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PstI (6)
SdaI (6) **SpeI (13)**

1 CCTGCAGGGCCACTAGTCGCCTTGCTGTGCCACTTTGGGACTTCCCTCCTAGCCTGAGCTTCAGTTTTCTGCCTGTTAGGCAGCCCCATGTCAACTG

Eco47III (165)
BamHI (156)

101 CACTTAGTAGGCCGGGTTTGATGCCCGACAAGACGTGAAGTGGTGGAGGTGGGCAGGATCCCAGCGCTACCATCTTCTTGAACCACTGATCTCAACACAT

201 CGGATTTCTGTTTCTCATCTGCAAAATGGGATCAGTGAGCTCAGGTGGGTACAAAATTTACAGGAAGTACTTTAGCCAAGCCCGCCCCCTGAAAGTT

EcoNI (372)

301 CCCCTCGGTGGGCTGTTAGGGTATTGTTTTTCATCTGTGGGGCTCCCTGATGCGTCCCACCCACCAAGCCTTGGAGAGGGTGGGATGGGAGGGTGGGGTGC

401 TTGGGGAGACAAGCTAGAGCTGGGCCCTCCCACCCACTGCCTCCCCCATCCCAGGGCCCCACCCAGTGACAAAAGCCCGTGGCACTTCTCTTACC

NaeI (564)

501 CGGTTGGCAGGGCGCTGGCCAGCCCTTCTTAAGGAAGCGATTTCCTGCCTCCCTGGCCGGCCGGGCTGGATGAGCCGGGAGCTCCCTGCTGCCG

601 GTCATACCACAGCCTTCTATGCGCCCTGGGGCCAGGACTGCTGCTGCTACTGCCATCCATTGGAGCCAGCACCCCTCCCGCCCATCTTCGGACAG

Tth111I (781)

701 CAACTCCAGCCAGCCCCGCGTCCCTGTGTCCACTTCTCTGACCCTCGGCCGCCACCCAGAAGGCTGGAGCAGGGACGCCGTCGCTCCGCCGCTG

SandI (808) **NaeI (831)** **BbrPI (897)**

801 CTCCCCTCGGGTCCCGTGCAGCCACGCCGGCCCCGGTGGCCGCCGAGCCCTGCCACTGGACACAGGATAAGGCCAGCGCACAGGCCCCACGTTG

NcoI (905) **NheI (943)** **Acc65I (999)**

901 GACACCATGGGGGTTCTCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAAATGGGTCGGATCTGTACGACGATGACGATAAGG

1001 TACCTAAGGATCAGCTTGGAGTTGATCCCGTCGTTTTACAACGCTGCTGACTGGGAAAACCTGGCGTTACCCAACCTAATCGCCTTGACGACATCCCC

32▶ al ProLysAspGlnLeuGlyValAspProValValLeuGlnArgArgAspTrpGluAsnProGlyValThrGlnLeuAsnArgLeuAlaAlaHisSPProP

FspI (1159)

1101 TTTCCGACGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCTTTGCCTGGTTTCCGGCA

65▶ oPheAlaSerTrpArgAsnSerGluGluAlaArgThrAspArgProSerGlnGlnLeuArgSerLeuAsnGlyGluTrpArgPheAlaTrpPheProAla

Bsu36I (1241)

1201 CCAGAAGCGGTGCCGAAAGCTGGCTGGAGTGCATCTTCTGAGGCCGATACTGCTGCTGCCCTCAAAGTGGCAGATGCACGGTTACGATGCGCCCA

99▶ ProGluAlaValProGluSerTrpLeuGluCysAspLeuProGluAlaAspThrValValValProSerAsnTrpGluMetHisGlyTyrAspAlaProI

1301 TCTACCAACGTAACCTATCCATTACGGTCAATCCGCCGTTTGTCCACGGAGAATCCGACGGGTTGTTACTCGCTCACATTTAATGTTGATGAAAG

132▶ IeTyrThrAsnValThrTyrProIeThrValAsnProPheValProThrGluTyrGlyCysTyrSerLeuThrPheAsnValAspGluSe

