

# Blue Heron pUCminusMCS

Vector	Cloning Information	Sequencing Primers
<p><b>Blue Heron Bio pUCminusMCS (3171 bp)</b></p> <p>(pUC119 derivative)</p> <p>no multiple cloning site</p> <p>amp resistant</p>	<p>Blue Heron pUCminusMCS is the DEFAULT vector choice. It lacks a Multiple Cloning Site to allow greater flexibility for <u>subcloning</u> and future manipulations. <b>Be sure to add flanking restriction sites to your gene.</b></p> <p>You may download the <a href="#">Blue Heron Bio pUCminusMCS map</a> which shows the sequence of the adaptors, and/or the <a href="#">Blue Heron Bio pUCminusMCS sequence</a> file.</p> <p>Blue Heron will design your gene with up to 50 bp unique flanking sequence to be cloned non-directionally into the Blue Heron Bio adaptors between the CTTTC and GAAAG "sticky ends". If a unique flanking sequence is used, a cloning information sheet will be posted in your File Area: Notes from Blue Heron folder and included with your packing slip when your gene is shipped. This unique flanking sequence will not contain common restriction sites.</p>	<p>M13/pUC Forward 23-Base Sequencing Primer: 5'-CCCAG TCACG ACGTT GTAAA ACG-3'</p> <p>M13/pUC Reverse 23-Base Sequencing Primer: 5'-AGCGG ATAAC AATTT CACAC AGG-3'</p>

## BLUEHERON

BIOTECHNOLOGY

## Blue Heron pUCminusMCS

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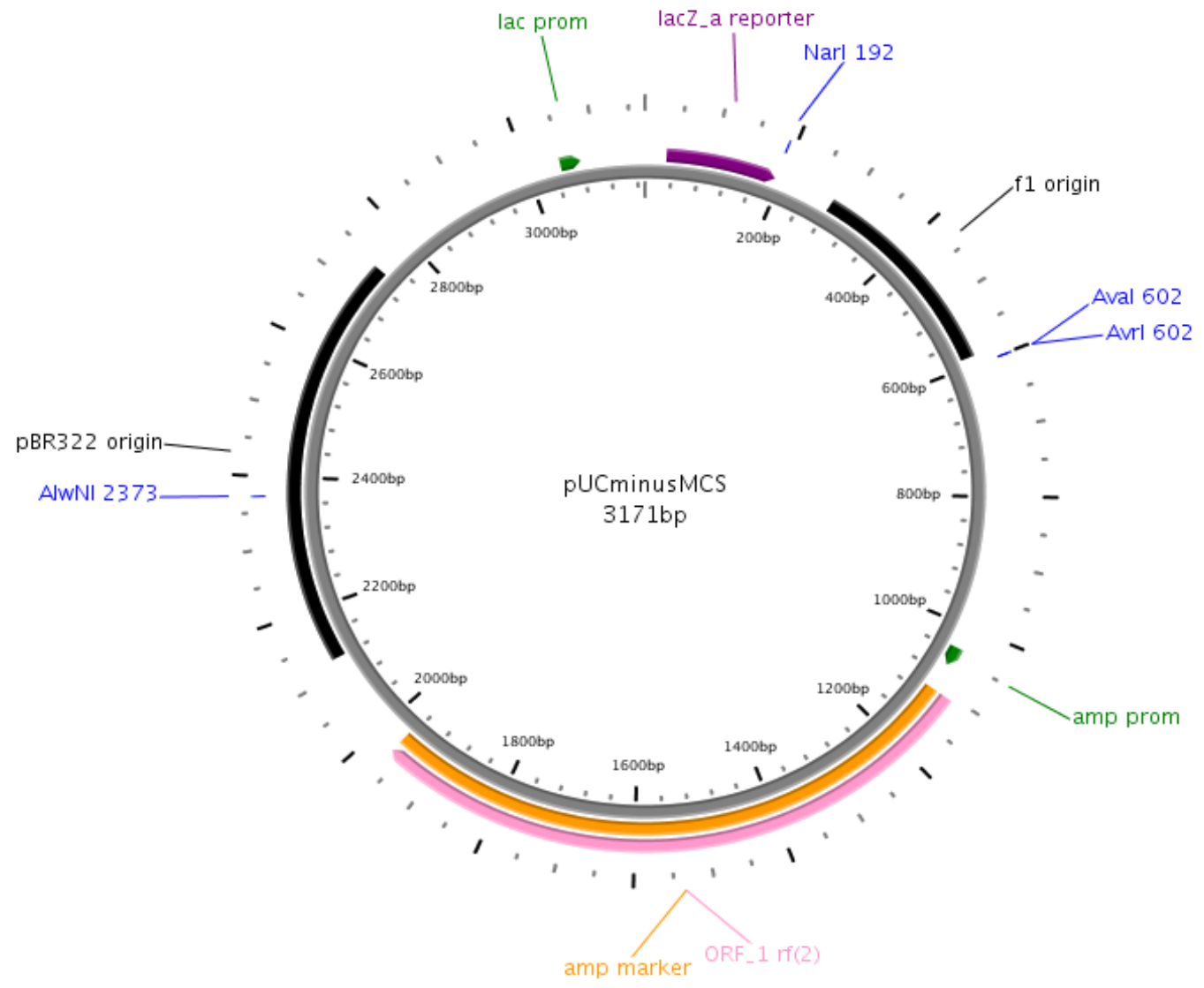
Sequence polylinker flanking the insert -multiple cloning site removed

