



Metallothionein Promoter

1 ATGATTACCG TTGCAGGACA GGATGTGGT CCGATGTGA CTAGCTCTTT GCTGCAGGCC GTCCTATCCT CTGGTTCOGA TAAGAGACCC AGAACTCCGG
TACTAATGGC AACGTCCTGT CCTACACCAC GGGCTACACT GATCGAGAAA CGACGTCGCG CAGGATAGGA GACCAAGGCT ATTCTCTGGG TCTTGAGGCC

Metallothionein Promoter

101 CCCCCACCG CCCACCGCCA CCCCATAACA TATGTGGTAC GCAAGTAAGA GTGCTGCGC ATGCCCATG TGCCCCACCA AGAGCTTTGC ATCCATAACA
GGGGGTGGC GGGTGGCGGT GGGGTATGT ATACACCATG CGTTTCATTCT CACGGACGCG TACGGGTGAC ACGGGTGTT TCTCGAAACG TAGGGTATGT

Metallothionein Promoter

201 AGTCCCCAAA GTGAGAAACC GAACCAATTC TTCGCGGGCA GAACAAAAGC TTCTGCACAC GTCTCCACTC GAATTGTGGAG CCGGCCGGCG TGTGCAAAAG
TCAGGGGTTT CACTCTTGG CTGTGGTTAAG AAGCGCCGT CTGTGTTTCG AAGACGTGTG CAGAGGTGAG CTTAAACCTC GGCCGGCCGC ACAGTITTC

HindIII EagI

Transcription Start Site

Metallothionein Promoter

301 AGGTGAATCG AACGAAAGAC CCGTGTGTAA AGCCGCGTTT CAAAATGTA TAAAACCGAG AGCATCTGGC CAATGTGCAT CAGTTGTGGT CAGCAGCAAA
TCCACTTAGC TTGCTTTCG GGCACACATT TCGGCGCAA GGTTTTACAT ATTTTGGTCT TCGTAGACCG GTTACACGTA GTCAACACCA GTCGTCGTTT

EcoRI **Signal Peptide**

+1 M A L Q I P S L L L S A A V V V L M V

401 ATCAAGTGAA TCATCTCAGT GCAACTAAAG GGAATTCTT AGAGATGGCT CTGCAGATCC CCAGCCTCCT CCTCTCAGCT GCTGTGGTGG TGCTGATGGT
TAGTTCACIT AGTAGAGTCA CGTTGATITC CCCTTAAGAA TCTCTACCGA GACGCTTAGG GGTCGGAGGA GGAGAGTGA GGACACACC ACGACTACCA

Spe-13 linker

Derp1 117-127

SpeI **I-Ab beta**

+1 V L S S P G T E G C Q I Y P P N V N K I G G G G T S G G G S G G S E

501 GCTGAGCAGC CCCGGGACTG AGGGCTGCCA AATTTACCCA CCAAAATGTA ACAAAATGG CCGGGGAGGT ACTAGTGGCG GTGGAAGTGG AGGGTCTGAA
CGACTCGTCG GGGCCCTGAC TCCCGACGST TTAATGGGT GGTITACAIT TTGTTTAAAC GCCCCCTCCA TGATCACCGC CACTTCACC TCCAGACTT

I-Ab beta

+1 R H F V Y Q F M G E C Y F T N G T Q R I R Y V T R Y I Y N R E E Y V

601 AGGCATTTG TGTACCAGTT CATGGGGAG TGCTACTTCA CCAACGGGAC GCAGCGCATA CGATATGTA CCAGATACAT CTACAACCGG GAGGAGTAGC
TCCGTAAGC ACATGGTCAA GTACCCGCTC ACGATGAAGT GGTTCGCTG GCTATACACT GGTCTATGTA GATGTTGGCC CTCCTCATGC

I-Ab beta

+1 V R Y D S D V G E H R A V T E L G R P D A E Y W N S Q P E I L E R T

701 TGCGCTACGA CAGCGACGTG GCGGAGCACC GCGCGGTGAC CGAGCTGGGG CGGCCAGACG CCGAGTACTG GAACAGCCAG CCGGAGATCC TGGAGCGAAC
ACCGATGCT GTGCTGCAC CCGCTCGTGG CCGCCACTG GCTCGACCCC GCCGCTGTC GGCTCATGAC CTGTGCGTIC GGCCTTAGG ACCTCGCTTG

