

pmKate2-zyxin vector restriction map

The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 base pairs long are not included – for the more complete enzyme list please refer to the Table of restriction sites.

Unique sites are shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). mKate2 amino acids are shown in red, Zyxin amino acids are shown in green, linker amino acids are shown in black.




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                                     BseR1
                                     BseR1|
                                     Bpm1|
                                     BseR1 ||
          Pvu1      Xmn1      SpAcc      Bgl2      BseR1 ||      BspE1
          |         |         |         |         |         |
TGGGAGGTGCCTTCCCCGCCGCCCTCCCCGATCGAGGAATCATTTCCTCCCTGCGCCTCTGGAGGAGGAGATCTTCCCTTCCCCGCCGCCTCCTCCGGA
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
ACCTCCACGGAAGGGCGGCCGGGGGAGGGGGCTAGCTCCTTAGTAAAGGGGGACGCGGAGACCTCCTCCTCTAGAAGGGAAGGGGCGGCCGGAGGAGGCCT
Zyxin > G G A F P P P P P I E E S F P P A P L E E E I F P S P P P P E

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          BseR1
          Bsu36 |
          BseR1 ||
          || |
          SpDon
          |
          Ahd1      Bts1
          |         |
GGAGGAGGGAGGCCTGAGGCCCCATACCGCCCCACCACAGCCCAGGGAGAAGGTGAGCAGTATTGATTTGGAGATCGACTCTCTGTCTCACTGCTG
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
CCTCCTCCCTCCCGGACTCCGGGGTATGGCGGGGTGGTGTGCGGGTCCCTCTTCCACTCGTCATAACTAAACCTCTAGCTGAGAGACAGGAGTGACGAC
Zyxin > E E G G P E A P I P P P P Q P R E K V S S I D L E I D S L S S L L

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          Sma1
          |
          Msc1
          |
GATGACATGACCAAGAATGATCCTTTCAAAGCCCGGGTGTTCATCTGGATATGTGCCCCACCAGTGGCCACTCCATTTCAGTTCCAAGTCCAGTACCAAGC
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
CTACTGTACTGGTTCTTACTAGGAAAGTTTCGGGCCACAGTAGACCTATACACGGGGGTGGTCACCGGTGAGGTAAGTCAAGGTTTCAGGTCATGGTTTCG
Zyxin > D D M T K N D P F K A R V S S G Y V P P P V A T P F S S K S S T K P

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          Pst1
          |
          BseY1
          SpAcc | AlwN1
          |     |
          |     |
CTGCAGCCGGGGGCACAGCACCCCTGCCTCCTTGAAGTCCCCTTCCAGCTCCCAGCCTCTGCCCCAGGTTCCGGCTCCGGCTCAGAGCCAGACACAGTT
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
GACGTCCGCCCCGTGTCGTGGGGACGGAGGAACCTTCAGGGGAAGGTCGAGGGTCCGAGACGGGGTCCAAGGCCGAGGCCGAGTCTCGGTCTGTGTCAA
Zyxin > A A G G T A P L P P W K S P S S S Q P L P Q V P A P A Q S Q T Q F

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Apa1
PspOM |
Bgl1 | |

BseY1 BseY1 Bsu36 BseY1 BseY1

1301 CCATGTTTCAGCCCCAGCCCCAGCCCAAGCCTCAGGTCCAACCTCCATGTCCAGTCCCAGACCCAGCCTGTGTCTTTGGCTAACACCCAGCCCCGAGGGCCC 1400
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
 GGTACAAGTCGGGGTCGGGGTCGGGTTCGGAGTCCAGGTTGAGGTACAGGTTCAGGGTCTGGGTTCGGACACAGAAACCGATTGTGGGTTCGGGGCTCCCGGG

Zyxin > H V Q P Q P Q P K P Q V Q L H V Q S Q T Q P V S L A N T Q P R G P

Bpm1 Bpm1 SpAcc

BseY1 |

1401 CCAGCCTCATCTCCGGCTCCAGCCCCAAGTTTTCTCCAGTGACTCCTAAGTTTACTCCTGTGGCTTCCAAGTTCAGTCTCGGAGCCCCAGGTGGATCTG 1500
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
 GGTCGGAGTAGAGCCGAGGTTCGGGGATTCAAAAGAGGTCAGTACTGAGGATTCAAATGAGGACACCGAAGTTCAAGTCAGGACCTCGGGGTCCACCTAGAC