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AGCTCCTTCTTCCAGCCCTTCTCTTTC *** -Gene-*** GAAAGTCCTCTCCAAGTACTGTAGCCTCCAATT
*                                     *                                     *                                     *
3141                                 3171                                 1                                     33
                    
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\*\*\* Your gene may be flanked by up to 18 bp to facilitate Blue Heron cloning. This will not contain any common restriction sites. If your gene is cloned with this sequence a cloning information sheet will be included with your gene shipment and electronically posted on your GeneMaker Secure Website File Area in the "Notes from Blue Heron" folder. We recommend you frame your gene with restriction sites to facilitate your future subcloning.

- Open reading frame
- Origin of replication
- Promoter
- Reporter gene
- Selectable marker
- Unique restriction site



# Blue Heron pUCminusMCS DNA Sequence

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1 GAAAGTCCTC TCCACTGACT GTAGCCTCCA ATTCACTGGC CGTCGTTTTA CAACGTCGTG ACTGGGAAAA CCCTGGCGTT ACCCAACTTA ATCGCCTTGC
101 AGCACATCCC CCTTTCGCCA GCTGGCGTAA TAGCGAAGAG GCCCGCACCG ATCGCCCTTC CCAACAGTTG CGCAGCCTGA ATGGCGAATG GCGCCTGATG
201 CGGTATTTTC TCCTTACGCA TCTGTGCGGT ATTTACACACC GCATACGTCA AAGCAACCAT AGTACGCGCC CTGTAGCGGC GCATTAAGCG CGGCGGGTGT
301 GGTGGTTACG CGCAGCGTGA CCGCTACACT TGCCAGCGCC CTAGCGCCCG CTCCTTTCGC TTTCTTCCCT TCCTTTCTCG CCACGTTCCG CGGCTTTCCC
401 CGTCAAGCTC TAAATCGGGG GCTCCCTTTA GGGTCCGAT TTAGTGCTTT ACGGCACCTC GACCCAAAA AACTTGATTT GGGTGATGGT TCACGTAATG
501 GGCCATCGCC CTGATAGACG GTTTTTCGCC CTTTGACGTT GGAGTCCACG TTCTTTAATA GTGGA CTCTT GTTC CAAACT GGAA CAACAC TCAACCCAT
601 CTCGGGCTAT TCTTTTGATT TATAAGGGAT TTTGCCGATT TCGGCCTATT GGTAAAAAAA TGAGCTGATT TAACAAAAAT TTAACGCGAA TTTTAACAAA
701 ATATTAACGT TTACAATTTT ATGGTGC ACTCAGTACAA TCTGCTCTGA TGCCGCATAG TTAAGCCAGC CCCGACACCC GCCAACACCC GCTGACGCGC
801 CCTGACGGGC TTGTCTGCTC CCGGCATCCG CTTACAGACA AGCTGTGACC GTCTCCGGGA GCTGCATGTG TCAGAGGTTT TCACCGTCAT CACCGAAACG
901 CGCGAGACGA AAGGGCCTCG TGATACGCCT ATTTTATATAG GTTAATGTCA TGATAATAAT GGTTCCTTAG ACGTCAGGTG GCAC TTTTCG GGGAAATGTG
1001 CGCGGAACCC CTATTTGTTT ATTTTCTAA ATACATTCAA ATATGTATCC GCTCATGAGA CAATAACCTT GATAAATGCT TCAATAATAT TGAAAAAGGA
1101 AGAGTATGAG TATCAACAT TTCCGTGTCG CCCTTATTCC CTTTTTGGC GCAATTTGCC TTCTGTTTT TGCTCACCCA GAAACGCTGG TGAAAGTAAA
