

SEQUENCE LISTING

<110> INTA-UNSAM-KAISER

<120> Bitransgenic Bovine

5

<130> INTA-UNSAM-KAISER

<160> 10

<170> PatentIn version 3.5

10

<210> 1

<211> 148

<212> PRT

<213> Homo sapiens

<400> 1

15

Met Lys Ala Leu Ile Val Leu Gly Leu Val Leu Leu Ser Val Thr Val

1 5 10 15

Gln Gly Lys Val Phe Glu Arg Cys Glu Leu Ala Arg Thr Leu Lys Arg

20 25 30

20

Leu Gly Met Asp Gly Tyr Arg Gly Ile Ser Leu Ala Asn Trp Met Cys

35 40 45

Leu Ala Lys Trp Glu Ser Gly Tyr Asn Thr Arg Ala Thr Asn Tyr Asn

50 55 60

25

Ala Gly Asp Arg Ser Thr Asp Tyr Gly Ile Phe Gln Ile Asn Ser Arg

65 70 75 80

Tyr Trp Cys Asn Asp Gly Lys Thr Pro Gly Ala Val Asn Ala Cys His

30

85 90 95

Leu Ser Cys Ser Ala Leu Leu Gln Asp Asn Ile Ala Asp Ala Val Ala

100 105 110

35

Cys Ala Lys Arg Val Val Arg Asp Pro Gln Gly Ile Arg Ala Trp Val

115 120 125

Ala Trp Arg Asn Arg Cys Gln Asn Arg Asp Val Arg Gln Tyr Val Gln

130 135 140

40

Gly Cys Gly Val

145

45

<210> 2

<211> 710

<212> PRT

<213> Homo sapiens

<400> 2

5 Met Lys Leu Val Phe Leu Val Leu Leu Phe Leu Gly Ala Leu Gly Leu
 1 5 10 15

 Cys Leu Ala Gly Arg Arg Arg Ser Val Gln Trp Cys Ala Val Ser Gln
 20 25 30
 10 Pro Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val
 35 40 45

 Arg Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys
 15 50 55 60

 Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly
 65 70 75 80
 20 Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val
 85 90 95

 Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr
 100 105 110
 25 Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu
 115 120 125

 Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp
 30 130 135 140

 Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro
 145 150 155 160
 35 Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys
 165 170 175

 Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys
 40 180 185 190

 Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr
 195 200 205
 45 Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp

	210	215	220
	Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu		
5	225	230	235 240
	Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys		
	245	250	255
10	Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His		
	260	265	270
	Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn		
	275	280	285
15	Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys		
	290	295	300
	Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys		
20	305	310	315 320
	Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly		
	325	330	335
25	Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys		
	340	345	350
	Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala		
	355	360	365
30	Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser		
	370	375	380
35	Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile		
	385	390	395 400
	Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly		
	405	410	415
40	Tyr Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu		
	420	425	430
	Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp		
45	435	440	445