I-Ab beta

+1 T R A E L D T V C R H N Y E G P E T H T S L R R L E Q P N V V I S L

801 GCGGGCCGAG CTGGACACGG TGTGCAGACA CAACTACGAG GGGCCGGAGA CCCACACCTC CTGCGGGCG CTTGAACAGC CCAATGTCGT CATCTCCCTG
CGCCCGCTC GACCTGTGCC ACACGTCGT GTTGATGCT CCGGCCCTCT GGTGTGGAG GGACCCGCC GAACPTGTCG GGTTCACGA GTAGAGGGAC

I-Ab beta

+1 S R T E A L N H H N T L V C S V T D F Y P A K I K V R W F R N G Q E

901 TCCAGGACAG AGGCCCTCAA CCACCACAAC ACTCTGGTCT GCTCAGTAC AGATTTCTAC CCAGCCAAGA TCAAAGTGG CTGGTCCCG AATGGCCAGG
AGGTCTGTG TCCGGGAGT GGTGTGTGTT TGAGACCAGA CGAGTCACTG TCTAAAGATG GGTGCGTCT AGTTTCACGC GACCAAGGCC TTACCGTCC

I-Ab beta

+1 E E T V G V S S T Q L I R N G D W T F Q V L V M L E M T P R R G E V

1001 AGGAGACGGT GGGGTCTCA TCCACACAGC TTATTAGGAA TGGGGACTGG ACCTTCCAGG TCCTGGTCAT GCTGGAGATG ACCCTCGCG GGGAGAGGT
TCCCTGCCA CCCCAGAGT AGGTGTGTCG AATAATCCTT ACCCTGACC TGGAAAGTCC AGGACCAGTA CGACCTTAC TGGGAGCCG CCCCTCCA

BstXI **Linker** **BamHI**

+1 V Y T C H V E H P S L K S P I T V E W R A Q S E S A W S K G G G S

1101 CTACACCTGT CACGTGGAGC ATCCAGCCT GAAGAGCCCC ATCACTGTGG AGTGGAGGGC ACAGTCTGAG TCTGCTGGA GCAAGGGAGG TGGAGGATCC
GATGTGGACA GTGCACCTCG TAGGGTCGGA CTCTCGGGG TAGTGACACC TCACTCCCG TGTCAACTC AGACGGACCT CGTTCCTCC ACCTCCTAGG

Basic Leucine Zipper

+1 T T A P S A Q L K K K L Q A L K K K N A Q L K W K L Q A L K K K L A

1201 ACTACAGCTC CATCAGTCA GTTGAAAAAG AAATGCAAG CACTGAAGAA AAAGAACGCT CAGCTGAAGT GGAAACTTCA AGCCCTCAAG AAGAACTCG
TGATGTGAG GTAGTCGAGT CAACTTTTTC TTAAACGTTG GTGACTTCT TTTCTGCGA GTCGACTTCA CCTTTGAAGT TCGGGAGTTC TTCTTTGAGC

