse I ScrF I
Hpa II Hpa II Hha I Sau96 I Ava II Mse I Hpa II
Bgl I Sau96 I Ase I Bcn I
ACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTTGTTGCCGG 4400
TGGTCGGTCCGGCTTCCCGCTCGCGTCTTACCAGGACGTTGAAATAGCGGAGGTAGGTTCAGATAAATTAACAACGGCC
4329 4336 4343 4353 4386 4397
4330 4337 4343 4353 4387 4397
4343 4397
Mae II
HinP I
Mae I Hha I
Alu I Mse I Fsp I Mae III
GAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGGCGAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACAGCTC 4480
CTTCGATCTCATTCATCAAGCGGTCAATTTATCAAACGCGTTGCAACAACGGTAACGATGTCCGTAGCACCACAGTGGCGAG
4403 4426 4435 4472
4405 4436 4436
4436 4441
Nla IV Sau3a
Hpa II Nla 3
Alu I Sau3a Mae III Nla 3
GTCGTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAG 4560
CAGCAAACCATAACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCGGCTCAATGTACTAGGGGTACAACACGTTTTTTTC
4503 4519 4530 4544
4507 4534 4537
4509
Pvu I
Sau96 I Hae III
Alu I Ava II Sau3a Eae I Nla 3
CGGTTAGCTCCTTCGGTCCCGATCGTTGTCAGAAGTAAGTTGGCCGCGAGTGTATCACTCATGGTTATGGCAGCACTG 4640
GCCAATCGAGGAAGCCAGGAGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCTGTGAC
4566 4575 4583 4603 4622
4575 4604
4582
Nla 3 Rsa I
Mae III Sca I Dde I
CATAATCTCTTACTGTATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGGAGTACTCAACCAAGTCATTCTGAGAATA 4720
GTATTAAGAGAATGACAGTACGGTAGGCATTTCTACGAAAAGACACTGACCACTCATGAGTTGGTTTCAGTAAGACTCTTAT
4658 4683 4693 4712

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4694

Aha II
 Hpa II
 ScrF I
 Bcn I

HinP I
 Hha I
 BstU I

Mse I
 Dra I HgiA I

GTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGC 4800
 CACATACGCCGCTGGCTCAACGAGAACGGGCCGAGTTATGCCCTATTATGGCGCGGTGTATCGTCTTGAATTTTCACG

 4748 4772 4790 4797
 4748 4773 4791
 4749 4773
 4751

Mae II
 Xmn I

Sau3a
 BstY I NspB II BstY I

Sau3a
 Mae III
 Taq I

TCATCATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCCTGTTGAGATCCAGTTTCGATGTAACCCACT 4880
 AGTAGTAACCTTTTGCAAGAAGCCCCGCTTTTGGAGAGTTCTTAGAATGGCGACAACCTCTAGGTCAAGCTACATTGGGTGA

 4810 4814 4840 4848 4857 4866 4871
 4814 4841 4858

HgiA I
 ApaL I

Sau3a

CGTGCACCCAACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGC 4960
 GCACGTGGGTTGACTAGAAGTCGTAGAAAATGAAAGTGGTCGCAAAGACCCACTCGTTTTTGTCTTCCGTTTTACGGCG

 4882 4894
 4882

Ssp I

AAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTcatACTCTTCTTTTTTCAATATTATGAAGCATTTTATCAGG 5040
 TTTTTTCCCTTATTCCCGCTGTGCCTTTACAACCTTATGAgtaTGAGAAGGAAAAAGTTATAATAACTTTCGTAAATAGTCC

 5017

HinP I
 Hha I
 BstU I

Nla 3
 BspH I

Nla IV

GTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGA 5120
 CAATAACAGAGTACTCGCCTATGTATAAACTTACATAAAATCTTTTTATTGTTTATCCCCAAGGCGGTGTAAGGGGCT

 5050 5099 5104
 5051 5105 5105

AAAGTGCCACCT 5132
 TTTCACGGTGGGA
 .

