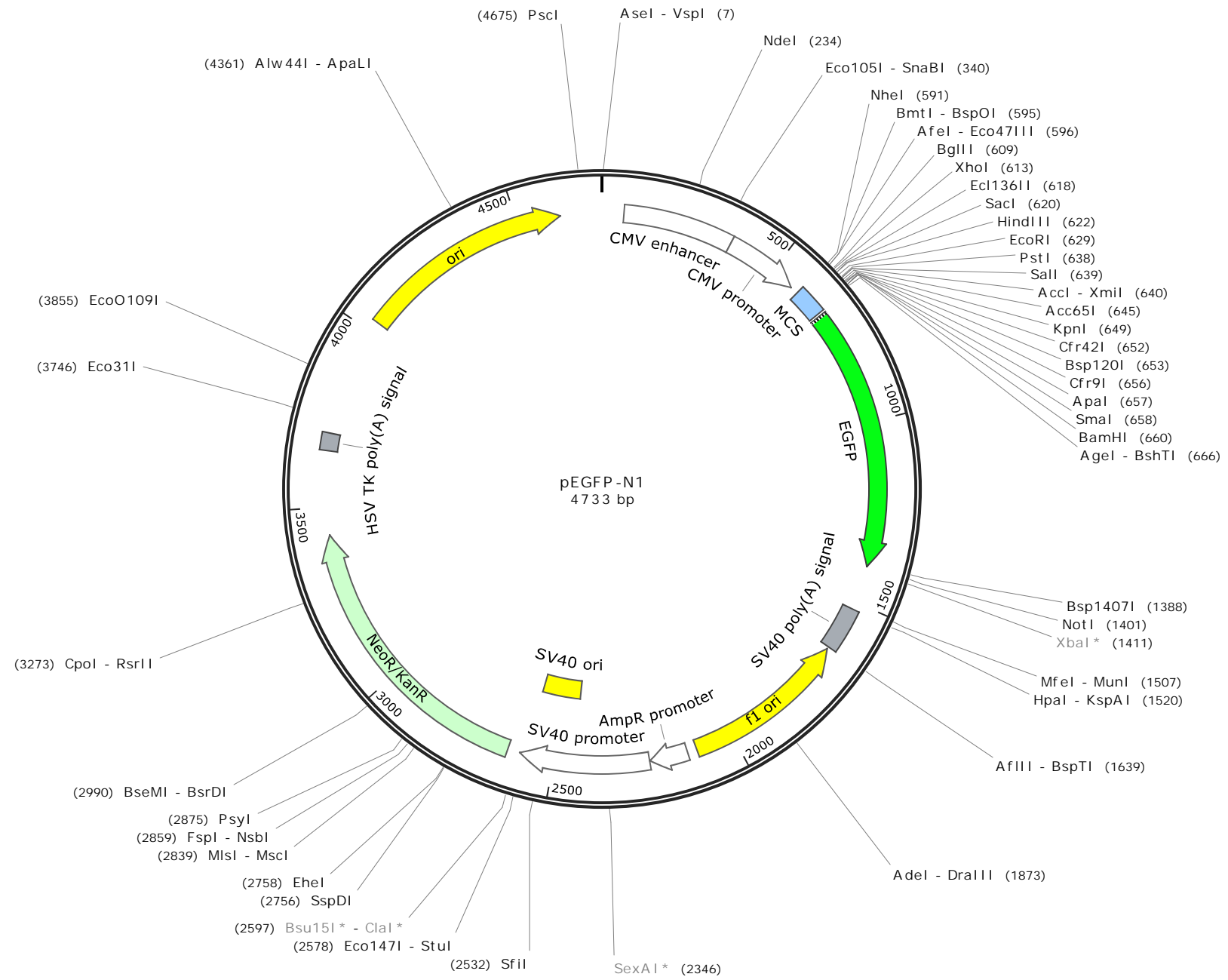
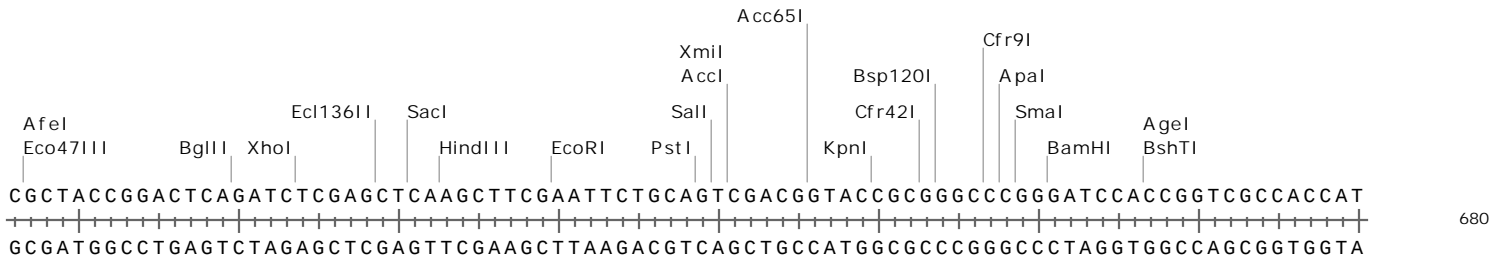
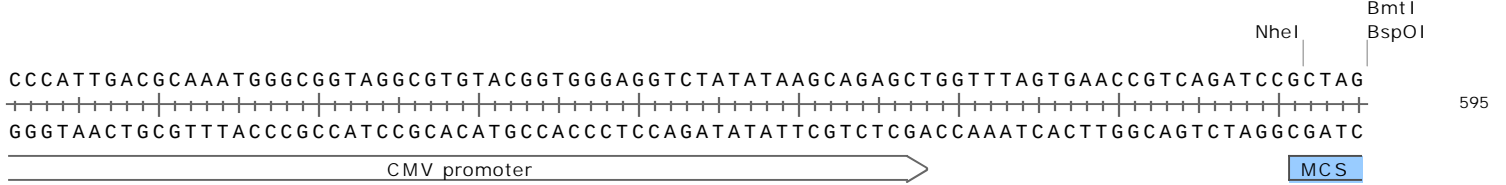
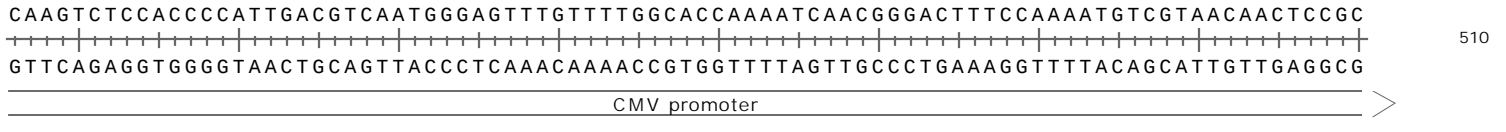