1401 CTGCTACAGGAAGGCCAGCGGAATATTTTTGATGGCGTTAACTCGCGTTTTCATCTGTGGTGCAACGGCGCTGGGTCGGTTACGGCCAGGACAGT

165▶ rTrpLeuGlnGluGlyGlnThrArgIleIlePheAspGlyValAsnSerAlaPheHisLeuTrpCysAsnGlyArgTrpValGlyTyrGlyGlnAspSer

1501 CGTTTGGCTGCTGAATTTGACCTGAGCGCATTTTTACGCGCCGAGAAAACCGCTCGCGGTGATGGTCTGCTTGGAGTGACGGCAGTTATCTGGAAG

199▶ ArgLeuProSerGluPheAspLeuSerAlaPheLeuArgAlaGlyGluAsnArgLeuAlaValMetValLeuArgTrpSerAspGlySerTyrLeuGluAla

AatII (1640)

1601 ATCAGGATATGTGGCGGATGAGCGGCATTTCCGTGACGTCTCGTTGCTGCATAAACCGACTACACAAATCAGCGATTTCCATGTTGCCACTCGCTTAA

232▶ spGlnAspMetTrpArgMetSerGlyIlePheArgAspValSerLeuLeuHisLysProThrThrGlnIleSerAspPheHisValAlaThrArgPheAs

1701 TGATGATTTACGCGCGCTGACTGGAGGCTGAAGTTCAGATGTGCGCGAGTTGCGTACTACTACGGTAACAGTTTCTTTATGGCAGGGTGAACCG

265▶ nAspAspPheSerArgAlaValLeuGluAlaGluValGlnMetCysGlyGluLeuArgAspTyrLeuArgValThrValSerLeuTrpGlnGlyGluThr

ClaI (1841)

1801 CAGGTCGCCAGCGGCACCGCCTTTCCGGCGTGAATATCGATGAGCGTGGTGGTTATGCCGATCGCGTCACACTACGCTGAACGTCGAAAACCCGA

299▶ GluValAlaSerGlyThrAlaProPheGlyGlyGluIleIleAspGluArgGlyGlyTyrAlaAspArgValThrLeuArgLeuAsnValGluAsnProL

1901 AACTGTGGAGCGCGAAATCCCGAATCTCTATCGTGGCGTGGTTGAATGCACACCGCGACGCGACGCTGATTGAAGCAGAAGCCTGCGATGTCGGTTT

332▶ yssLeuTrpSerAlaGluIleProAsnLeuTyrArgAlaValAlaGluLeuHisThrAlaAspGlyThrLeuIleGluAlaGluAlaCysAspValGlyPh

2001 CCGCGAGTGGGATGAAAATGGTCTGCTGCTGAACGGCAAGCGTTGCTGATTCGAGGCGTTAACCGTCAAGGATCATCCTCTGCATGGTCAG

365▶ eArgGluValArgIleGluAsnGlyLeuLeuLeuLeuAsnGlyLysProLeuLeuIleArgGlyValAsnArgHisGluHisHisSPProLeuHisGlyGln

EcoRV (2130)

2101 GTCATGGATGAGCAGACGATGGTGCAGGATATCCTGCTGATGAAGCAGAACAACCTTAACCGCGTGGCTGTTTCGATTATCCGAACCATCCGCTGTGGT

399▶ ValMetAspGluGlnThrMetValGlnAspIleLeuLeuMetLysGlnAsnAsnPheAsnAlaValArgCysSerHisSyrProAsnHisSPProLeuTrpT

SspI (2247)