	Arg	Pro	Val	Glu	Gly	Tyr	Leu	Ala	Val	Ala	Val	Val	Arg	Arg	Ser	Asp	
	450						455						460				
5	Thr	Ser	Leu	Thr	Trp	Asn	Ser	Val	Lys	Gly	Lys	Lys	Ser	Cys	His	Thr	
	465					470					475					480	
	Ala	Val	Asp	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met	Gly	Leu	Leu	Phe	
					485					490					495		
10	Asn	Gln	Thr	Gly	Ser	Cys	Lys	Phe	Asp	Glu	Tyr	Phe	Ser	Gln	Ser	Cys	
				500					505					510			
	Ala	Pro	Gly	Ser	Asp	Pro	Arg	Ser	Asn	Leu	Cys	Ala	Leu	Cys	Ile	Gly	
15			515					520					525				
	Asp	Glu	Gln	Gly	Glu	Asn	Lys	Cys	Val	Pro	Asn	Ser	Asn	Glu	Arg	Tyr	
		530					535					540					
20	Tyr	Gly	Tyr	Thr	Gly	Ala	Phe	Arg	Cys	Leu	Ala	Glu	Asn	Ala	Gly	Asp	
	545					550					555					560	
	Val	Ala	Phe	Val	Lys	Asp	Val	Thr	Val	Leu	Gln	Asn	Thr	Asp	Gly	Asn	
					565					570					575		
25	Asn	Asn	Glu	Ala	Trp	Ala	Lys	Asp	Leu	Lys	Leu	Ala	Asp	Phe	Ala	Leu	
					580				585					590			
30	Leu	Cys	Leu	Asp	Gly	Lys	Arg	Lys	Pro	Val	Thr	Glu	Ala	Arg	Ser	Cys	
		595						600					605				
	His	Leu	Ala	Met	Ala	Pro	Asn	His	Ala	Val	Val	Ser	Arg	Met	Asp	Lys	
	610						615					620					
35	Val	Glu	Arg	Leu	Lys	Gln	Val	Leu	Leu	His	Gln	Gln	Ala	Lys	Phe	Gly	
	625					630					635					640	
	Arg	Asn	Gly	Ser	Asp	Cys	Pro	Asp	Lys	Phe	Cys	Leu	Phe	Gln	Ser	Glu	
40					645					650					655		
	Thr	Lys	Asn	Leu	Leu	Phe	Asn	Asp	Asn	Thr	Glu	Cys	Leu	Ala	Arg	Leu	
				660					665					670			
45	His	Gly	Lys	Thr	Thr	Tyr	Glu	Lys	Tyr	Leu	Gly	Pro	Gln	Tyr	Val	Ala	
		675						680					685				

Gly Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala
 690 695 700

5 Cys Glu Phe Leu Arg Lys
 705 710

<210> 3
 <211> 459
 10 <212> DNA
 <213> *Homo sapiens*
 <400> 3

atgaaggctc tcattgttct ggggcttgct ctcctttctg ttacgggtcca gggcaaggctc 60
 15 ttgaaagggt gtgagttggc cagaactctg aaaagattgg gaatggatgg ctacagggga 120
 atcagcctag caaactggat gtgtttggcc aaatgggaga gtggttaca cacacgagct 180
 acaaactaca atgctggaga cagaagcact gattatggga tatttcagat caatagccgc 240
 20 tactggtgta atgatggcaa aaccccagga gcagttaatg cctgtcattt atcctgcagt 300
 gctttgctgc aagataacat cgctgatgct gtagcttggtg caaagaggggt tgtccgtgat 360
 25 ccacaaggca ttagagcatg ggtggcatgg agaaatcggt gtcaaaacag agatgtccgt 420
 cagtatgttc aaggttgtgg agtgtaactc cagaatttt 459

<210> 4
 30 <211> 2159
 <212> DNA
 <213> *Homo sapiens*
 <400> 4

atgaaacttg tcttcctcgt cctgctgttc ctcggggccc tcggactgtg tctggctggc 60
 35 cgtaggagga gtgttcagt gtgcgccgta tccaaccg aggccacaaa atgcttcaa 120
 tggcaaagga atatgagaaa agtgcgtggc cctcctgtca gctgcataaa gagagactcc 180
 40 cccatccagt gtatccaggc cattgcggaa aacagggccg atgctgtgac ccttgatggt 240
 ggtttcatat acgaggcagg cctggccccc taaaactgc gacctgtagc ggcggaagtc 300
 45 tacgggaccg aaagacagcc acgaactcac tattatgccg tggctgtggt gaagaagggc 360