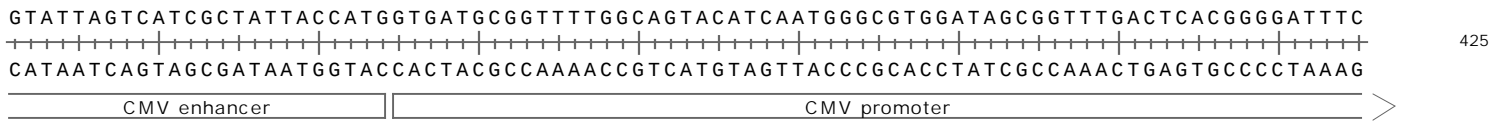
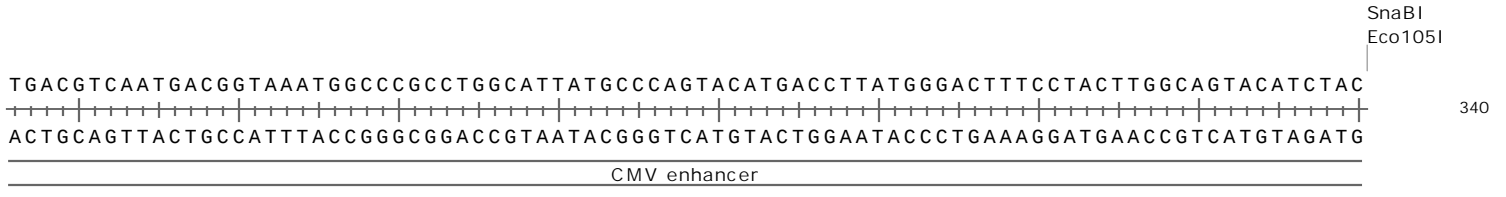
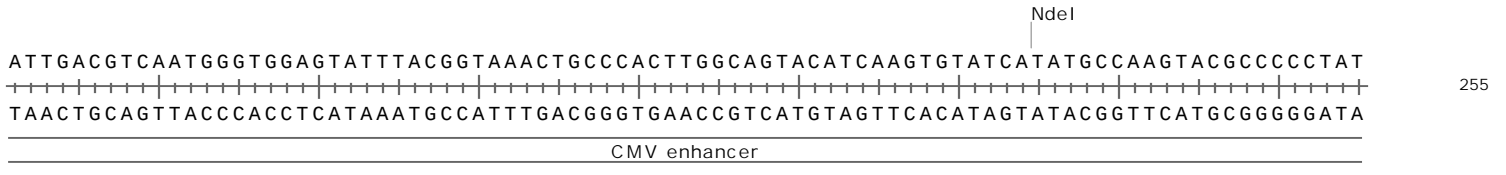