Zyxin > P A S S P A P A P K F S P V T P K F T P V A S K F S P G A P G G S G

Bpm1 BseY1 BseY1

1501 GGTCACAACCAAATCAAAAATTGGGGCACCCCGAAGCTCTTTCTGCTGGCACAGGCTCCCCTCAACCTCCCAGCTTCACCTATGCCAGCAGAGGGAGAA 1600
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
 CCAGTGTGGTTAGTTTTTAACCCCGTGGGGCTTCGAGAAAGACGACCGTGTCCGAGGGGAGTTGGAGGGTTCGAAGTGGATACGGGTTCGTCTCCCTCTT

Zyxin > S Q P N Q K L G H P E A L S A G T G S P Q P P S F T Y A Q Q R E K

Bsg1 Dra3 BstAP SexA1 PspOM PspOM SpAcc

Apa1 PspOM | | | SpAcc

1601 GCCCGAGTGCAGGAGAAGCAGCACCCCGTGCACCCACCGGCTCAGAACCAAAACCAGGTGCGCTCCCCTGGGGCCCCAGGGCCCCCTGACTCTGAAGGAG 1700
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
 CGGGGCTCACGTCTCTCGTTCGTGGGGCACGGGGTGGCCGAGTCTTGGTTTTGGTCCACGCGAGGGGACCCCGGGGTCCCAGGGGACTGAGACTTCTC

Zyxin > P R V Q E K Q H P V P P P A Q N Q N Q V R S P G A P G P L T L K E

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                BseY1
          BseR1 | BstAP
    Eco57 Pvu2| | Bpm1 |
          | | | | |
1701 GTGGAGGAGCTGGAGCAGCTGACCCAGCAGCTAATGCAGGACATGGAGCATCCTCAGAGGCAGAATGTGGCTGTCAACGAACTCTGCGGCCGATGCCATC
    |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1800
    CACCTCCTCGACCTCGTCGACTGGGTCGTCGATTACGTCTGTACCTCGTAGGAGTCTCCGTCTTACACCGACAGTTGCTTGAGACGCCGGCTACGGTAG
Zyxin > V E E L E Q L T Q Q L M Q D M E H P Q R Q N V A V N E L C G R C H Q

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                                Ale1
                                BspM1|
                                Bpm1|
                                BfuA1|
          Srf1
    Sma1 | BtgZ1 Pvu2 | SpDon Aar1| Fsp1
          | | | | |
1801 AACCCCTGGCCCGGGCGCAGCCAGCCGTCGCCGCTCTAGGGCAGCTGTTCCACATCGCCTGCTTCACCTGCCACCAGTGTGCCGAGCAGCTCCAGGGCCA
    |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1900
    TTGGGGACCGGGCCCGCTCGGTCGGCAGGCGCGAGATCCCGTCGACAAGGTGTAGCGGACGAAGTGGACGGTGGTTCACACCGCTCGTCGAGGTCCCGGT
Zyxin > P L A R A Q P A V R A L G Q L F H I A C F T C H Q C A Q Q L Q G Q

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                                BspM1
                                BfuA1
                                Aar1
          SpAcc Kas1| SpAcc Bpm1 | SpAcc SpAcc Bpm1 |
          | | | | |
1901 GCAGTTCTACAGTCTGGAGGGGGCGCCGTACTIONGCGAGGGCTGTTACTACTGACACCCTGGAGAAGTGTAACACCTGCGGGGAGCCCATCACTGACCGCATG
    |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2000
    CGTCAAGATGTCAGACCTCCCCCGGCATGACGCTCCCGACAATGTGACTGTGGGACCTCTTACATTGTGGACGCCCTCGGGTAGTACTGGCGGTAC
Zyxin > Q F Y S L E G A P Y C E G C Y T D T L E K C N T C G E P I T D R M

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    Bpu10
    BbvC1
    Sph1| Stul Bts1 SpDon | Bpm1
          | | | | |
2001 CTGAGGGCCACGGGCAAGGCTATCACCCGCACTGCTTACCTGTGTGGTCTGCGCCCCCCCCCTGGAGGGCACCTCCTTCATCGTGGACCAGGCCAACC
    |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2100
    GACTCCCGGTGCCCGTTCCGGATAGTGGGCGTGACGAAGTGGACACACCAGACGCGGGCGGGGGACCTCCCGTGGAGGAAGTAGCACCTGGTCCGGTTGG
Zyxin > L R A T G K A Y H P H C F T C V V C A R P L E G T S F I V D Q A N R