2201 ACACGCTGTGCGACCGCTACGGCCTGTATGTGGTGGATGAAGCAATATTGAAACCCACGGCATGGTGCATGAATCGTCTGACCGATGATCCGCGCTG

432▶ yrThrLeuCysAspArgTyrGlyLeuTyrValValAspGluAlaAsnIleGluThrHisGlyMetValProMetAsnArgLeuThrAspAspProArgTr

BsaBI (2343)

2301 GCTACCGCGATGAGCGAACCGTAACCGAATGGTGCAGCGCATCGTAATCACCCGAGTGTGATCATCTGGTCTGGGGAATGAATCAGGCCACGGC

465▶ pLeuProAlaMetSerGluArgValThrArgMetValGlnArgAspArgAsnHisSPProSerValIleIleTrpSerLeuGlyAsnGluSerGlyHisGly

2401 GCTAATCACGACGCGCTGTATCGCTGGATCAAATCTGTCGATCCTTCCGCCCGTGCAGTATGAAGCGGGGAGCCGACACCAGGCCACCGATATTA

499▶ AlaAsnHisAspAlaLeuTyrArgTrpIleLysSerValAspProSerArgProValGlnTyrGluGlyGlyAlaAspThrThrAlaThrAspIleI

BssHII (2515) **BbsI (2534)**

2501 TTTGCCCGATGTACGCGCGCTGGATGAAGACCAAGCCCTCCCGGCTGTGCCGAAATGGTCCATCAAAAAATGGCTTTCGCTACTGGAGAGACGCGCCC

532▶ IeCysProMetTyrAlaArgValAspGluAspGlnProPheProAlaValProLysTrpSerIleLysLysTrpLeuSerLeuProGlyGluThrArgPr

2601 GCTGATCCTTTGGAATACGCCACGCGATGGGTAACAGTCTTGGCGGTTTCGCTAAACTGCGAGCGGCTTTCGTCAGTATCCCGTTTACAGGGCGGC

565▶ oLeuIleLeuCysGluTyrAlaHisAlaMetGlyAsnSerLeuGlyGlyPheAlaLysTyrTrpGlnAlaPheArgGlnTyrProArgLeuGlnGlyGly

2701 TTCGTCGGGACTGGGTGGATCAGTCGCTGATTAATATGATGAAAACGGCAACCCGTGGTGGTTCACGGCGGTGATTTGGCGATACGCCAACGATC

599▶ PheValTrpAspTrpValAspGlnSerLeuIleLysTyrAspGluAsnGluAsnProTrpSerAlaTyrGlyGlyAspPheGlyAspThrProAsnAspA

Eco47III (2852)