Vector for fusing EGFP to the C-terminus of a partner protein.





GGTGAGCAAGGGCGAGGAGCTGTTACACGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAACCGGCCACAAGTTCAGC
CCACTCGTTCGCTCCTCGACAAGTGGCCCCACCACGGGTAGGACCAGCTCGACCTGCCGCTGCATTTGCCGGTGTTC AAGTCCG

765

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
1 a EGFP

GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCT
CACAGGCCGCTCCCGCTCCCGCTACGGTGGATGCCGTTTCGACTGGGACTTCAAGTAGACGTGGTGGCCGTTTCGACGGGCACGGGA

850

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
EGFP

GGCCACCCCTCGTGACCACCCCTGACCTACGGCGTGCAAGTCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAA
CCGGGTGGGAGCACTGGTGGGACTGGATGCCGCACGTCACGAAGTCGGCGATGGGGCTGGTGTACTTCGTCGTGCTGAAGAAGTT

935

Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys
EGFP

GTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAG
CAGGGGTACGGGCTTCCGATGCAGGTCTTCGCGTGGTAGAAGAAGTTCTGCTGCCGTTGATGTTCTGGGGCGGGCTCCACTTC

1020

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
EGFP

TTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGG
AAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTAGCTGAAGTTCCTCCTGCCGTTGTAGGACCCCGTGTTCGACC

1105

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
EGFP

AGTACAACACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAA
TCATGTTGATGTTGTCGGTGTTCGAGATATAGTACCGGCTGTTCTGCTTCTTGGCCGTTAGTTCCACTTGAAGTTCCTAGGGCGGTGTT

1190

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
EGFP

CATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAAC
GTAGCTCCTGCCGTCGCACGTCGAGCGGCTGGTGGATGGTCTGTTGTGGGGGTAGCCGCTGCCGGGGCACGACGACGGGCTGTTG