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                                                                                      Bpu10
                                                                                      |
2101  GGCCCCACTGTGTCCCCGACTACCACAAGCAGTACGCCCCGAGGTGCTCCGTCTGCTCTGAGCCCATCATGCCTGAGCCTGGCCGAGATGAGACTGTGCG
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 2200
      CCGGGGTGACACAGGGGCTGATGGTGTCGTCATGCGGGGCTCCACGAGGCAGACGAGACTCGGGTAGTACGGACTCGGACCGGGCTCTACTCTGACACGC
Zyxin > P H C V P D Y H K Q Y A P R C S V C S E P I M P E P G R D E T V R

                                                                                      SpAcc
                                                                                      |
2201  AGTGGTCGCCCTGGACAAGAAGTTCACATGAAGTGTTACAAGTGTGAGGACTGCGGGAAGCCCCTGTTCGATTGAGGCAGATGACAATGGCTGCTTCCCC
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 2300
      TCACCAGCGGGACCTGTTCTTGAAGGTGTACTTCACAATGTTCAACTCCTGACGCCCTTCGGGGACAGCTAACTCCGTCTACTGTTACCGACGAAGGGG
Zyxin > V V A L D K N F H M K C Y K C E D C G K P L S I E A D D N G C F P

                                                                                      SpDon
                                                                                      Ale1 |
                                                                                      Nco1 ||
      Pml1 |                Bts1 |                BamH1 | Agel |
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 2400
2301  CTGGACGGTCACGTGCTCTGTCGGAAGTGCCACACTGCTAGAGCCCAGACGGATCCACCGGTCGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGC
      GACCTGCCAGTGCACGAGACAGCCTTCACGGTGTGACGATCTCGGGTCTGCCTAGGTGGCCAGCGGTGGTACCCTCGCTCGACTAATTCCTCTTGTACG
Zyxin/mKate2 > L D G H V L C R K C H T A R A Q T D P P V A T M V S E L I K E N M H

      BsrG1 |                ApaL1 |                SpAcc |
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 2500
2401  ACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAAT
      TGTACTTCGACATGTACCTCCCGTGGCACTTGTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTTCGGGATGCTCCCGTGGGTCTGGTACTCTTA
mKate2 > M K L Y M E G T V N N H H F K C T S E G E G K P Y E G T Q T M R I

      CAAGGCGGTCGAGGGCGGCCCTCTCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAAAAACCTTCATCAACCACACCCAGGGCATC
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 2600
2501  GTTCCGCCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTTCGAAGTACATGCCGTCGTTTTTGAAGTAGTTGGTGTGGGTCCCCTAG
mKate2 > K A V E G G P L P F A F D I L A T S F M Y G S K T F I N H T Q G I

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                                     SpDon              Bbs1              Bpm1
                                     |                    |                    |
                CCCGACTTCTTTAAGCAGTCCTTCCCCGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCC
2601  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
                GGGCTGAAGAAATTCGTCAGGAAGGGGCTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCGGCACGACTGGCGATGGGTCTGTGGTCGG
mKate2  > P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L

                                     BseY1      StuI      BsaI
                                     |          |          |
                TCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTC
2701  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
                AGGTCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCACCTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAG
mKate2  > Q D G C L I Y N V K I R G V N F P S N G P V M Q K K T L G W E A S

                                     BglI              BglI              BssS1              Eco57
                                     |                    |                    |                    |
                CACCGAGACCCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAGCCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGACC
2801  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
                GTGGCTCTGGGACATGGGGCGACTGCCGCCGGACCTTCCGTCTCGGCTGTACCGGGACTTCGAGCACCCGCCCGGTGGACTAGACGTTGAACTTCTGG
mKate2  > T E T L Y P A D G G L E G R A D M A L K L V G G G H L I C N L K T

                                     Bbs1              SpAcc              BsaI
                                     |                    |                    |
                ACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCCGGCGTCTACTATGTGGACAGAAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCT
2901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
                TGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAGATGATACACCTGTCTTCTGACCTTTCTTAGTTCTCCGGCTGTTTCTCTGGA
mKate2  > T Y R S K K P A K N L K M P G V Y Y V D R R L E R I K E A D K E T Y