2801 GCCAGTTCGTATGAACGGTCTGGTCTTTGCCGACCGCACGCCGATCCAGCGCTGACGGAAGCAAACACCAGCAGCAGTTTTTCCAGTTCCTTTATC
632▶ r g l n P h e C y s M e t A s n G l y L e u V a l P h e A l a A s p A r g T h r P r o H i s P r o A l a L e u T h r G l u A l a L y s H i s G l n G l n G l n P h e P h e G l n P h e A r g L e u S e
2901 CGGGCAAACCATCGAAGTGACCAGCGAATACCTGTTCCGTCATAGCGATAACGAGCTCCTGCACTGGATGGTGGCGCTGGATGGTAAGCCGCTGGCAAGC
665▶ r G l y G l n T h r I l e G l u V a l T h r S e r G l u T y r L e u P h e A r g H i s S e r A s p A s n G l u L e u L e u H i s T r p M e t V a l A l a L e u A s p G l y L y s P r o L e u A l a S e r
3001 GGTGAAGTGCCTCTGGATGTCGCTCCACAAGGTAACAGTTGATTGAACTGCCTGAACTACCGCAGCCGGAGAGCGCCGGCAACTCTGGCTCACAGTAC
699▶ G l y G l u V a l P r o L e u A s p V a l A l a P r o G l n G l y L y s G l n L e u I l e G l u L e u P r o G l u L e u P r o G l n P r o G l u S e r A l a G l y G l n L e u T r p L e u T h r V a l A
3101 GCGTAGTGAACCGAACCGCACCATGGTCAGAAAGCCGGGCACATCAGCGCCTGGCAGCAGTGGCGTCTGGCGGAAAACCTCAGTGTGACGCTCCCCGC
732▶ r g V a l V a l G l n P r o A s n A l a T h r A l a T r p S e r G l u A l a G l y H i s I l e S e r A l a T r p G l n G l n T r p A r g L e u A l a G l u A s n L e u S e r V a l T h r L e u P r o A l
3201 CGGTCCCACGCCATCCCGCATCTGACCACAGCGAAATGGATTTTTGCATCGAGCTGGGTAATAAGCGTTGGCAATTTAACCGCCAGTCAGGCTTTCTT
765▶ a A l a S e r H i s A l a l l e P r o H i s L e u T h r T h r S e r G l u M e t A s p P h e C y s I l e G l u L e u G l y A s n L y s A r g T r p G l n P h e A s n A r g G l n S e r G l y P h e L e u
3301 TCACAGATGTGGATTGGCGATAAAAAACAACCTGCTGACGCCGCTGCGCGATCAGTTCACCCGTGCACCCTGGATAACGACATTTGGCGTAAGTGAAGCGA
799▶ S e r G l n M e t T r p l l e G l y A s p L y s L y s G l n L e u L e u T h r P r o L e u A r g A s p G l n P h e T h r A r g A l a P r o L e u A s p A s n A s p l l e G l y V a l S e r G l u A l a T
3401 CCCGATTGACCTAACCGCTGGTCTGAAAGCGTGAAGCGCGGGCCATTACCAGGCCAAGCAGCGTTGTTGCACTGCACGGCAGATACACTTGTCTGA
832▶ h r A r g I l e A s p P r o A s n A l a T r p V a l G l u A r g T r p L y s A l a A l a G l y H i s T y r G l n A l a G l u A l a L e u L e u G l n C y s T h r A l a A s p T h r L e u A l a A s
3501 TGCGGTGCTGATTACGACCGCTCAGCGTGGCAGCATCAGGGGAAAACCTTATTTATCAGCCGAAAACCTACCGGATTGATGGTAGTGGTCAAATGGCG
865▶ p A l a V a l L e u I l e T h r T h r A l a H i s A l a T r p G l n H i s G l n G l y L y s T h r L e u P h e I l e S e r A r g L y s T h r T y r A r g I l e A s p G l y S e r G l y G l n M e t A l a
3601 ATTACCGTTGATGTTGAAGTGGCGAGCGATACCCGCATCCGCGCGGATTGGCTGAACTGCCAGCTGGCGCAGGTAGCAGAGCGGGTAAACTGGCTCG
899▶ I l e T h r V a l A s p V a l G l u V a l A l a S e r A s p T h r P r o H i s P r o A l a A r g I l e G l y L e u A s n C y s G l n L e u A l a G l n V a l A l a G l u A r g V a l A s n T r p L e u G

BbsI (3786)

Bst1107I (3779)

BspLU11I (3776) BsiWI (3787)

3701 GATTAGGGCCGAAGAAAATATCCCGACCGCCTTACTGCCGCTGTTTTGACCCTGGGATCTGCCATTGTCCAGACATGTATACCCCGTACGCTTTCCC
932▶ l y L e u G l y P r o G l n G l u A s n T y r P r o A s p A r g L e u T h r A l a A l a C y s P h e A s p A r g T r p A s p L e u P r o L e u S e r A s p M e t T y r T h r P r o T y r V a l P h e P r
3801 GAGCGAAAACGGTCTGCGCTGCGGGACGCGCAATTGAATTATGGCCACACCAGTGGCGCGGCGACTTCCAGTTCAACATCAGCCGCTACAGTCAACAG
965▶ o S e r G l u A s n G l y L e u A r g C y s G l y T h r A r g G l u L e u A s n T y r G l y P r o H i s G l n T r p A r g G l y A s p P h e G l n P h e A s n I l e S e r A r g T y r S e r G l n G l n

NdeI (3974)

3901 CAACTGATGGAACACAGCCATCGCCATCTGCTGACCGGGAAGAGGCACATGGCTGAATATCGACGGTTTCCATATGGGGATTGGTGGCGACGACTCCT
999▶ G l n L e u M e t G l u T h r S e r H i s A r g H i s L e u L e u H i s A l a G l u G l u G l y T h r T r p L e u A s n I l e A s p G l y P h e H i s M e t G l y l l e G l y G l y A s p A s p S e r T

NheI (4096)

EcoRI (4090)

4001 GGAGCCCGTCAGTATCGGCGGAATTACAGCTGAGCGCCGCTGCTACCATTACAGTTGGTCTGGTGTCAAAAATAATAATCTAGTCGAGAATTCGCTAG
1032▶ r p S e r P r o S e r V a l S e r A l a G l u L e u G l n L e u S e r A l a G l y A r g T y r H i s T y r G l n L e u V a l T r p C y s G l n L y s ●●●
4101 CTCGACATGATAAGATACATTGATGAGTTTGGACAAACCAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTAT

MfeI (4270)

4201 TTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAATTGCATTCATTTATGTTTCAGTTTCAG

DraI (4319)

DraI (4358)

SwaI (4361)

4301 GGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTAGATCCATTTAAATGTTAATTAAGTACCATGACCAAATCCCTTAACG

4401 TGAGTTTTCTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAAACAAA

4501 AAACCACCGCTACCAGCGGTGGTTTGTGGCCGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTG

4601 TTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTCAAGAACTCTGTAGCACCCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAG

4701 TGGCGATAAGTCTGTCTTACCAGGTTGGACTCAAGACGATAGTTACCAGATAAGGCGCAGCGGTCGGGCTGAACGGGGGTTCTGTGCACACAGCCAGC

4801 TTGGAGCGAACGACCTACCCGAAGTGAATACCTACAGCGTGAAGCTATGAGAAAGCGCCACGCTTCCGAAGGGAGAAAGCGGACAGGTATCCGGTAA

4901 CGGCAGGGTCGGAACAGGAGAGCGCAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTGTGCGGTTTCGCCACCTCTGACTTGAGCG

BspLU11I

5001 TCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAACACGCCAGCAACCGGCCTTTTTACGGTTCCTGGCCTTTTGTGGCCTTTTGTCTC

AseI (5137)

SfiI (5188)

MseI (5199)

5101 ATGTTCTTAATTAATTTTTCAAAGTAGTTGACAATTAATCATCGGCATAGTATATCGGCATAGTATAATACGACTCACTATAGGAGGGCCATCATGG

1▶MetA

5200 CCAAGTTGACCAAGTGTGTCCAGTGTCTCACAGCCAGGGATGTGGCTGGAGCTGTTGAGTCTGGACTGACAGGTTGGGGTTCTCCAGAGATTTTGTGGG

5300 GGATGACTTTGCAGGTGTGGTCAAGATGATGTACCCCTGTTTCATCTCAGCAGTCCAGGACCAGTGGTGCCTGACAACACCCCTGGCTGGGTGGGTG

5400 AGAGGACTGGATGAGCTGATGCTGAGTGGAGTGGTGGTCTCCACCAACTTACAGGATGCCAGTGGCCCTGCCATGACAGAGATTGGAGAGCAGCCCT

5500 GGGGGAGAGAGTTTGCCTGAGAGACCCAGCAGGCAACTGTGTGCACTTTGTGGCAGAGGAGCAGGACTGAGGATAAGAAATTGAGTTTCAGAAAAGGGGG

SfiI (5597)

5600 CCTGAGTGGCCCTTTTTTCAACTTAATTAA