ggagctttc agctgaacga actgcaaggt ctgaagtcct gccacacagg ccttcgcagg 420
 accgctggat ggaatgtccc tatagggaca cttcgtccat tcttgaattg gacgggtcca 480
 5 cctgagccca ttgaggcagc tgtggccagg ttcttctcag ccagctgtgt tcccggtgca 540
 gataaaggac agttcccca cctgtgtcgc ctgtgtgcgg ggacagggga aaacaaatgt 600
 10 gccttctcct ccaggaacc gtacttcagc tactctggtg ctttcaagtg tctgagagac 660
 ggggctggag acgtggcttt tatcagagag agcacagtgt ttgaggacct gtcagacgag 720
 gctgaaaggg acgagtatga gttactctgc ccagacaaca ctcggaagcc agtggacaag 780
 15 ttcaaagact gccatctggc cgggtccct tctcatgccg ttgtggcacg aagtgtgaat 840
 ggcaaggagg atgccatctg gaatcttctc cgccaggcac aggaaaagtt tggaaaggac 900
 aagtcaccga aattccagct ctttggctcc cctagtgggc agaaagatct gctgttcaag 960
 20 gactctgcca ttgggttttc gagggtgccc ccgaggatag attctgggct gtaccttggc 1020
 tccggctact tcaactgcat ccagaacttg aggaaaagtg aggaggaagt ggctgcccg 1080
 25 cgtgcgcggg tcgtgtggtg tgcggtgggc gagcaggagc tgcgcaagtg taaccagtgg 1140
 agtggcttga gcgaaggcag cgtgacctgc tcctcggcct ccaccacaga ggactgcatc 1200
 gccctggtgc tgaaaggaga agctgatgcc atgagtttgg atggaggata tgtgtacact 1260
 30 gcaggcaaat gtggtttggt gcctgtcctg gcagagaact acaaatccca acaaagcagt 1320
 gacctgatc ctaactgtgt ggatagacct gtggaaggat atcttgctgt ggcggtggtt 1380
 35 aggagatcag aactagcct tacctggaac tctgtgaaag gcaagaagtc ctgccacacc 1440
 gccgtggaca ggactgcagg ctggaatata cccatgggcc tgctcttcaa ccagacgggc 1500
 tcctgcaaat ttgatgaata tttagtcaa agctgtgccc ctgggtctga cccgagatct 1560
 40 aatctctgtg ctctgtgtat tggcgacgag cagggtgaga ataagtgcgt gcccaacagc 1620
 aacgagagat actacggcta cactggggct ttccggtgcc tggctgagaa tgctggagac 1680
 45 gttgcatttg tgaaagatgt cactgtcttg cagaacactg atggaataa caatgaggca 1740

tgggctaagg atttgaagct ggcagacttt gcgctgctgt gcctcgatgg caaacggaag 1800
 cctgtgactg aggctagaag ctgccatctt gccatggccc cgaatcatgc cgtgggtgtct 1860
 5 cggatggata aggtggaacg cctgaaacag gtgttgctcc accaacaggc taaatttggg 1920
 agaaatggat ctgactgccc ggacaagttt tgcttattcc agtctgaaac caaaaacctt 1980
 10 ctgttcaatg acaacactga gtgtctggcc agactccatg gcaaaacaac atatgaaaaa 2040
 tatttgggac cacagtatgt cgcaggcatt actaatctga aaaagtgtc aacctcccc 2100
 ctccctggaag cctgtgaatt cctcaggaag taaaaccgaa gaagatggcc cagctcccc 2159
 15
 <210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 20 <220>
 <223> Reverse LTF
 <400> 5
 ctcgagttac ttcctgagga attc 24
 25
 <210> 6
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 30 <223> Forward LTF
 <400> 6
 ctcgagatga aacttgtctt cctc 24
 35
 <210> 7
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Forward Lysozyme
 40 <400> 7
 ctcgagatga aggtctctcat tggt 24
 45
 <210> 8
 <211> 27
 <212> DNA

<213> Artificial Sequence
<220>
<223> Reverse Lysozyme
<400> 8
5 ctcgagagtt actacactcc acaacct 27

<210> 9
<211> 27
<212> DNA
10 <213> Artificial Sequence
<220>
<223> Forward B-casein
<400> 9
15 attattgtca gtgaggatgg ggctgga 27

<210> 10
<211> 27
<212> DNA
20 <213> Artificial Sequence
<220>
<223> Reverse B-casein
<400> 10
gctagcaatg atctgattta gtggctg 27

25