                                     NotI
                                     |
                ACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAAACCTGGGGCACAGATGAGCGGCCGCGACTCTAGATCATAATCAGCCATA
3001  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
                TGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTCTACTCTGCCGGCGCTGAGATCTAGTATTAGTCGGTAT
mKate2  > V E Q H E V A V A R Y C D L P S K L G H R *

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                                     Bsm1
                                     MfeI |           HpaI
                                     ||           |
                SpDon   DraI
                |       |
3101  CCACATTTGTAGAGGTTTTACTTGGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTAT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
      GGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATA

polyA   PsiI   polyA           polyA           BtsI BsmI
|       |       |               |               |       |
3201  TGCAGCTTATAATGGTTACAAAATAAAGCAATAGCATCACAAATTTACAAAATAAAGCATTTTTTTCAGTGCATTCTAGTTGTGGTTTGTCCAAACTCATC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
      ACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTTTAAAGTGTTTATTTTCGTAATAAAGTACGTAAGATCAACACCAACAGGTTTGTAGTAG

                AflII           SpDon           SspI
                |               |               |
3301  AATGTATCTTAAGGCGTAAATTTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
      TTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAG

                PsiI                                           BsaXB           DrdI
                |                                               |               |
3401  GGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAGAACGTGGACTCCAACG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
      CCGTTTTAGGGAATTTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGACCTGAGGTTGC

                                     BtgZI
                BsaXa           Dra3|
                |               ||
3501  TCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGCACTAAATCG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
      AGTTTCCCCTTTTTGGCAGATAGTCCCCTACCGGGTGTGCACTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGC

                                     NaeI
                SpAcc           NgoM4 |           BsrBI
                |               |       |           |
3601  GAACCCATAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
      CTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGACACCGCTCTTTTCTTCCCTTCTTTTCGCTTTCTTCGCCCCGATCCCCG

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Found:

Aar1	Aat2	Afe1	Afl2	Age1	Ahd1	Ale1	AlwN1	Apa1	Apal1	Ase1	Avr2	BamH1	Bbs1
BbvC1	BciV1	BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb
BseR1	BseY1	Bsg1	Bsm1	BsmB1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1
BstAP	BstB1	Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57
EcoR1	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1
Nsi1	PflF1	Pml1	polyA	PshA1	Psi1	PspOM	Pst1	Pvu1	Pvu2	Rsr2	Sac1	Sap1	SexA1
Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Srf1	Ssp1	Stu1	Xba1	Xho1	Xmn1		

Unique:

Afe1	Afl2	Age1	Ahd1	Ase1	BamH1	BbvC1	BsaXa	BsaXb	Bsg1	BsmB1	BspE1	BspLU	BsrD1
BsrG1	BssH2	Clal	Ecl2	EcoR1	Hind3	Hpa1	Mfe1	Nde1	Nhe1	Not1	PflF1	Pml1	PshA1
Pst1	Pvu1	Rsr2	Sac1	Sfi1	SnaB1	Srf1	Xba1	Xho1					

Not found:

Acc65	Acc1	Asc1	AsiS1	Baela	Baelb	Bcgl1a	Bcgl1b	Bcl1	Blp1	BmgB1	BsiW1	BstE2	BstX1
BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT
Fse1	FspA1	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	PflM1	Pme1	R4atB	R4atL	R4atP	R4atR
Sac2	Sall	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Swa1	T3RNA	T7RNA	T7Ter	PISce	Xcm1

Excluded by site complexity:

Acc1	Acil	Afl3	Alu1	Alw1	Apo1	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfa1	Bme15
BsaA1	BsaH1	BsaJ1	BsaW1	BseM2	BsiE1	BsiH1	Bs11	BsmA1	BsmF1	Bsp12	BspCa	BspCb	Bsr1
BsrF1	BssK1	BstF5	BstN1	BstU1	BstY1	Btg1	Cac8	CviJ1	Dde1	Eae1	EcoO1	Fau1	Fnu4H
Fok1	Hae2	Hae3	Hga1	Hha1	Hinc2	Hinf1	HinP1	Hpa2	Hph1	Hpy99	Hpy1	Hpy3	HpyC3
HpyC4	HpyC5	Mae3	Mbo2	Mnl1	Mse1	Msl1	MspA1	Mwo1	Nci1	Nla3	Nla4	Nsp1	Ple1
PpuM1	Rsa1	Sau3A	Sau96	SfaN1	Sfc1	Sml1	Sty1	Taq1	Tat1	Tfi1	Tse1	Tsp45	Tsp50
TspR1													