Restriction Endonucleases site usage

Aat II	5	Bsm I	1	EcoR I	-	Nco I	3	Sau96 I	12
Acc I	1	BspH I	2	EcoR V	-	Nde I	1	Sca I	2
Afl II	1	BspM I	1	Esp I	1	Nhe I	1	ScrF I	21
Aha II	9	BspM II	1	Fsp I	1	Nla 3	27	Sec I	17
Alu I	24	BssH II	2	Hae II	2	Nla IV	20	Sfi I	1
Apa I	-	BstB I	1	Hae III	22	Not I	2	Sma I	2

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ApaL I	2	BstE II	-	HgiA I	6	Nru I	-	SnaB I	2
Ase I	5	BstN I	11	Hha I	18	Nsi I	4	Spe I	1
Asp718	-	BstU I	19	HinC II	4	NspB II	9	Sph I	4
Ava I	3	BstX I	-	HinD III	1	NspH I	5	Spl I	-
Ava II	6	BstY I	10	Hinf I	15	PaeR7 I	-	Ssp I	2
Avr II	1	Bsu36 I	-	HinP I	18	PflM I	1	Stu I	1
Bal I	1	Cla I	1	Hpa I	1	PpuM I	1	Sty I	4
BamH I	1	Cfr10 I	2	Hpa II	20	Pst I	1	Taq I	9
Ban I	4	Dde I	11	Kpn I	-	Pvu I	1	Tth111 I	-
Ban II	9	Dra I	3	Mae I	9	Pvu II	3	Tth111 II	4
Bbe I	-	Dra III	-	Mae II	14	Rsa I	10	Xba I	-
Bbv II	4	Eae I	6	Mae III	17	Rsr II	-	Xca I	-
Bcl I	1	Eag I	3	Mlu I	1	Sac I	3	Xho I	-
Bcn I	10	Eco47 III	-	Mse I	15	Sac II	1	Xma I	2
Bgl I	5	EcoN I	-	Nae I	1	Sal I	1	Xmn I	2
Bgl II	1	EcoO109 I	2	Nar I	-	Sau3a	25		

Enzyme	Site	Use	Site position (Fragment length)	Fragment order	
Acc I	gt/mkac	1	1(371) 2	372(4761) 1	
Afl II	c/taaag	1	1(1811) 2	1812(3321) 1	
Avr II	c/ctagg	1	1(2123) 2	2124(3009) 1	
Bal I	tgg/cca	1	1(389) 2	390(4743) 1	
BamH I	g/gatcc	1	1(2109) 2	2110(3023) 1	
Bcl I	t/gatca	1	1(2227) 2	2228(2905) 1	
Bgl II	a/gatct	1	1(2216) 2	2217(2916) 1	
Bsm I	gaatgc	1/-1	1(2888) 1	2889(2244) 2	
BspM I	acctgc	4/8	1(2677) 1	2678(2455) 2	
BspM II	t/ccgga	1	1(1578) 2	1579(3554) 1	
BstB I	tt/cgaa	1	1(2649) 1	2650(2483) 2	
Cla I	at/cgat	1	1(362) 2	363(4770) 1	
Esp I	gc/tnagc	1	1(1298) 2	1299(3834) 1	
Fsp I	tgc/gca	1	1(4434) 1	4435(698) 2	
HinD III	a/agctt	1	1(2017) 2	2018(3115) 1	
Hpa I	gtt/aac	1	1(1894) 2	1895(3238) 1	
Mlu I	a/cgct	1	1(2103) 2	2104(3029) 1	
Nae I	gcc/ggc	1	1(2751) 1	2752(2381) 2	
Nde I	ca/tatg	1	1(712) 2	713(4420) 1	
Nhe I	g/ctagc	1	1(2092) 2	2093(3040) 1	
PflM I	ccannnn/ntgg	1	1(1373) 2	1374(3759) 1	
PpuM I	rg/gwccy	1	1(1469) 2	1470(3663) 1	
Pst I	ctgca/g	1	1(2002) 2	2003(3130) 1	
Pvu I	cgat/cg	1	1(4581) 1	4582(551) 2	
Sac II	ccgc/gg	1	1(1132) 2	1133(4000) 1	
Sal I	g/tcgac	1	1(371) 2	372(4761) 1	
Sfi I	ggccnnnn/nggcc	1	1(61) 2	62(5071) 1	
Spe I	a/ctagt	1	1(479) 2	480(4653) 1	
Stu I	agg/cct	1	1(17) 2	18(5115) 1	
ApaL I	g/tgcac	2	1(3635) 1	3636(1246) 2	4882(251) 3
BspH I	t/catga	2	1(4041) 1	4042(1008) 2	5050(83) 3
BssH II	g/cgctc	2	1(1940) 2	1941(2) 3	1943(3190) 1
Cfr10 I	r/ccggy	2	1(2751) 1	2752(1543) 2	4295(838) 3
EcoO109 I	rg/gnccy	2	1(1254) 2	1255(215) 3	1470(3663) 1
Hae II	rgcgc/y	2	1(3195) 1	3196(370) 3	3566(1567) 2
Not I	gc/ggccgc	2	1(6) 3	7(2937) 1	2944(2189) 2
Sca I	agt/act	2	1(1924) 2	1925(2768) 1	4693(440) 3
Sma I	ccc/ggg	2	1(355) 3	356(1742) 2	2098(3035) 1