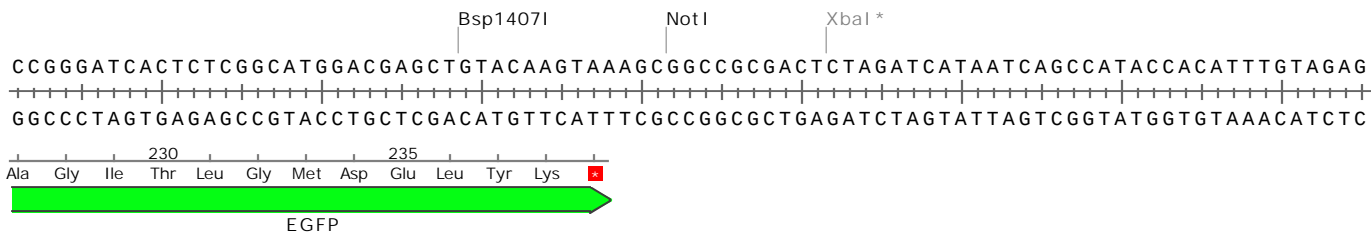
1275

Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
EGFP

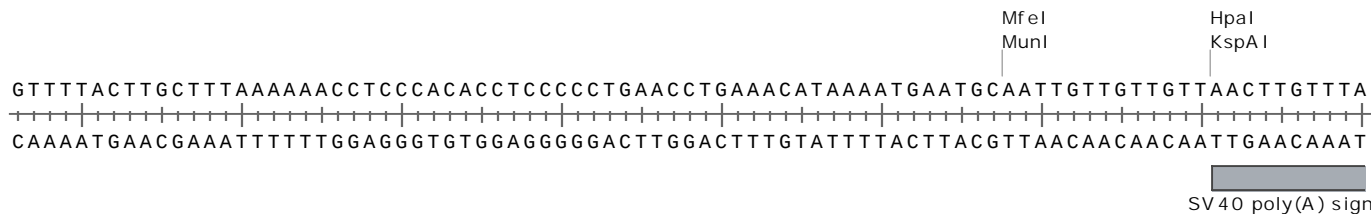
CACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTTCGTGACCGCCG
GTGATGGACTCGTGGGTCAGGCGGGACTCGTTTTCTGGGGTGTCTTTCGCGCTAGTGTACCAGGACGACCTCAAGCACTGGCGGC

1360

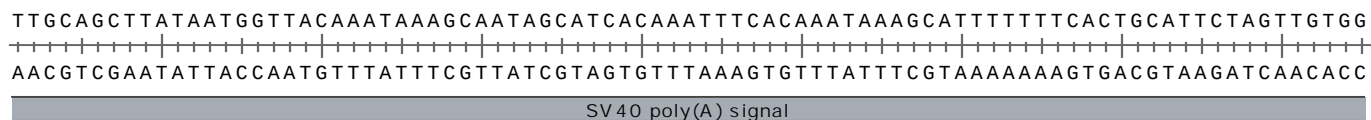
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
EGFP