	6x His Basic Leucine Zippe			Sall	ADH poly A							
+1	· A Q H H H H H ·			SbfI								
1301	CCCAGCATCA	TCATCATCAT	CATTGAGTCG	ACCTGCAGGC	ATGCAAGCTA	TTCGATGCAC	ACTCACATTG	TTCTCCTAAT	ACGATAATAA	AACTTTCCAT		
	GGGTCGTAGT	AGTAGTAGTA	GTAACCTCAGC	TGGACGTCCG	TACGTTTCGAT	AAGCTACGTG	TGAGTGTAA	AAGAGGATTA	TGCTATTATT	TTGAAAGGTA		
	ADH poly A											
1401	GAAAAATATG	GAAAAATATA	TGAAAATTGA	GAAATCCAAA	AACTGATAA	ACGCTCTACT	TAATTAAAAT	AGATAAATGG	GAGCGGCAGG	AATGGCGGAG		
	CTTTTTATAC	CTTTTTATAT	ACTTTTAACT	CITTAGGTTT	TTTGACTATT	TGCGAGATGA	ATTAATTTTA	TCTATTATTG	CTCGCCGTCC	TTACCCGCTC		
	ADH poly A											
1501	CATGGCCAAG	TTCTCCCGCC	AATCAGTCGT	AAAACAGAAG	TCGTGGAAAG	CGGATAGAAA	GAATGTTTGA	TTTGACGGGC	AAGCATGTCT	GCTATGTGGC		
	GTACCGGTTT	AAGGAGGCGG	TTAGTCAGCA	TTTTGTCTTC	AGCACCTTTC	GCCTATCTTT	CITACAAGCT	AAACTGCCCG	TTCGTACAGA	CGATACACCG		
	ADH poly A											
1601	GGATTGCGGA	GGAATTGCAC	TGGAGACCAG	CAAGGTTCTC	ATGACCAAGA	ATATAGCGGT	GAGTGAGCGG	GAAGCTCGGT	TTCTGTCCAG	ATCGAACTCA		
	CCTAACGCCT	CCTTAACGTG	ACCTCTGGTC	GITCCAAGAG	TACTGGTTCT	TATATCGCCA	CTCACTCGCC	CITCGAGCCA	AAGACAGGTC	TAGCTTGAGT		
	Spe mutator											
1701	AAACTTGTC	AGCCAGTCGC	TGTCGAAACT	AATTAAGTTA	ATGAGTTTTT	CATGTTAGTT	TCGCGCTGAG	CAACAATTAA	GTTTATGTTT	CAGTTTCGGT		
	TTTGAACAGG	TCGGTCAGCG	ACAGCTTTGA	TTAATTCAAT	TACTCAAAAA	GTACAATCAA	AGCGCGACTC	GTTGTTAATT	CAAATACAAA	GTCAGCCGA		
	ADH poly A											
1801	TAGATTTGCG	TGAAGGACTT	GCCACTTTCA	ATCAATACTT	TAGAACAAAA	TCAAAAATCA	TTCTAATAGC	TTGGTGTTC	TCITTTTTTT	TAATGATAAG		
	ATCTAAAGCG	ACTTCTGAA	CGGTGAAAGT	TAGTTATGAA	ATCTTGTTTT	AGTTTTGAGT	AAGATTATCG	AACCACAAGT	AGAAAAAATA	ATTACTATTC		
	ADH poly A											
1901	CAITTTGTG	TTTATACTTT	TTATATTTTG	ATATTAACC	ACCTATGAAG	TCTATTTTAA	TCGCCAGATA	AGCAATATAT	TGTGTAAATA	TTTGTATCT		
	GTAAACAGC	AAATATGAAA	AATATAAAGC	TATAATTTGG	TGGATACTTC	AGATAAAATP	AGCGGTCTAT	TCGTTATATA	ACACTTTTAT	AAACATAAGA		
	ADH poly A											
2001	TTATCAGGAA	ATTGAGGAG	ACGGGGAAGT	TACTATCTAC	TAAAAGCCAA	ACAATTTCTT	ACAGTTTTAC	TCTCTCTACT	CTAGAGTAGC	TTGGCACTGG		
	AATAGTCCTT	TAAAGTCCTC	TGCCCTTCA	ATGATAGATG	ATTTTCGGTT	TGTTAAAGAA	TGTCAAAATG	AGAGAGATGA	GATCTCATCG	AACCGTGACC		
	ADH poly A											
2101	CCGTCGTTTT	ACAACGTCGT	GACTGGGAAA	ACCCTGGCGT	TACCCAACCT	AATGCGCTTG	CAGCACATCC	CCCTTTCGCC	AGCTGGCGTA	ATAGCGAAGA		
	GGCAGCAAAA	TGTTGCAGCA	CTGACCTTTT	TGGGACCACA	ATGGGTTGAA	TTAGCGGAAC	GTCGTGTAGG	GGGAAAGCGG	TCGACCCGAT	TATCGCTTCT		
	ADH poly A											
2201	GGCCCGCACC	GATCGCCCTT	CCCAACAGTT	GCGCAGCCTG	AATGGCGAAT	GCGCCCTGAT	GCGGTATTTT	CTCCTTACGC	ATCTGTGCGG	TATTTACAC		
	CCGGCGTG	CTAGCGGAAA	GGGTTGTCAA	CGCGTCGAC	TTACCGCTTA	CCGCGGACTA	CGCCATAAAA	GAGGAATGCG	TAGACACGCC	ATAAAGTGTG		
	ADH poly A											
2301	CGCATATGGT	GCACTCTCAG	TACAATCTGC	TCTGATGCGG	CATAGTTAAG	CCAGCCCGGA	CACCCGCCAA	CACCCGCTGA	CGCGCCTGA	CGGGCTTGT		
	GCGTATACCA	CGTGAGAGTC	ATGTTAGACG	AGACTACGGC	GTATCAATTC	GGTCGGGGCT	GTGGGCGGTT	GTGGGCGACT	GCGCGGACT	GCCCGAACAG		
	ADH poly A											
2401	TGCTCCCGCC	ATCCGCTTAC	AGACAAGCTG	TGACCGTCTC	CGGGAGCTGC	ATGTGTGAGA	GGTTTTACCC	GTCATCACCG	AAACGCGCGA	GACGAAAGGG		
	ACGAGGGCCG	TAGCGGAATG	TCTGTTGAC	ACTGGCAGAG	GCCCTCGAGC	TACACAGTCT	CCTAAAGTGG	CAGTAGTGCC	TTTGGCGGCT	CTGCTTTCCC		
	ADH poly A											
2501	CCTCGTGATA	CGCCTATTTT	TATAGGTTAA	TGTCATGATA	ATAATGGTTT	CTTAGACGTC	AGGTGGCACT	TTTCGGGGAA	ATGTGCGCGG	AACCCCTATT		
	GGAGCACTAT	GCGGATAAAA	ATATCCAATT	ACAGTACTAT	TATTACAAA	GAATCTGCAG	TCCACCGTGA	AAAGCCCTTT	TACACCGGCC	TTGGGGATAA		
	ADH poly A											
2601	TGTTTATTTT	TCTAAATACA	TTCAAATATG	TATCCGCTCA	TGAGACAATA	ACCCTGATAA	ATGCTTCAAT	AATATGAAA	AAGGAAGAGT	ATGAGTATTC		
	ACAAATAAAA	AGATTTATGT	AGITTTATAC	ATAGCGGAGT	ACTCTGTTAT	TGGGACTATT	TACGAAGTTA	TTATACTTTT	TTCTTCTCA	TACTCATAAG		

pUC 18

APr

2701 AACATTTCCG TGTGCCCTT ATTCCCTTTT TTGGGSCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA
TTGTAAGGC ACAGCGGGAA TAAGGGAAA AACCGCTAA AACGGAAGGA CAAAACGAG TGGGTCTTTG CGACCACCTT CATTTTCTAC GACTTCTAGT

pUC 18

APr

2801 GTTGGGTGCA CGAGTGGGT ACATCGAACT GGATCTCAAC AGCGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT GAGCACTTTT
CAACCCACGT GCTCACCCAA TGTAGCTTGA CCTAGAGTTG TCGCCATTCT AGGAACTCTC AAAAGCGGGG CTTCTTGCAA AAGGTTACTA CTCGTGAAA

pUC 18

APr

2901 AAAGTTCTGC TATGTGGCG GGTATTATCC CGTATGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTAATCTCA GAATGACTTG GTTGAAGTACT
TTTCAAGACG ATACACCGCG CCATAATAGG GCATAACTGC GGCCTGTTCT CGTTGAGCCA GCGGCGTATG TGATAAGAGT CTTACTGAAC CAACTCATGA

pUC 18

APr

3001 CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT
GTGGTCAGTG TCTTTTCGTA GAATGCCTAC CGTACTGTCA TTCTCTTAAT ACGTCACGAC GGTATTGGTA CTCACTAATG TGACGCCGGT TGAATGAAGA

pUC 18

APr

3101 GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT GATCGTITGG AACCGGAGCT GAATGAAGCC
CTGTTGCTAG CCTCTGGCT TCCTCGATTG GCGAAAAAC GTGTTGTACC CCCTAGTACA TTGAGCCGAA CTAGCAACCC TTGGCCTCGA CTTACTTCGG

pUC 18

APr

3201 ATACCAAACG ACGAGCGTGA CACCACGATG CCTGTAGCAA TGGCAACAAC GTTTCGCAAA CTAATTAATG GCGAACTACT TACTCTAGCT TCCCGGCAAC
TATGGTTTGC TGCTCGCACT GTGGTGCTAC GGACATCGTT ACCGTTGTTG CAACGCGTTT GATAATTGAC CGCTTGATGA ATGAGATCGA AGGCGCGTTG

pUC 18

APr

3301 AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG GAGCCGGTGA
TTAATTATCT GACCTACCTC CGCCTAATTC AACGTCCTGG TGAAGACGCG AGCCGGGAAG GCCGACCGAC CAAATAAOGA CTAATTTAGAC CTCGGCCACT

pUC 18

APr

3401 GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA
CGCACCCAGA GCGCCATAGT AACGTCGTGA CCCCCTCTA CCATTCGGGA GGGCATAGCA TCAATAGATG TGCTGCCCTC CAGTCCGTTG ATACCTACTT

pUC 18

APr

3501 CGAAATAGAC AGATCGTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT TTAACACTTC
GCTTTATCTG TCTAGCGACT CTATCCACGG AGTGACTAAT TCGTAACCAT TGACAGTCTG GTTCAAATGA GTATATATGA AATCTAACTA AATTTTGAAG