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SnaB I	tac/gta	2	1(818) 3	819(1403) 2	2222(2911) 1	
Ssp I	aat/att	2	1(377) 2	378(4639) 1	5017(116) 3	
Xma I	c/ccggg	2	1(355) 3	356(1742) 2	2098(3035) 1	
Xmn I	gaann/nmttc	2	1(346) 2	347(4463) 1	4810(323) 3	
Ava I	c/ycgrg	3	1(355) 4	356(1210) 2	1566(532) 3	2098(
Dra I	ttt/aaa	3	1(4078) 1	4079(19) 4	4098(692) 2	4790(
Eag I	c/ggccg	3	1(7) 4	8(1128) 3	1136(1809) 2	2945(
Nco I	c/catgg	3	1(840) 3	841(1149) 2	1990(213) 4	2203(
Pvu II	cag/ctg	3	1(1840) 2	1841(628) 4	2469(675) 3	3144(
Sac I	gagct/c	3	1(1044) 2	1045(726) 3	1771(377) 4	2148(
Ban I	g/gyrcc	4	1(945) 4	946(1360) 1	2306(760) 5	3066(
Bbv II	gaagac 2/6	4	4163(970) 3			
HinC II	gty/rac	4	1(1107) 2	1108(699) 3	1807(274) 5	2081(
Nsi I	atgca/t	4	2423(2710) 1			
Sph I	gcatg/c	4	1(371) 4	372(91) 5	463(532) 3	995(
Sty I	c/cwwgg	4	1895(3238) 1			
Tth111 II	caarca 11/9	4	1(109) 3	110(91) 4	201(72) 5	273(
Aat II	gacgt/c	5	1230(3903) 1			
Ase I	at/taat	5	1(202) 4	203(72) 5	275(957) 3	1232(
Bgl I	gccnnnn/nggc	5	2437(2696) 1			
NspH I	rcatg/y	5	1(840) 3	841(1149) 2	1990(134) 4	2124(
Ava II	g/gwcc	6	2203(2930) 1			
Eae I	y/ggCCR	6	1(2268) 1	2269(1627) 2	3896(33) 4	3929(
HgiA I	gwgw/c	6	3935(1198) 3			
Aha II	gr/cgyc	9	1(0) 6	1(600) 2	601(53) 5	654(
Ban II	grgcy/c	9	738(186) 3	924(4209) 1		
Mae I	c/tag	9	1(348) 4	349(138) 5	487(2605) 1	3092(
NspB II	cmg/ckg	9	3151(1235) 2	4386(747) 3		
Taq I	t/cga	9	1(62) 6	63(623) 3	686(72) 5	758(
Bcn I	ccs/gg	10	1129(3200) 1	4329(804) 2	275(957) 3	1232(
			2437(885) 4	3322(1811) 1		
			1(1117) 2	1118(353) 5	1471(160) 7	1631(
			2485(1868) 1	4353(222) 6	4575(558) 4	
			1(7) 7	8(382) 5	390(746) 3	1136(
			2945(216) 6	3161(1442) 2	4603(530) 4	
			1(1044) 3	1045(726) 4	1771(377) 5	2148(
			3636(1161) 2	4797(85) 7	4882(251) 6	
			1(0) 10	1(600) 3	601(53) 9	654(
			738(186) 5	924(154) 6	1078(1592) 2	2670(
			2749(2002) 1	4751(382) 4		
			1(1044) 2	1045(543) 3	1588(36) 8	1624(
			1771(13) 10	1784(264) 5	2048(100) 7	2148(
			2455(20) 9	2475(2658) 1		
			1(15) 10	16(465) 5	481(1613) 1	2094(
			2125(125) 8	2250(644) 4	2894(923) 2	3817(
			4070(335) 6	4405(728) 3		
			1(1132) 1	1133(511) 6	1644(175) 9	1819(
			1841(628) 4	2469(675) 3	3144(518) 5	3662(
			3907(941) 2	4848(285) 7		
			1(363) 4	364(9) 10	373(1864) 1	2237(
			2479(172) 8	2651(45) 9	2696(263) 6	2959(
			3422(1444) 2	4866(267) 5		
			1(355) 7	356(1) 10	357(758) 3	1115(
			1139(959) 1	2098(1) 11	2099(646) 5	2745(
			3701(696) 4	4397(351) 8	4748(385) 6	

