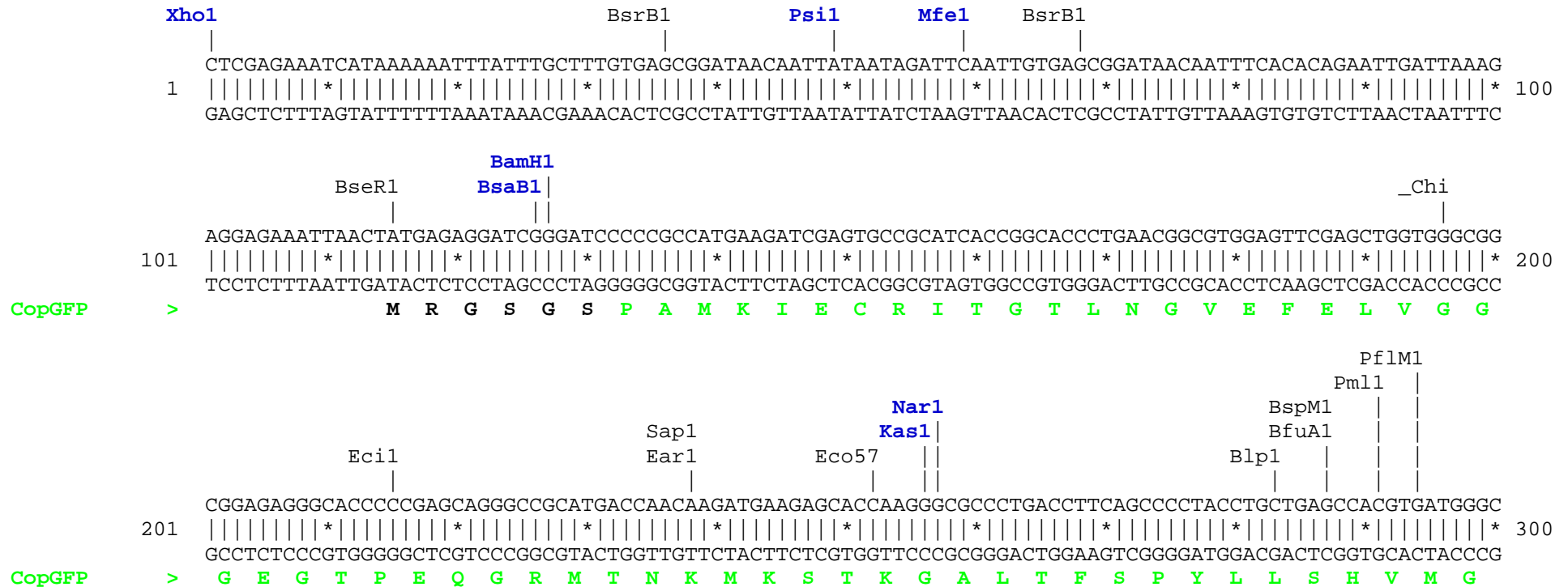


pCop-Green-B vector restriction map

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 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction sites.

Unique sites shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). Amino acids coded by vector's backbone sequence are shown in black.



BseY1 Bsg1 Xmn1

301 TACGGCTTCTACCACTTCGGCACCTACCCCAGCGGCTACGAGAACCCTTCTGCACGCCATCAACAACGGCGGCTACACCAACACCCGCATCGAGAAGT
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 400
 ATGCCGAAGATGGTGAAGCCGTGGATGGGGTCGCCGATGCTCTTGGGGAAGGACGTGCGGTAGTTGTTGCCGCCGATGTGGTTGTGGGCGTAGCTCTTCA
CopGFP > Y G F Y H F G T Y P S G Y E N P F L H A I N N G G Y T N T R I E K