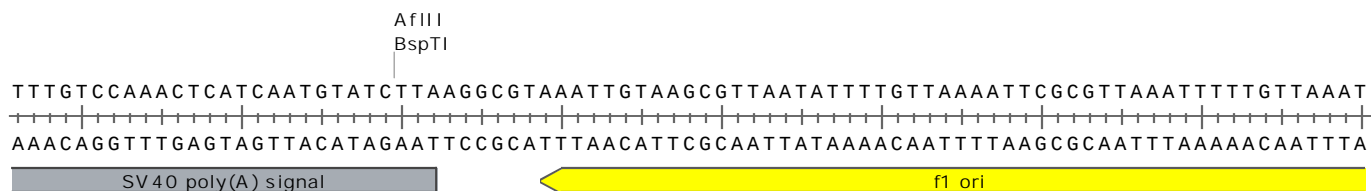
1445



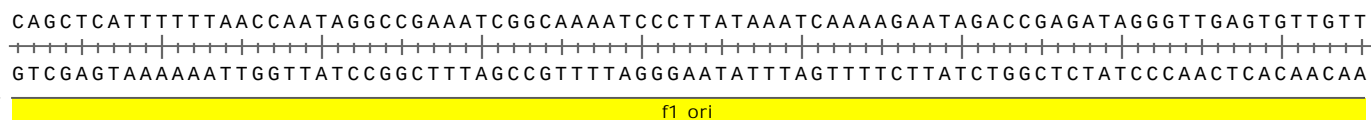
1530



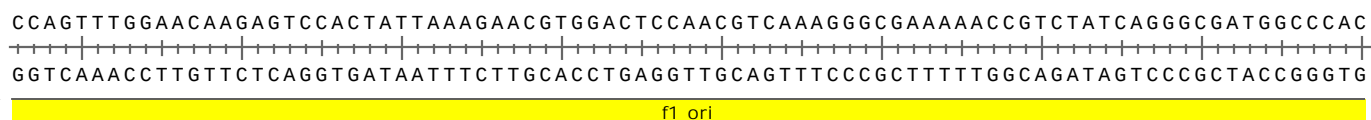
1615



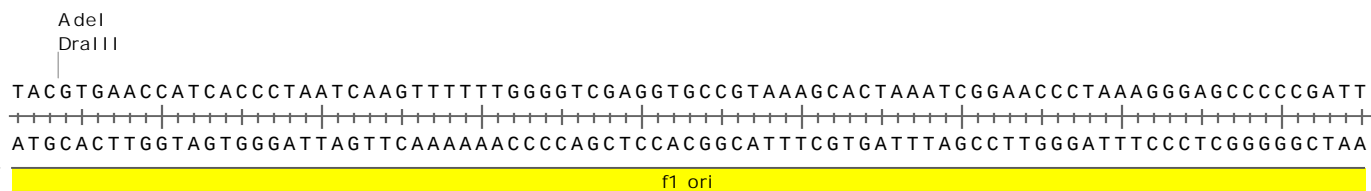
1700



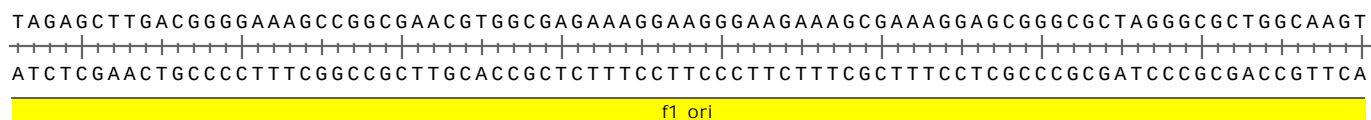
1785



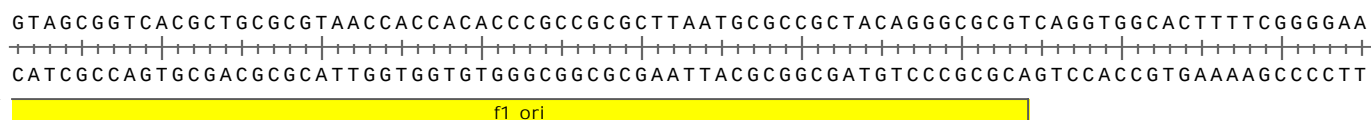
1870



1955



2040



2125



2210

TCAATAATATTGAAAAAGGAAGAGTCTCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAG
AGTTATTATAACTTTTTCTTCTCAGGACTCCGCTTTCTTGGTTCGACACCTTACACACAGTCAATCCCACACCTTTTCAGGGGTC

AmpR promoter

SV40 promoter

GCTCCCCAGCAGGCAGAAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGG
CGAGGGGTCGTCCGCTTTCATACGTTTTCTGACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTTCAGGGGTCGAGGGGTCGTCC

SexAI *

SV40 promoter

CAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCGCCCATCCCGCCCTAACTCCGCC
GTCTTCATACGTTTTCTGACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTATGGGCGGGGATTGAGGCGGG

SV40 promoter

SV40 ori

AGTTCCGCCATTCTCCGCCCATGGCTGACTAATTTTTTTTATTTATGCAAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCC
TCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAATAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGG

SfiI

SV40 promoter

SV40 ori

AGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTTCGAAAGATCGATCAAGAGACAGGATGAGGATCGTTTTCGCATGATTG
TCTTCATCACTCCTCCGAAAAACCTCCGGATCCGAAAAACGTTTCTAGCTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTAAC

StuI
Eco147I

Clal *
Bsu151 *

SV40 promoter

1
Met Ile
NeoR/KanR

SV40 ori

AACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTG
TTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGAC

Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys
NeoR/KanR

CTCTGATGCCGCCGTGTTCCGGCTGTGACGCGAGGGGCGCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAA
GAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTT

SspDI EheI

Ser Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu
NeoR/KanR

CTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCTTGCAGCTGTGCTCGACGTTGTCACTGAAGCGG
GACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCC

MisI
MscI

FspI
NsbI

PsyI

Leu Gln Asp Glu Ala Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val Leu Asp Val Val Thr Glu Ala
NeoR/KanR

GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCAT
 CTTCCCTGACCGACGATAAACCCTTACACGGCCCGTCTTAGAGGACAGTAGAGTGAACGAGGACGGCTCTTTTCATAGGTAGTA