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BstY I	r/gatcy	10	1(1549) 1 2778(1185) 2 4072(768) 3	1550(560) 5 3963(11)11 4840(17) 9	2110(107) 7 3974(86) 8 4857(276) 6	2217() 4060()
Rsa I	gt/ac	10	1(424) 3 812(51)10 1571(355) 5	425(273) 6 863(157) 8 1926(2768) 1	698(81) 9 1020(169) 7 4694(439) 2	779() 1189()
BstN I	cc/wgg	11	1(234) 8 763(309) 6 3061(288) 7	235(17)11 1072(556) 4 3349(121) 9	252(55)10 1628(671) 3 3470(13)12	307() 2299() 3483()
Dde I	c/tnag	11	1(55)12 1844(75)11 3597(409) 6	56(1244) 1 1919(441) 4 4006(166) 9	1300(396) 7 2360(272) 8 4172(540) 3	1696() 2632() 4712()
Sau96 I	g/gncc	12	1(563) 3 1118(138)10 2485(1772) 1 4575(558) 4	564(163) 8 1256(215) 7 4257(79)11	727(30)12 1471(160) 9 4336(17)13	757() 1631() 4353()
Mae II	a/cgt	14	1(1)15 614(41)13 925(258) 8 4025(416) 3	2(400) 4 655(84)11 1183(390) 5 4441(373) 6	402(200) 9 739(81)12 1573(650) 2 4814(319) 7	602() 820() 2223()
Hinf I	g/antc	15	1(890) 2 1448(114)10 2640(58)13 3222(75)11	891(272) 8 1562(304) 7 2698(37)16 3297(396) 6	1163(38)15 1866(722) 3 2735(422) 5 3693(517) 4	1201() 2588() 3157() 4210()
Mse I	t/taa	15	1(349) 5 1813(83)10 4028(52)13 4152(235) 8	350(138) 9 1896(1197) 1 4080(5)16 4387(39)14	488(1048) 2 3093(59)11 4085(14)15 4426(365) 4	1536() 3152() 4099() 4791()
Mae III	/gtnac	17	1(542) 4 1180(170)10 2008(826) 2 3858(283) 7 4683(188) 9	543(31)18 1350(445) 5 2834(845) 1 4141(331) 6 4871(262) 8	574(55)17 1795(80)14 3679(63)15 4472(58)16	629() 1875() 3742() 4530()
Sec I	c/cnngg	17	1(63)14 307(49)15 1133(494) 3 2098(26)16 3061(421) 5	64(9)17 356(1)18 1627(115) 9 2124(79)12 3482(1651) 1	73(162) 8 357(484) 4 1742(248) 7 2203(95)11	235() 841() 1990() 2298()
Hha I	gcg/c	18	1(1940) 1 2596(176) 8 3197(33)15 3667(174) 9 4436(337) 4	1941(2)18 2772(332) 5 3230(270) 7 3841(109)10 4773(332) 6	1943(2)19 3104(65)14 3500(67)13 3950(393) 3 5105(28)17	1945() 3169() 3567() 4343()
HinP I	g/gcg	18	1(1940) 1 2596(176) 8 3197(33)15 3667(174) 9 4436(337) 4	1941(2)18 2772(332) 5 3230(270) 7 3841(109)10 4773(332) 6	1943(2)19 3104(65)14 3500(67)13 3950(393) 3 5105(28)17	1945() 3169() 3567() 4343()
BstU I	cg/cg	19	1(5)17 1159(400) 6 1944(161)13 2949(219)10 3949(330) 9	6(534) 4 1559(381) 7 2105(668) 1 3168(2)20 4279(493) 5	540(594) 2 1940(2)18 2773(170)12 3170(198)11 4772(332) 8	1134() 1942() 2943() 3368() 5104()
Hpa II	c/cgg	20	1(356) 8	357(12)20	369(356) 9	725()