Fse1
Nae1
Eag1

Bsg1 Eco57 Pml1 NgoM4

401 ACGAGGACGGCGGCGTGCTGCACGTGAGCTTTCAGCTACCGCTACGAGGCCGGCCGCGTGATCGGCGACTTCAAGGTGGTGGGCACCCGGCTTCCCCGAGGA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
 TGCTCCTGCCGCCGACGACGTGCACTCGAAGTCGATGGCGATGCTCCGGCCGGCGCACTAGCCGCTGAAGTTCACCACCCGTTGGCCGAAGGGGCTCCT
CopGFP > Y E D G G V L H V S F S Y R Y E A G R V I G D F K V V G T G F P E D

Nco1
BspM1
BfuA1 Eco57

Bsg1 Aar1 _Chi

501 CAGCGTGATCTTCACCGACAAGATCATCCGAGCAACGCCACCGTGGAGCACCTGCACCCCATGGGCGATAACGTGCTGGTGGGCAGCTTCGCCCGCACC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
 GTCGCACTAGAAGTGGCTGTTCTAGTAGGCGTCGTTGCGGTGGCACCTCGTGGACGTGGGGTACCCGCTATTGCACGACCACCCGTCGAAGCGGGCGTGG
CopGFP > S V I F T D K I I R S N A T V E H L H P M G D N V L V G S F A R T

BseY1 Pst1 PspOM Apa1

601 TTCAGCCTGCGGACGGCGGCTACTACAGCTTCGTGGTGGACAGCCACATGCACTTCAAGAGCGCCATCCACCCAGCATCCTGCAGAACGGGGGCCCA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
 AAGTCGGACGCGCTGCCGCCGATGATGTCGAAGCACCACCTGTCCGTGTACGTGAAGTTCGCGGTAGGTGGGGTTCGTAGGACGTCTTGCCCCGGGGT
CopGFP > F S L R D G G Y Y S F V V D S H M H F K S A I H P S I L Q N G G P

Found:

Aar1	Aat2	Acl1	Ahd1	AlwN1	Apa1	ApaL1	Ase1	BamH1	Bbs1	Bcg1a	Bcg1b	BciV1	BfuA1
Bgl1	Blp1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BseR1	BseY1	Bsg1	Bsm1	BsmB1	BspE1
BspH1	BspLU	BspM1	BsrB1	BsrD1	BssS1	BstAP	BstZ1	Bts1	_Chi	Dra1	Drd1	Eag1	Ear1
Eci1	Eco57	EcoK	Fse1	Fsp1	Hind3	Kas1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4
Nhe1	PflF1	PflM1	Pml1	Psi1	PspOM	Pst1	Pvu1	Pvu2	Sap1	Scal	Ssp1	Xba1	Xho1

Xmn1

Unique:

Aar1	Aat2	Ahd1	AlwN1	Apa1	Ase1	BamH1	Bbs1	Bcg1a	Bcg1b	Bgl1	Bpu10	Bsa1	BsaB1
BspE1	BspLU	BstAP	BstZ1	Eag1	EcoK	Fse1	Fsp1	Hind3	Kas1	Mfe1	Msc1	Nae1	Nar1
Nde1	NgoM4	Nhe1	PflF1	Psi1	PspOM	Pst1	Pvu2	Xba1	Xho1				

Not found:

Acc65	Afe1	Afl2	Age1	Ale1	Asc1	AsiS1	Avr2	Bae1a	Bae1b	BbvC1	Bcl1	BfrB1	Bgl2
BmgB1	BsaXa	BsaXb	BsiW1	BsrG1	BssH2	BstB1	BstE2	BstX1	Bsu36	Clal	Dra3	EcoN1	EcoR1
EcoRV	ScFRT	FspA1	Hpa1	I_Ceu	Kpn1	loxP	Mlu1	Not1	Nru1	Nsi1	Pac1	Pme1	PshA1
Rsr2	Sac1	Sac2	Sall	SanD1	Sbf1	SexA1	Sfi1	Sgf1	SgrA1	Sma1	SnaB1	Spe1	Sph1
Srf1	Stu1	Swal	PISce	Xcm1									

Excluded by site complexity:

Acc1	Ac11	Afl3	Alu1	Alw1	Apo1	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfa1	Bme15
BsaA1	BsaH1	BsaJ1	BsaW1	BseM2	BsiE1	BsiH1	Bsl1	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													