1201 AGATGCTGAA GATCAGTTGG GTGCACGAGT GGGTACATC GAACTGGATC TCAACAGCGG TAAGATCCTT GAGAGTTTTC GCCCGAAGA ACGTTTTCCA
1301 ATGATGAGCA CTTTAAAGT TCTGCTATGT GGCGCGGTAT TATCCCGTAT TGACGCGGG CAAGAGCAAC TCGGTTCGCG CATACTACTAT TCTCAGAAATG
1401 ACTTGGTTGA GTACTACCA GTCACAGAAA AGCATCTTAC GGATGGCATG ACAGTAAGAG AATTAATGCG TGCTGCCATA ACCATGAGTG ATAACACTGC
1501 GGCCAACTTA CTTCTGACAA CGATCGGAGG ACCGAAGGAG CTAACCGCTT TTTTGCACAA CATGGGGGAT CATGTAAC TC GCCTTGATCG TTGGGAAACG
1601 GAGCTGAATG AAGCCATACC AAACGACGAG CGTGACACCA CGATGCCTGT AGCAATGGCA ACAACGTTGC GCAAAC TATT AACTGGCGAA CTACTTACTC
1701 TAGCTTCCCG GCAACAATTA ATAGACTGGA TGGAGGCGGA TAAAGTTGCA GGACCACTTC TGCCCTCGGC CCTTCCGGCT GGCTGGTTTA TTGCTGATAA
1801 ATCTGGAGCC GGTGAGCGTG GGTCTCGCGG TATCATTGCA GCACTGGGGC CAGATGGTAA GCCCTCCCGT ATCGTAGTTA TCTACACGAC GGGGAGTCAG
1901 GCAACTATGG ATGAACGAAA TAGACAGATC GCTGAGATAG GTGCCTCACT GATTAAGCAT TGGTAACTGT CAGACCAAGT TTACTCATAT ATACTTTAGA
2001 TTGATTTAAA ACTTCATTTT TAATTTAAAA GGATCTAGGT GAA GATCCTT TTTGATAATC TCATGACCAA AATCCCTTAA CGTGAGTTTTT CGTTCCTACTG
2101 AGCGTCAGAC CCCGTAGAAA AGATCAAAGG ATCTTCTTGA GATCCTTTTTT TCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC GCTACCAGCG
2201 GTGGTTTGTT TGCCGGATCA AGAGCTACCA ACTCTTTTTT C GAAGGTAAC TGGCTT CAGC AGAGCGCAGA TACCAAATAC TGTCCTTCTA GTGTAGCCGT
2301 AGTTAGGCCA CCACTTCAAG AACTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC TGTTACCAGT GGCTGCTGCC AGTGCCGATA AGTCGTGTCT
2401 TACCGGTTTG GACTCAAGAC GATAGTTACC GGATAAGGCG CAGCGTTCGG GCTGAAACGG GGGTTCTGTC ACACAGCCCA GCTTGGAGCG AACGACCTAC
2501 ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAAGC CCACGCTTCC CGAAGGGAGA AAGGCGGACA GGTA TCCGCT AAGCGGCAGG GTCGGAACAG
2601 GAGAGCGCAC GAGGGAGCTT CCAGGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTCCGGT TTCGCACCT CTGACTTGAG CGTCGATTTT TGTGATGCTC
2701 GTCAGGGGGG CGGAGCCTAT GGAAAACGC CAGCAACGCG GCCTTTTTAC GGTTCCTGGC CTTTTGCTGG CCTTTTGTCT ACATGTTCTT TCCTGCGTTA
2801 TCCCCTGATT CTGTGGATAA CCGTATTACC GCCTTTGAGT GAGCTGATAC CGCTCGCCGC AGCCGAACGA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG
2901 CGGAAGAGCG CCCAATACGC AAACCGCCTC TCCC CGCGCG TTGGCCGATT CATTAATGCA GCTGGCACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA
3001 GCGCAACGCA ATTAATGTGA GTTAGCTCAC TCATAGGCA CCC CAGGCTT TACACTTTAT GCTTC CGGCT CGTATGTTGT GTGGAATTGT GAGCGGATAA
3101 CAATTTACA CAGGAAACAG CTATGACCAT GATTACGCCA AGCTCCTTCC TCTTCCAGCC CTTCTCTTTT C
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# Blue Heron pUCminusMCS Restriction Map

RESTRICTION MAP: ALL ENZYMES

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Enzyme      Cuts    [ ----- Base 5' to Cleave Sites ----- ]
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AatII       1       974
AccI        0
AclI        3       707  1291  1664
AcyI        3       191   971  1353
AflIII      0
AflIII      1       2781
AgeI        0
AhaIII      3       1315  2007  2026
AluI        17      121   407   664   842   861  1540  1603  1703
           2224  2481  2527  2617  2843  2961  3025  3120  3142
AlwNI       1       2372
ApaBI       0
ApaI        0
ApaLI       3       724  1221  2467
ApoI        2       677   688
AscI        0
AsuI        7       140   500   913  1529  1751  1768  1847
AsuII       0
  
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AvaI	1	601									
AvaII	2	1529	1751								
AvrII	0										
BalI	0										
BamHI	0										
BclI	0										
BetI	3	1597	2428	2575							
BglI	2	181	1775								
BglII	0										
BsaAI	1	494									
BsaBI	0										
BseMII	2	745	1406								
BsePI	0										
BsiYI	9	275	601	602	855	2303	2582	2748	2766	2940	
Bsp1407I	0										
BspHI	3	948	1053	2061							
BspLU11I	1	2781									
BspMII	0										
BstEII	0										
BstXI	1	35									
Cac8I	14	119	123	143	334	348	391	767	1780		
		2171	2731	2768	2854	2963	2992				
CauII	5	821	856	1357	1708	2404					
Cfr10I	2	389	1808								
CfrI	3	37	1500	2942							

ClaI	0								
CviJI	53	24	39	121	141	175	393	407	421
		502	606	644	664	765	769	809	842
		861	915	1502	1540	1603	1613	1703	1769
		1778	1782	1808	1849	1861	2224	2253	2296
		2307	2372	2451	2476	2481	2527	2617	2715
		2741	2759	2770	2843	2862	2944	2961	3025
		3047	3068	3120	3142	3158			
CviRI	11	99	726	864	1223	1467	1555	1748	1838
		2173	2469	2958					
DdeI	6	731	966	1392	1932	2098	2507		
DpnI	14	151	1212	1248	1265	1523	1569	1587	1928
		2033	2045	2123	2131	2142	2217		
DraII	1	913							
DraIII	1	497							
DrdI	3	541	810	2679					
DsaI	0								
Eam1105I	1	1893							
Eco47III	0								
EcoNI	0								
EcoRI	0								
EcoRII	5	71	2620	2633	2754	3042			
EcoRV	0								
EspI	0								
Fnu4HI	22	100	173	277	291	313	753	862	1149
		1378	1473	1500	1839	2167	2373	2376	2441
		2584	2739	2857	2860	2878	2959		
FnuDII	14	266	290	310	686	797	900	902	1002
		1334	1827	2157	2738	2936	2938		







PstI	0								
PvuI	2	152	1524						
PvuII	2	121	2961						
RsaI	3	263	736	1412					
RsrII	0								
SacI	0								
SacII	0								
SalI	0								
SanDI	0								
SauI	0								
ScaI	1	1412							
ScrFI	10	73 2756	821 3044	856	1357	1708	2404	2622	2635
SduI	5	423	728	1225	1310	2471			
SecI	3	71	2621	3042					
SexAI	0								
SfeI	5	19	271	1647	2325	2516			
SfiI	0								
SgfI	0								
SgrAI	0								
SmaI	0								
SmlI	4	1268	2136	2413	2675				
SnaBI	0								
SpeI	0								
SphI	0								

SplI	0								
SrfI	0								
Sse8387I	0								
Sse8647I	0								
SspI	2	702	1088						
StuI	0								
StyI	0								
SwaI	0								
TaqI	3	459	1239	2683					
TatI	2	734	1410						
TfiI	2	2807	2947						
TseI	13	99	172	312	861	1472	1838	2166	2372
		2375	2440	2859	2877	2958			
Tsp45I	5	57	316	844	1420	1631			
Tsp4CI	10	20	166	520	850	885	1453	1968	2281
		2751	2822						
TspEI	10	29	677	688	714	1460	1715	2021	3009
		3084	3101						
TspRI	11	19	40	1474	1501	1848	1953	2102	2373
		2386	2892	3001					
Tth1111I	0								
VspI	3	1718	2953	3012					
XbaI	0								
XcmI	0								
XhoI	0								
XhoII	6	1246	1263	2031	2043	2129	2140		

XmaIII	0	
XmnI	1	1293

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