pUC 18

3601 ATTTTAAAT TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTT CACTGAGCGT CAGACCCCGT
TAAAATTAAT ATTTTCTAG ATCCACTTCT AGGAAAAACT ATTAGAGTAC TGGTTTTAGG GAATTGCACT CAAAAGCAAG GTGACTCGCA GTCTGGGGCA

pUC 18

3701 AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTPTTCTG CCGGTAATCT GCTGCTTGA AACAAAAAAA CCACCCTAC CAGCGGTGGT TTGTTTGGCG
TCTTTCTAG TTTCTAGAA GAACCTTAGG AAAAAAGAC GCGCATTAGA CGACGAACGT TTGTTTTTTT GGTGGCGATG GTGCCACCA AACAAACGGC

mutation?

pUC 18

3801 GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACAGGCT TCAGCAGAGC GCAGATACCA AATACTGTTT TTCTAGTGTG GCCGTAGTTA GGCCACCACT
CTAGTTCTCG ATGGTTGAGA AAAAGGCTTC CATTGACCGA AGTCGTCTCG CGTCTATGGT TTATGACAAG AAGATCACAT CGGCATCAAT CCGGTGGTGA

pUC 18

3901 TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT AATCCTGTTA CCACTGGCTG CTGCCAGTGG CGATAAGTGG TGTCTTACC GGTGGACTC
AGTCTTGTAG ACATCGTGCC GGATGTATGG AGCGAGACGA TTAGGACAAT GGTCAACGAC GACGGTCACC GCTATTCAGC ACAGAATGCC CCAACCTGAG

pUC 18

4001 AAGACGATAG TTACC GGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGTTC CGTGACACACA GCCAGCTTG GAGCGAAOGA CCTACACCGA ACTGAGATAC
TTCTGCTATC AATGGCTAT TCCGCGTCCG CAGCCCGACT TGCCCCCAA GCACGTTGTG CGGTTCGAAC CTCGCTTGTG GGATGTGGCT TGACTCTATG

pUC 18

4101 CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCGAAG GGAGAAAGCG GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGG
GATGTCGCAC TCGATACTCT TTCGCGGTGC GAAGGGCTTC CCTCTTTCCG CCTGTCCATA GGCCATTCCG CTTCCACCC TGTCTCTCTC GCGTGTCTCC

pUC 18

4201 AGCTTCCAGG GGAAACGCC TGGTATCTTT ATAGTCTGT CCGGTTTCCG CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG
TCGAAGGTCC CCCTTTCCGG ACCATAGAAA TATCAGGACA GCCCAAAGCG GTGGAGACTG AACTCGCAGC TAAAACACT ACGAGCAGTC CCCCCTCCTC

pUC 18

ORI

4301 CCTATGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG
GGATACCTTT TTGCGGTCGT TGCGCCGAA AAATGCCAAG GACCGGAAA CGACCGGAAA ACGAGTGTAC AAGAAAGGAC GCAATAGGGG ACTAAGACAC

pUC 18

4401 GATAACCGTA TTACCGCCTT TGAGTGAGCT GATACCGCTC GCGCAGCCG AACGACCGAG CGCAGCGAGT CAGTGAGOGA GGAAGCGGAA GAGGCCCCAA
CTATTGGCAT AATGGCGGAA ACTCACTCGA CTATGGCGAG CCGGTCGCGC TTGCTGGCTC GCGTCGCTCA GTCACTCGCT CCTTCGCCTT CTCGCGGGTT

pUC 18

4501 TACGCAAACC GCCTCTCCCC GCGCGTTGGC CGATTCAATTA ATGCAGCTGG CACGACAGGT TTCCCGACTG GAAAGCGGGC AGTGAGCGCA ACGCAATTAA
ATGCGTTTGG CGGAGAGGGG CCGCAACCG GCTAAGTAAT TAGTTCGACC GTGCTGTCCA AAGGGTGAC CTTTCGCCG TCACTCGCGT TGCCTTAATT

pUC 18

P(LAC)

4601 TGTGAGTTAG CTCACTCAIT AGGCACCCCA GGCTTTACAC TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT TCACACAGGA
ACACTCAATC GAGTGAGTAA TCCGTGGGGT CCGAAATGTG AAATACGAAG GCCGAGCATA CAACACACCT TAACACTGCG CTATTGTATA AGTGTGTCTT

pUC 18

4701 AACAGCTATG AC
TTGTCGATAC TG