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			1115(24)18	1139(441) 4	1580(18)19	1598(
			2099(646) 1	2745(8)21	2753(287)10	3040(
			3529(147)13	3676(26)17	3702(190)12	3892(
			4296(34)16	4330(67)15	4397(110)14	4507(
			4749(384) 7			
Nla IV	ggn/ncc	20	1(230) 7	231(72)17	303(424) 5	727(
			946(171)12	1117(138)15	1255(215) 9	1470(
			1471(160)13	1631(479) 4	2110(196)11	2306(
			2464(602) 2	3066(286) 6	3352(39)19	3391(
			4163(94)16	4257(41)18	4298(211)10	4509(
			5099(34)20			
ScrF I	cc/ngg	21	1(234)11	235(17)19	252(55)15	307(
			356(1)21	357(406) 5	763(309) 9	1072(
			1115(24)18	1139(489) 2	1628(470) 3	2098(
			2099(200)13	2299(446) 4	2745(316) 8	3061(
			3349(121)14	3470(13)20	3483(218)12	3701(
			4397(351) 7	4748(385) 6		
Hae III	gg/cc	22	1(8)22	9(10)20	19(43)16	62(
			71(6)23	77(314) 7	391(173)11	564(
			727(30)17	757(380) 6	1137(120)13	1257(
			1689(51)15	1740(1206) 1	2946(216) 9	3162(
			3336(11)19	3347(18)18	3365(434) 4	3799(
			4257(80)14	4337(267) 8	4604(529) 2	
Alu I	ag/ct	24	1(53)24	54(992) 1	1046(252) 8	1298(
			1611(55)23	1666(106)15	1772(70)18	1842(
			1962(57)22	2019(130)12	2149(321) 4	2470(
			2532(291) 6	2823(141)10	2964(22)25	2986(
			3081(64)19	3145(118)14	3263(226) 9	3489(
			3625(257) 7	3882(521) 3	4403(100)16	4503(
			4566(567) 2			
Sau3a	/gatc	25	1(361) 6	362(4)26	366(701) 2	1067(
			1123(428) 5	1551(560) 3	2111(107)11	2218(
			2229(534) 4	2763(16)20	2779(161)10	2940(
			2952(937) 1	3889(75)14	3964(11)24	3975(
			3983(78)13	4061(12)22	4073(105)12	4178(
			4519(18)18	4537(46)16	4583(258) 8	4841(
			4858(36)17	4894(239) 9		
Nla 3	catg/	27	1(108)15	109(4)28	113(91)16	204(
			276(166)12	442(18)25	460(322) 8	782(
			842(391) 4	1233(147)14	1380(205)10	1585(
			1636(16)26	1652(339) 7	1991(38)23	2029(
			2204(234) 9	2438(346) 5	2784(148)13	2932(
			2977(346) 6	3323(720) 1	4043(491) 2	4534(
			4544(78)18	4622(36)24	4658(393) 3	5051(

540 sites found

No Sites found for the following Restriction Endonucleases

Apa I	gggcc/c	Eco47 III	agc/gct	Paer7 I	c/tcgag
Asp718	g/gtacc	EcoN I	cctnn/nmnagg	Rsr II	cg/gwccg
Ebe I	ggcgc/c	EcoR I	g/aattc	Spl I	c/gtacg
BstE II	g/gtnacc	EcoR V	gat/atc	Tth111 I	gacn/nngtc
BstX I	ccannnnn/ntgg	Kpn I	ggtac/c	Xba I	t/ctaga

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Bsu36 I	cc/tnagg	Nar I	gg/cgcc	Xca I	gta/tac
Dra III	cacnnn/gtg	Nru I	tcg/cga	Xho I	c/tcgag

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