90 95 100 105 110 115
 Gly Arg Asp Trp Leu Leu Gly Glu Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys Val Ser Ile Met

NeoR/KanR

2975

BsrDI
 BseMI

GGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCATTGACCACCAAGCGAAACATCGCATCGAGCGAGCA
 CCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTTCGCTTTGTAGCGTAGCTCGCTCGT

120 125 130 135 140
 Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala

NeoR/KanR

3060

CGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCA
 GCATGAGCCTACCTTCGGCCAGAACAGCTAGTCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTTCGGCTTGACAAGCGGT

145 150 155 160 165 170
 Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala

NeoR/KanR

3145

GGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGG
 CCGAGTTCGGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACC

175 180 185 190 195 200
 Arg Leu Lys Ala Ser Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys Leu Pro Asn Ile Met Val Glu Asn Gly

NeoR/KanR

3230

CpOI
 RsrI I

CCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCT
 GGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCTGTATCGCAACCGATGGGCACTATAACGA

205 210 215 220 225
 Arg Phe Ser Gly Phe Ile Asp Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala Thr Arg Asp Ile Ala

NeoR/KanR

3315

GAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATC
 CTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGGCGAGGGCTAAGCGTTCGCGTAGCGGAAGATAG

230 235 240 245 250 255
 Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe Tyr

NeoR/KanR

3400

GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTC
 CGGAAGAAGTCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAG

260 265
 Arg Leu Leu Asp Glu Phe Phe

NeoR/KanR

3485

GATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATC
 CTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCTAG

3570

TCATGCTGGAGTTCTTCGCCACCCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGAC
 AGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCTCTGTTATGGCCTTCTTGGGCGCGATACTG

3655

HSV TK poly(A) signal

GGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGGTCGTTTGTTCATAAACGCGGGGTTCCGGTCCCAGGGCTGGCACTCTGTC 3740
CCGTTATTTTTCTGTCTTATTTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCAAGCCAGGGTCCCAGCCGTGAGACAG

HSV TK poly(A) signal

Eco311

GATACCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCTTTTCCCACCCCACCCCCAAGTTCGGGTGAAGGCC 3825
CTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCCACTTCCGG

EcoO109I

CAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACCTTCA 3910
GTCCCAGAGCGTCGGTTGCAGCCCCGCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTGAAGT

TTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAATCCCTAACGTGAGTTTTCGTTCCACTGA 3995
AAAAATTAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACT

GCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAC 4080
CGCAGTCTGGGGCATCTTTTCTAGTTTCTAGAAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTG

ori

CACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGAT 4165
GTGGCGATGGTCGCCACCAAACAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTA

ori

ACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTA 4250
TGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGGAGACGAT

ori

ATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGCTTACCGGGTGGACTCAAGACGATAGTTACCGGATAAGGGCGC 4335
TAGGACAATGGTCACCGACGACGGTCACCGCTATTGAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCG

ori

Alw 441
ApaI

AGCGGTCGGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGA 4420
TCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGTGGATGTGGCTTGACTCTATGGATGTCGCACT

ori

GCTATGAGAAAGCGCCACGCTTCCCAGGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCCGAACAGGAGAGCGCACG 4505
CGATACTCTTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCTGTCCATAGGCCATTGCGCGTCCCAGCCTTGTCTCTCGCGTGC

ori



























AGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTGCATTTTTGTGAT 4590
TCCCTCGAAGGTCCCCCTTTCGCGACCATAGAAATATCAGGACAGCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTA

ori

GCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGTGTCCTTTTGTCTCA 4675
CGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTGCTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGT

ori

Enzymes	Sites	
AccI	1	640
Acc65I	1	645
Adel	1	1873
AfeI	1	596
AfII	1	1639
AgeI	1	666
Alw44I	1	4361
Apal	1	657
ApaLI	1	4361
AseI	1	7
BamHI	1	660
BglII	1	609
BmtI	1	595
BseMI	1	2990
BshTI	1	666
Bsp120I	1	653
Bsp1407I	1	1388
BspOI	1	595
BspTI	1	1639
BsrDI	1	2990
Bsu15I	1*	2597*
Cfr9I	1	656
Cfr42I	1	652
Clal	1*	2597*
CpoI	1	3273
DraIII	1	1873
Ecl136II	1	618
Eco31I	1	3746
Eco47III	1	596
Eco105I	1	340
Eco147I	1	2578
EcoO109I	1	3855
EcoRI	1	629
EheI	1	2758
FspI	1	2859
HindIII	1	622
HpaI	1	1520
KpnI	1	649
KspAI	1	1520
MfeI	1	1507
MisI	1	2839
MscI	1	2839
MunI	1	1507
NdeI	1	234
NheI	1	591
NotI	1	1401
NsbI	1	2859
PscI	1	4675
PstI	1	638
PsyI	1	2875
RsrII	1	3273
SacI	1	620
Sall	1	639
SexAI	1*	2346*
Sfil	1	2532
SmaI	1	658
SnaBI	1	340
SspDI	1	2756
StuI	1	2578
VspI	1	7
XbaI	1*	1411*
XhoI	1	613
XmiI	1	640

Feature	Location	Size (bp)			Type
✓ CMV enhancer /note = human cytomegalovirus immediate early enhancer	61 .. 364	304			enhancer
✓ CMV promoter /note = human cytomegalovirus (CMV) immediate early promoter	365 .. 568	204			promoter
✓ MCS /note = multiple cloning site of fluorescent protein plasmids	591 .. 671	81			misc_feature
✓ EGFP ▶ 3 segments /product = enhanced GFP /note = mammalian codon-optimized /translation = M,V,SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLT LKFICTTGKLPVPWPPTLVTTTLYGVQCFSRYPDHMKQHDFK SAMPEGYVQERTIFFKDDGNYKTRAEVKFEEDTLVNRIELKGI DFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIE DGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALS KDPNEKRDMVLLFEVTAAGITLGMDELYK* 239 amino acids = 26.9 kDa	679 .. 1398	720			CDS
✓ SV40 poly(A) signal /note = SV40 polyadenylation signal	1521 .. 1642	122			polyA_signal
✓ f1 ori /direction = LEFT /note = f1 bacteriophage origin of replication; arrow indicates direction of (+) strand syynthesis	1649 .. 2104	456			rep_origin
✓ AmpR promoter /gene = bla	2131 .. 2235	105			promoter
✓ SV40 promoter /note = SV40 enhancer and early promoter	2237 .. 2594	358			promoter
✓ SV40 ori /note = SV40 origin of replication	2445 .. 2580	136			rep_origin
✓ NeoR/ KanR /gene = aph(3')-II (or nptII) /product = aminoglycoside phosphotransferase from Tn5 /note = confers resistance to neomycin, kanamycin, and G418 (Geneticin) /translation = MIEQDGLHAGSPAAWVERLFGYDWAQQTIGCSDAAVFRLSAQGRPVLFVKTDL S GALNELODEAARLSWLATTGVP CAAVLDVV TEAGR DWLLLGEVPGQDLLSSHLAPA EKVSIMADAMRRLHTLDPATCPF DHQAKHRIERARTRMEAGLVDQDDLDEEHQGLAPAE LFARLKA SMPDGEDLVVTHGDA CLPNIMVENGRFSGFIDCGR LGVADRYQDIALATRDIAEELGGEWADRFVLVYGI AAPDSORIA FYRIIDFFF* 264 amino acids = 29.0 kDa	2629 .. 3423	795			CDS
✓ HSV TK poly(A) signal /note = herpesvirus thymidine kinase polyadenylation signal	3655 .. 3702	48			misc_feature
✓ ori /direction = RIGHT /note = high-copy-number ColE1/pMB1/pBR322/pUC origin of replication	4031 .. 4619	589			rep_origin

Description: Vector for fusing EGFP to the C-terminus of a partner protein.

Created: Thursday, Apr 26, 2012

Last Modified: Friday, Jan 4, 2013

Accession Number: U55762

Code Number:

Sequence Author: Clontech

DNA Type: Synthetic DNA

Laboratory Host Organism: Mammalian Cells

Bacterial Transformation Strain: Unspecified

Dam⁺ Dcm⁺ EcoKI⁺

Comments:

References: