

SEQUENCE LISTING

<110> EUROIMMUN Medizinische Labordiagnostika AG
 <120> Diagnosis of blistering autoimmune diseases
 <130> 18PP205EP
 <160> 31
 <170> PatentIn version 3.5
 <210> 1
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> sense LAMB4 Primer
 <400> 1
 ataggtctca catgcaattt caactgaccc tttttttgca ccttg 45
 <210> 2
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> asense LAMB4 Primer
 <400> 2
 ataggtctcg tcgaggctat agcacctagc atattttttt tcttg 45
 <210> 3
 <211> 48
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> LAMB4-Stop Primer
 <400> 3
 ataggtctcc tcgagctagc tatagcacct agcatatttt ttttcttg 48
 <210> 4
 <211> 5758
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> pTriEx-1
 <400> 4
 ggggaattgt gagcggataa caattccccg gagttaatcc gggaccttta attcaaccca 60
 acacaatata ttatagttaa ataagaatta ttatcaaadc atttgtatat taattaaaat 120
 actatactgt aaattacatt ttattttaca tcaaaggaga tataccatgg cgatatcccc 180
 ggagctcgtg gatccgaatt ctgagatctc ggcgcgcctg caggtcgacg gtaccggttc 240
 gaagcttgcg gccgcacagc tgtatacacg tgcaagccag ccagaactcg ccccggaaga 300
 ccccgaggat ctcgagcacc accatcacca tcaccatcac taagtgatta acctcaggtg 360

caggctgcct atcagaaggt ggtggctggt gtggccaatg ccctggctca caaataccac	420
tgagatcgat ctttttccct ctgccaaaaa ttatggggac atcatgaagc cccttgagca	480
tctgacttct ggctaataaa ggaaatttat tttcattgca atagtgtgtt ggaatTTTTT	540
gtgtctctca ctcggaagga catatgggag ggcaaatcat ttaaaacatc agaatgagta	600
tttggtttag agtttggcaa catatgccca tatgtaacta gcataacccc ttggggcctc	660
taaacgggtc ttgaggggtt ttttgctgaa agcatgcgga ggaaattctc cttgaagttt	720
ccctggtgtt caaagtaaag gagtttgcac cagacgcacc tctgttctact ggtccggcgt	780
attaaaacac gatacattgt tattagtaca tttattaagc gctagattct gtgcgttggt	840
gatttacaga caattgttgt acgtatttta ataattcatt aaatttataa tctttaggg	900
ggtatgttag agcgaaaatc aatgattttt cagcgtcttt atatctgaat ttaaatatta	960
aatcctcaat agatttgtaa aataggtttc gattagtttc aaacaaggggt tgTTTTTccg	1020
aaccgatggc tggactatct aatggatttt cgctcaacgc cacaaaactt gccaaatctt	1080
gtagcagcaa tctagctttg tcgatattcg tttgtgtttt gttttgtaat aaaggttcga	1140
cgctcgttcaa aatattatgc gcttttgtat ttctttcatc actgtcgtta gtgtacaatt	1200
gactcgacgt aaacacgtta aatagagctt ggacatatTTT aacatcgggc gtgttagctt	1260
tattaggccg attatcgtcg tcgtcccaac cctcgtcgtt agaagttgct tccgaagacg	1320
atTTTgcat agccacacga cgcctattaa ttgtgtcggc taacacgtcc gcgatcaaat	1380
ttgtagttga gctTTTTgga attatttctg attgcgggCG tttttgggCG ggtttcaatc	1440
taactgtgcc cgattttaat tcagacaaca cgttagaaag cgatggtgca ggcggtggta	1500
acatttcaga cggcaaatct actaatggcg gcggtggtgg agctgatgat aaatctacca	1560
tcggtggagg cgcaggcggg gctggcggcg gaggcggagg cggaggtggt ggcggtgatg	1620
cagacggcgg tttaggctca aatgtctctt taggcaacac agtcggcacc tcaactattg	1680
tactggtttc gggcgccgtt tttggtttga ccggtctgag acgagtgcga ttttttctg	1740
ttctaatagc ttccaacaat tgttgtctgt cgtctaaagg tgcagcgggt tgaggttccg	1800
tcggcattgg tggagcgggc ggcaattcag acatcgatgg tgggtggtggt ggtggaggcg	1860
ctggaatgtt aggcacggga gaagggtgtg gcggcgggtc cgccggtata atTTTgttctg	1920
gtttagtttg ttcgcgcacg attgtgggca ccggcgcagg cgccgctggc tgcacaacgg	1980
aaggtcgtct gcttcgaggc agcgcttggg gtggtggcaa ttcaatatta taattggaat	2040
acaaatcgta aaaatctgct ataagcattg taatttcgct atcgtttacc gtgccgatat	2100
ttaacaaccg ctcaatgtaa gcaattgtat tgtaaagaga ttgtctcaag ctcggaacgc	2160
tgcgctcggc cgttcggctg cggcgagcgg tatcagctca ctcaaaggcg gtaatacgg	2220
tatccacaga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc cagcaaaagg	2280
ccaggaaccg taaaaaggcc gcgttgctgg cgTTTTTcca taggctccgc cccctgacg	2340
agcatcacia aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga ctataaagat	2400

accaggcggtt	tccccctgga	agctccctcg	tgcgctctcc	tgttccgacc	ctgccgctta	2460
ccggatacct	gtccgccttt	ctcccttcgg	gaagcggtggc	gctttctcaa	tgctcacgct	2520
gtaggtatct	cagttcgggtg	taggtcggtc	gctccaagct	gggctgtgtg	cacgaacccc	2580
ccgttcagcc	cgaccgctgc	gccttatccg	gtaactatcg	tcttgagtcc	aacccggtaa	2640
gacacgactt	atcgccactg	gcagcagcca	ctggtaacag	gattagcaga	gcgaggatg	2700
taggcgggtg	tacagagttc	ttgaagtggg	ggcctaacta	cggctacact	agaaggacag	2760
tatttggtat	ctgcgctctg	ctgaagccag	ttaccttcgg	aaaaagagtt	ggtagctctt	2820
gatccggcaa	acaaaccacc	gctggtagcg	gtgggttttt	tgtttgcaag	cagcagatta	2880
cgcgcagaaa	aaaaggatct	caagaagatc	ctttgttacc	aatgcttaat	cagtgaggca	2940
cctatctcag	cgatctgtct	atttcgttca	tccatagttg	cctgactccc	cgctcgtgtg	3000
ataactacga	tacgggaggg	cttaccatct	ggccccagtg	ctgcaatgat	accgcgagac	3060
ccacgctcac	cggctccaga	tttatcagca	ataaaccagc	cagccggaag	ggccgagcgc	3120
agaagtggtc	ctgcaacttt	atccgcctcc	atccagtcta	ttaattgttg	ccgggaagct	3180
agagtaagta	gttcgccagt	taatagtttg	cgcaacgttg	ttgccattgc	tacaggcatc	3240
gtggtgtcac	gctcgtcggt	tggtatggct	tcattcagct	ccggttccca	acgatcaagg	3300
cgagttacat	gatcccccct	gttggtgcaa	aaagcgggta	gctccttcgg	tcctccgatac	3360
gttggtcagaa	gtaagttggc	cgcagtggtta	tcactcatgg	ttatggcagc	actgcataat	3420
tctcttactg	tcatgccatc	cgtaagatgc	ttttctgtga	ctgggtgagta	ctcaaccaag	3480
tcattctgag	aatagtgtat	gcggcgaccg	agttgctctt	gcccggcgtc	aatacgggat	3540
aataccgctc	cacatagcag	aacttttaaa	gtgctcatca	ttggaaaacg	ttcttcgggg	3600
cgaaaactct	caaggatctt	accgctgttg	agatccagtt	cgatgtaacc	cactcgtgca	3660
cccaactgat	cttcagcatc	ttttactttc	accagcgttt	ctgggtgagc	aaaaacagga	3720
aggcaaaatg	ccgcaaaaaa	gggaataagg	gcgacacgga	aatgttgaat	actcatactc	3780
ttcctttttc	aatattattg	aagcatttat	caggggttatt	gtctcatgtc	cgcgcgtttc	3840
ctgcatcttt	taatcaaata	ccaagatgtg	tataaaccac	caaactgcca	aaaaatgaaa	3900
actgtcgaca	agctctgtcc	gtttgctggc	aactgcaagg	gtctcaatcc	tatttgtaat	3960
tattgaataa	taaaacaatt	ataaatgtca	aatttgtttt	ttattaacga	tacaaaccaa	4020
acgcaacaag	aacatttgta	gtattatcta	taattgaaaa	cgcgtagtta	taatcgctga	4080
ggtaatat	aaaatcattt	tcaaagtatt	cacagttaat	ttgcgacaat	ataattttat	4140
tttcacataa	actagacgcc	ttgtcgtctt	cttcttcgta	ttccttctct	ttttcatttt	4200
tctcttcata	aaaattaaca	tagttattat	cgtatccata	tatgtatcta	tcgtatagag	4260
taaat	gttgtcataa	atatatatgt	cttttttaat	ggggtgtata	gtaccgctgc	4320
gcatagtttt	tctgtaattt	acaacagtgc	tattttctgg	tagttcttcg	gagtgtgttg	4380
ctttaattat	taaatttata	taatcaatga	atttgggatc	gtcgggtttt	tacaatatgt	4440

tgccggcata	gtacgcagct	tcttctagtt	caattacacc	atttttttagc	agcaccggat	4500
taacataact	ttccaaaatg	ttgtacgaac	cgttaaacaa	aaacagttca	cctccctttt	4560
ctatactatt	gtctgcgagc	agttgtttgt	tgttaaaaat	aacagccatt	gtaatgagac	4620
gcacaaacta	atatcacaaa	ctggaaatgt	ctatcaatat	atagttgctc	tagttattaa	4680
tagtaatcaa	ttacgggggtc	attagttcat	agcccatata	tggagttccg	cgttacataa	4740
cttacggtaa	atggcccgcg	tggctgaccg	ccaacgacc	cccgcccatt	gacgtcaata	4800
atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	attgacgtca	atgggtggac	4860
tatttacggt	aaactgccca	cttggcagta	catcaagtgt	atcatatgcc	aagtacgcc	4920
cctattgacg	tcaatgacgg	taaatggccc	gcctggcatt	atgcccagta	catgacctta	4980
tgggactttc	ctacttgga	gtacatctac	gtattagtca	tcgctattac	catgcatggt	5040
cgaggtgagc	cccacgttct	gcttcactct	ccccatctcc	ccccctccc	cacccccaat	5100
tttgtattta	tttatttttt	aattattttg	tgcagcgatg	ggggcggggg	gggggggggg	5160
gcgcgcgcc	ggcggggcgg	ggcggggcga	ggggcggggc	ggggcgaggc	ggagagggtgc	5220
ggcggcgacc	aatcagagcg	gcgcgcctcc	aaagtttcct	tttatggcga	ggcggcgggc	5280
gcggcgggcc	tataaaaagc	gaagcgcgcg	gcgggcggga	gtcgcctgcga	cgctgccttc	5340
gccccgtgcc	ccgctccgcc	gccgcctcgc	gccgcccgcc	ccggctctga	ctgaccgcgt	5400
tactcccaca	ggtgagcggg	cgggacggcc	cttctccttc	gggctgtaat	tagcgcttgg	5460
tttaatgacg	gcttgtttct	tttctgtggc	tgcgtgaaag	ccttgagggg	ctccgggagg	5520
gccctttgtg	cggggggagc	ggctcggggc	tgtccgcggg	gggacggctg	ccttcggggg	5580
ggacggggga	gggcgggggt	cggcttcttg	cgtgtgaccg	gcggctctag	agcctctgct	5640
aaccatgttc	atgccttctt	ctttttccta	cagctcctgg	gcaacgtgct	ggttattgtg	5700
ctgtctcatc	attttgga	agaattggat	cggaccgaaa	ttaatacgac	tcactata	5758

aaattaatac	gactcactat	aggggaattg	tgagcggata	acaattcccc	ggagttaatc	480
cgggaccttt	aattcaaccc	aacacaatat	attatagtta	aataagaatt	attatcaaat	540
catttgtata	ttaattaaaa	tactatactg	taaattacat	tttattttaca	atcaaaggag	600
atataccatg	caatttcaac	tgaccctttt	tttgcacctt	gggtgggtca	gttactcaaa	660
agctcaagat	gactgcaaca	ggggtgcctg	tcatcccacc	actggtgatc	tcctggtggg	720
caggaacacg	cagcttatgg	cttcttctac	ctgtgggctg	agcagagccc	agaaatactg	780
catcctcagt	tacctggagg	gggaacaaaa	atgcttcac	tgtgactcta	gatttccata	840
tgatccgtat	gaccaaccca	acagccacac	cattgagaat	gtcattgtaa	gttttgaacc	900
agacagagaa	aagaaatgg	ggcaatctga	aaatggtctt	gatcatgtca	gcatcagact	960
ggacttagag	gcattatttc	ggttcagcca	ccttatcctg	acctttaaga	cttttcggcc	1020
tgctgcaatg	ttagttgaac	gttccacaga	ctatggacac	aactggaaag	tgttcaaata	1080
ttttgcaaaa	gactgtgcca	cttcctttcc	taacatcaca	tctggccagg	cccagggagt	1140
gggagacatt	gtttgtgact	ccaaatactc	ggatattgaa	ccctcaacag	gtggagaggt	1200
gtttttaaaa	gttttggatc	ccagttttga	aattgaaaac	ccttatagcc	cctacatcca	1260
agaccttgtg	acattgacaa	acctgaggat	aaactttacc	aagctccaca	cccttgggga	1320
tgctttgctt	ggaaggaggc	aaaatgattc	ccttgataaa	tactactatg	ctctgtacga	1380
gatgattgtt	cggggaagct	gcttttgcaa	tggccatgct	agcgaatgtc	gccctatgca	1440
gaagatgcgg	ggagatgttt	tcagccctcc	tggaatggtt	cacggtcagt	gtgtgtgtca	1500
gcacaataca	gatggtccga	actgtgagag	atgcaaggac	ttcttccagg	atgctccttg	1560
gaggccagct	gcagacctcc	aggacaacgc	ttgcagatcg	tgcagctgta	acagccactc	1620
cagccgctgt	cactttgaca	tgactacgta	cctggcaagc	ggtggcctca	gcgggggcgt	1680
gtgtgaagac	tgccagcaca	acactgaggg	gcagcactgc	gaccgctgca	gacccctctt	1740
ctacagggac	ccgctcaaga	ccatctcaga	tccttacgcg	tgcattcctt	gtgaatgtga	1800
ccccgatggg	accatatctg	gtggcatttg	tgtgagccac	tctgatcctg	ccttaggggtc	1860
tgtggctggc	cagtgccttt	gtaaagagaa	cgtggaagga	gccaaatgcg	accagtgcaa	1920
accaaccac	tatggactaa	gcgccaccga	ccccctgggc	tgccagccct	gcgactgtaa	1980
cccccttggg	agtctgccat	tcttgacctg	tgatgtggat	acaggccaat	gcttgtgcct	2040
gtcatatgtc	accggagcac	actgcgaaga	atgcactggt	ggatactggg	gcctgggaaa	2100
tcatctccat	gggtgttctc	cctgtgactg	tgatattgga	ggtgcttatt	ctaactgtgtg	2160
ctcacccaag	aatgggcagt	gtgaatgccg	cccacatgtc	actggccgta	gctgctctga	2220
accagcccct	ggctacttct	ttgctccttt	gaatttctat	ctctacgagg	cagaggaagc	2280
cacaacactc	caaggactgg	cgcctttggg	ctcggagacg	tttggccaga	gtcctgctgt	2340
tcacgttgtt	ttaggagagc	cagttcctgg	gaaccctggt	acatggactg	gacctggatt	2400
tgccaggggt	ctccctgggg	ctggcttgag	atttgctgtc	aacaacattc	cctttcctgt	2460

ggacttcacc	attgccattc	actatgaaac	ccagtctgca	gctgactgga	ctgtccagat	2520
tgtggtgaac	ccccctggag	ggagtgaagca	ctgcataccc	aagactctac	agtcaaagcc	2580
tcagtctttt	gccttaccag	cggctacgag	aatcatgctg	cttcccacac	ccatctgttt	2640
agaaccagat	gtacaatatt	ccatagatgt	ctatTTTTct	cagcctttgc	aaggagagtc	2700
ccacgctcat	tcacatgtcc	tgggtggactc	tcttggcctt	attccccaaa	tcaattcatt	2760
ggagaatttc	tgcagcaagc	aggacttaga	tgagtatcag	cttcacaact	gtgttgaaat	2820
tgcctcagca	atgggacctc	aagtgtccc	gggtgcctgt	gaaaggctga	tcatcagcat	2880
gtctgccaag	ctgcatgatg	gggctgtggc	ctgcaagtgt	cacccccagg	gctcagtcgg	2940
atccagctgc	agccgacttg	gaggccagtg	ccagtgtaaa	cctcttgtgg	tcgggctgtg	3000
ctgtgacagg	tgctcaactg	gaagctatga	tttggggcat	cacggctgtc	acccatgtca	3060
ctgccatcct	caaggatcaa	aggacactgt	atgtgaccaa	gtaacaggac	agtgcccctg	3120
ccatggagag	gtgtctggcc	gccgctgtga	tcgctgcctg	gcaggctact	ttggatttcc	3180
cagctgccac	ccttgccctt	gtaatagggt	tgctgaactt	tgtgatcctg	agacagggtc	3240
atgcttcaat	tgtggaggct	ttacaactgg	cagaaactgt	gaaagggtga	ttgatggtta	3300
ctatggaaat	ccttcttcag	gacagccctg	tcgtccttgc	ctgtgtccag	atgatccctc	3360
aagcaatcag	tattttgccc	attcctgtta	tcagaatctg	tggagctcag	atgtaatctg	3420
caattgtctt	caaggttata	cgggtactca	gtgtggagaa	tgctctactg	gtttctatgg	3480
aaatccaaga	atttcaggag	caccttgcca	accatgtgcc	tgcaacaaca	acatagatgt	3540
aaccgatcca	gagtcctgca	gccgggtaac	aggggagtg	cttcgatgtt	tgcacaacac	3600
tcagggcgca	aactgccagc	tctgcaaacc	aggtcactat	ggatcagccc	tcaatcagac	3660
ctgcagaaga	tgctcctgcc	atgcttccgg	cgtgagtcct	atggagtgtc	cccctggtgg	3720
gggagcttgc	ctctgtgacc	ctgtcactgg	tgcatgtcct	tgtctgccga	atgtcacagg	3780
cctggcctgt	gaccgttgtg	ctgatggata	ctggaatctg	gtccctggca	gaggatgtca	3840
gtcatgtgac	tgtgacccta	ggacctctca	aagtagccac	tgtgaccagc	ttacaggcca	3900
gtgtccgtgt	aaattagggt	acggcgggaa	acgttgcagt	gagtgccagg	aaaattatta	3960
tggtgatcca	cctgggcgat	gcattccatg	tgattgtaac	agggcaggta	cccagaagcc	4020
catctgtgat	ccagacacag	gcatgtgccg	ctgccgggag	ggtgtcagcg	gccagagatg	4080
tgatcgctgt	gcccggggac	acagccagga	attccctact	tgtcttcaat	gtcacttgtg	4140
ctttgatcag	tgggaccaca	ccatttcttc	cctctccaaa	gcggtgcaag	ggttaatgag	4200
actggctgct	aacatggaag	ataaaagaga	gaccctgcct	gtctgtgagg	cagacttcaa	4260
agacctcaga	gggaacgtgt	ctgaaataga	aaggattttg	aaacatcctg	ttttcccatc	4320
tgggaaattc	ttaaaagtca	aggattatca	tgactctgtt	agaagacaaa	tcatgcagct	4380
aaatgaacaa	ctgaaagcag	tgtatgaatt	tcaagatctg	aaagatacaa	tagaaagagc	4440
aaagaatgaa	gcagacctct	tacttgaaga	ccttcaggaa	gaaattgatt	tgcaatccag	4500

tgtcctaata	gcaagcattg	cggactcctc	agaaaacatc	aagaaatatt	atcacatatc	4560
atcatctgct	gaaaagaaaa	ttaatgaaac	tagttccacc	attaatacct	ctgcaaatatc	4620
aaggaatgac	ttacttacca	tcttagatac	actaacctca	aaaggaaact	tgtcattgga	4680
aagattaaaag	cagattaaga	taccagatat	ccaaatattg	aatgaaaagg	tgtgaggaga	4740
tccaggaaat	gtgccatgtg	tgcccttgcc	ctgtggcggt	gctctctgca	cggggccggaa	4800
ggggcacagg	aagtgtaggg	gtcccggctg	tcacggctcc	ctgaccctct	caacgaatgc	4860
cctccaaaaa	gccaggaag	caaatccat	tattcgtaat	ttggacaaac	aggttcgtgg	4920
gttgaaaaat	cagatcgaaa	gtataagtga	acaggcagaa	gtctccaaaa	acaatgcctt	4980
acagctgagg	gaaaaactgg	gaaatataag	aaaccaaagt	gactctgaag	aagaaaacat	5040
caatcttttc	atcaaaaaag	tgaaaaactt	tttgttagag	gaaaacgtgc	ctccagaaga	5100
catcgagaag	gttgcaaatg	gtgtgcttga	cattcaccta	ccaattccat	cccaaatctt	5160
aaccgatgaa	cttgtcaaaa	tacagaaaca	tatgcaactc	tgtgaggatt	acaggacaga	5220
tgaaaacagg	ttaaatgaag	aagcagatgg	agcccaaaag	cttttggtga	aggccaaagc	5280
agctgagaaa	gcagcaaata	ttctattaaa	tcttgacaaa	acattgaacc	agttacaaca	5340
agctcaaadc	actcaaggac	gggcaaactc	taccattaca	cagctgactg	ccaatataac	5400
aaaaataaaa	aagaatgtgc	tgaggctga	aaatcaaacc	agggaatga	agagtgaagt	5460
ggagttagca	aagcagcgat	cagggtgga	ggatggactt	tccctgctgc	agaccaagtt	5520
gcaaaggcat	caagaccacg	ctgtcaatgc	gaaagttcag	gctgaatctg	cccaacacca	5580
ggctgggagt	cttgagaagg	aatttggtga	gctgaaaaaa	caatatgcta	ttctccaacg	5640
taagacaagc	actacaggac	taacaaagga	gacattagga	aaagttaaag	agctaaaaga	5700
tgcggcagaa	aaattggctg	gagatacaga	ggccaagata	agaagaataa	cagatttaga	5760
aaggaaaaatc	caagatttga	atctaagtag	acaagcaaaa	gctgatcaac	tgagaatatt	5820
ggaagatcaa	gttggttgcca	ttaaaaatga	aattgttgaa	caagaaaaaa	aatatgctag	5880
gtgctatagc	ctcgagcacc	accatcacca	tcaccatcac	taagtgatta	acctcaggtg	5940
caggctgcct	atcagaagg	ggtggctggt	gtggccaatg	ccctggctca	caaataccac	6000
tgagatcgat	ctttttccct	ctgccaaaaa	ttatggggac	atcatgaagc	cccttgagca	6060
tctgacttct	ggctaataaa	ggaaatttat	tttcattgca	atagtgtgtt	ggaatttttt	6120
gtgtctctca	ctcggaagga	catatgggag	ggcaaatcat	ttaaaacatc	agaatgagta	6180
tttggttttag	agtttggtgca	catatgccca	tatgtaacta	gcataacccc	ttggggcctc	6240
taaacgggtc	ttgaggggtt	ttttgctgaa	agcatgcgga	ggaaattctc	cttgaagttt	6300
ccctgggtgtt	caaagtaaag	gagtttgcac	cagacgcacc	tctgttccact	ggtccggcgt	6360
attaaaacac	gatacattgt	tattagtaca	tttattaagc	gctagattct	gtgcgttggt	6420
gatttacaga	caattgttgt	acgtatttta	ataattcatt	aaatttataa	tctttaggg	6480
ggtatgttag	agcgaaaatc	aaatgatttt	cagcgtcttt	atatctgaat	ttaaatatta	6540

aatcctcaat	agattttgtaa	aatagggtttc	gatttagtttc	aaacaagggt	tgtttttccg	6600
aaccgatggc	tggactatct	aatggattttt	cgctcaacgc	cacaaaactt	gccaaatctt	6660
gtagcagcaa	tctagctttg	tcgatattcg	tttgtgtttt	gttttgtaat	aaagggttcga	6720
cgtcgttcaa	aatattatgc	gcttttgtat	ttctttcatc	actgtcgtta	gtgtacaatt	6780
gactcgacgt	aaacacgtta	aatagagctt	ggacatatatt	aacatcgggc	gtgttagctt	6840
tattaggccg	attatcgtcg	tcgtcccaac	cctcgtcggt	agaagttgct	tccgaagacg	6900
attttgccat	agccacacga	cgcctattaa	ttgtgtcggc	taacacgtcc	gcgatcaaat	6960
ttgtagttga	gctttttgga	attattttctg	attgcgggcg	tttttgggcg	ggtttcaatc	7020
taactgtgcc	cgattttaat	tcagacaaca	cgttagaaag	cgatggtgca	ggcggtggtta	7080
acatttcaga	cggcaaatct	actaatggcg	gcggtggtgg	agctgatgat	aaatctacca	7140
tcggtggagg	cgcaggcggg	gctggcggcg	gaggcggagg	cggagggtgt	ggcggtgatg	7200
cagacggcgg	tttaggtcga	aatgtctctt	taggcaacac	agtcggcacc	tcaactattg	7260
tactggtttc	gggcgccgtt	tttggtttga	ccggtctgag	acgagtgcga	tttttttcgt	7320
ttctaatagc	ttccaacaat	tgttgtctgt	cgctctaaagg	tgcagcgggt	tgaggttccg	7380
tcggcattgg	tggagcgggc	ggcaattcag	acatcgatgg	tgggtggtggt	ggtggaggcg	7440
ctggaatgtt	aggcacggga	gaagggtggtg	gcggcggtgc	cgccggtata	atgtgttctg	7500
gtttagtttg	ttcgcgcacg	attgtgggca	ccggcgcagg	cgccgctggc	tgcacaacgg	7560
aaggctcgtct	gcttcgaggc	agcgcttggg	gtggtggcaa	ttcaatatta	taattggaat	7620
acaaatcgta	aaaatctgct	ataagcattg	taatttcgct	atcgtttacc	gtgccgatata	7680
ttaacaaccg	ctcaatgtaa	gcaattgtat	tgtaaagaga	ttgtctcaag	ctcggaacgc	7740
tgcgctcggg	cgttcggctg	cggcgagcgg	tatcagctca	ctcaaaggcg	gtaatacggg	7800
tatccacaga	atcaggggat	aacgcaggaa	agaacatgtg	agcaaaaggc	cagcaaaagg	7860
ccaggaaccg	taaaaaggcc	gcgttgctgg	cgtttttcca	taggctccgc	ccccctgacg	7920
agcatcacia	aaatcgacgc	tcaagtcaga	ggtggcgaaa	cccgacagga	ctataaagat	7980
accaggcggt	tccccctgga	agctccctcg	tgcgctctcc	tgttccgacc	ctgccgctta	8040
ccggatacct	gtccgccttt	ctcccttcgg	gaagcgtggc	gctttctcaa	tgctcacgct	8100
gtaggtatct	cagttcgggtg	taggtcggtt	gctccaagct	gggctgtgtg	cacgaacccc	8160
ccgttcagcc	cgaccgctgc	gccttatccg	gtaactatcg	tcttgagtcc	aaccgggtaa	8220
gacacgactt	atcgccactg	gcagcagcca	ctggtaacag	gattagcaga	gcgaggatatg	8280
taggcgggtg	tacagagttc	ttgaagtggg	ggcctaacta	cggctacact	agaaggacag	8340
tatttggtat	ctgcgctctg	ctgaagccag	ttaccttcgg	aaaaagagtt	ggtagctctt	8400
gatccggcaa	acaaaccacc	gctggtagcg	gtgggtttttt	tgtttgcaag	cagcagatta	8460
cgcgcagaaa	aaaaggatct	caagaagatc	ctttgttacc	aatgcttaat	cagtgaggca	8520
cctatctcag	cgatctgtct	atctcgttca	tccatagttg	cctgactccc	cgtcgtgtag	8580

ataactacga	tacgggaggg	cttaccatct	ggccccagtg	ctgcaatgat	accgcgagac	8640
ccacgctcac	cggctccaga	tttatcagca	ataaaccagc	cagccggaag	ggccgagcgc	8700
agaagtggtc	ctgcaacttt	atccgcctcc	atccagtcta	ttaattgttg	ccgggaagct	8760
agagtaagta	gttcgccagt	taatagtttg	cgcaacgttg	ttgccattgc	tacaggcatc	8820
gtggtgtcac	gctcgtcgtt	tggatatggct	tcattcagct	ccggttccca	acgatcaagg	8880
cgagttacat	gatcccccat	gttgtgcaaa	aaagcggtta	gctccttcgg	tcctccgatac	8940
gttgtcagaa	gtaagttggc	cgcagtgtta	tcactcatgg	ttatggcagc	actgcataat	9000
tctcttactg	tcatgccatc	cgtaagatgc	ttttctgtga	ctggtgagta	ctcaaccaag	9060
tcattctgag	aatagtgtat	gcggcgaccg	agttgctctt	gcccggcgtc	aatacgggat	9120
aataccgcgc	cacatagcag	aactttaaaa	gtgctcatca	ttggaaaacg	ttcttcgggg	9180
cgaaaactct	caaggatctt	accgctgttg	agatccagtt	cgatgtaacc	cactcgtgca	9240
cccaactgat	cttcagcatc	ttttactttc	accagcgttt	ctgggtgagc	aaaaacagga	9300
aggcaaaatg	ccgcaaaaaa	gggaataagg	gcgacacgga	aatgttgaat	actcatactc	9360
ttcctttttc	aatattattg	aagcatttat	cagggttatt	gtctcatgtc	cgcgcgtttc	9420
ctgcatcttt	taatcaaadc	ccaagatgtg	tataaaccac	caaactgcca	aaaaatgaaa	9480
actgtcgaca	agctctgtcc	gtttgctggc	aactgcaagg	gtctcaatcc	tatttgtaat	9540
tattgaataa	taaaacaatt	ataaatgtca	aatttgtttt	ttattaacga	tacaaaccaa	9600
acgcaacaag	aacatttgta	gtattatcta	taattgaaaa	cgcgtagtta	taatcgctga	9660
ggtaatatth	aaaatcattt	tcaaattgatt	cacagttaat	ttgcgacaat	ataattttat	9720
tttcacataa	actagacgcc	ttgtcgtctt	cttcttcgta	ttccttctct	ttttcatttt	9780
tctcttcata	aaaattaaca	tagttattat	cgtatccata	tatgtatcta	tcgtatagag	9840
taaatttttt	gttgtcataa	atatatatgt	cttttttaat	ggggtgtata	gtaccgctgc	9900
gcatagttht	tctgtaattt	acaacagtgc	tattttctgg	tagttcttcg	gagtgtgttg	9960
ctttaattat	taaatttata	taatcaatga	atttgggata	gtcgggtttg	tacaatatgt	10020
tgccggcata	gtacgcagct	tcttctagtt	caattacacc	atttttttagc	agcaccggat	10080
taacataact	ttccaaaatg	ttgtacgaac	cgttaaacaa	aaacagttca	cctccctttt	10140
ctatactatt	gtctgcgagc	agttgtttgt	tgttaaaaat	aacagccatt	gtaatgagac	10200
gcacaaacta	atatcacaaa	ctggaaatgt	ctatcaatat	atagttgctc	tagttattaa	10260
tagtaatcaa	ttacggggtc	attagttcat	agcccatata	tggagttccg	cgttacataa	10320
cttacggtaa	atggcccgcc	tggctgaccg	cccaacgacc	cccgccatt	gacgtcaata	10380
atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	attgacgtca	atgggtggac	10440
tatttacggg	aaactgcccc	cttggcagta	catcaagtgt	atcatatgcc	aagtacgccc	10500
cctattgacg	tcaatgacgg	taaatggccc	gcctggcatt	atgccagta	catgacctta	10560
tgggactttc	ctacttgga	gtacatctac	gtattagtca	tcgctattac	catgcatggt	10620

cgaggtgagc	cccacgttct	gcttcactct	ccccatctcc	ccccctccc	cacccccaat	10680
tttgtattta	tttatttttt	aattattttg	tgcagcgatg	ggggcggggg	gggggggggg	10740
gcgcgcgcca	ggcggggcgg	ggcggggcga	ggggcggggc	ggggcgaggc	ggagaggtgc	10800
ggcggcagcc	aatcagagcg	gcgcgctccg	aaagtttcct	tttatggcga	ggcggcggcg	10860
gcggcgggcc	tataaaaagc	gaagcgcgcg	gcggggcg			10897

<210> 6
 <211> 10900
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pTriEx-1-LAMB4(IF1) [human] (dHis)

<400> 6	
ggagtcgctg	cgacgctgcc
ttcgccccgt	gccccgctcc
gccgcccgcct	cgcgccgccc
60	
gccccggctc	tgactgaccg
cgttactccc	acaggtgagc
gggcggggacg	gcccttctcc
120	
ttcgggctgt	aattagcgct
tggtttaatg	acggcttggt
tcttttctgt	ggctgcgtga
180	
aagccttgag	gggctccggg
agggcccttt	gtgcgggggg
agcggctcgg	ggctgtccgc
240	
ggggggacgg	ctgccttcgg
gggggacggg	gcagggcggg
gttcggcttc	tggcgtgtga
300	
ccggcggtc	tagagcctct
gctaaccatg	ttcatgcctt
cttctttttc	ctacagctcc
360	
tgggcaacgt	gctggttatt
gtgctgtctc	atcattttgg
caaagaattg	gatcggaccg
420	
aaattaatac	gactcactat
aggggaattg	tgagcggata
acaattcccc	ggagttaatc
480	
cgggaccttt	aattcaaccc
aacacaatat	attatagtta
aataagaatt	attatcaaat
540	
catttgata	ttaattaaaa
tactatactg	taaattacat
tttatttaca	atcaaaggag
600	
atataccatg	caatttcaac
tgaccctttt	tttgcacctt
gggtggctca	gttactcaaa
660	
agctcaagat	gactgcaaca
ggggtgcctg	tcattcccacc
actggtgatc	tcctggtggg
720	
caggaacacg	cagcttatgg
cttcttctac	ctgtgggctg
agcagagccc	agaaatactg
780	
catcctcagt	tacctggagg
gggaacaaaa	atgcttcatc
tgtgactcta	gatttccata
840	
tgatccgtat	gaccaaccca
acagccacac	cattgagaat
gtcattgtaa	gttttgaacc
900	
agacagagaa	aagaaatggt
ggcaatctga	aaatggtcct
gatcatgtca	gcatcagact
960	
ggacttagag	gcattatttc
ggttcagcca	ccttatcctg
acctttaaga	cttttcggcc
1020	
tgctgcaatg	ttagtgtgaac
gttccacaga	ctatggacac
aactggaaag	tgttcaaata
1080	
ttttgcaaaa	gactgtgcc
cttcctttcc	taacatcaca
tctggccagg	cccagggagt
1140	
gggagacatt	gtttgtgact
ccaaatactc	ggatattgaa
ccctcaacag	gtggagaggt
1200	
gtttttaaaa	gttttggatc
ccagttttga	aattgaaaac
ccttatagcc	cctacatcca
1260	
agaccttggtg	acattgacaa
acctgaggat	aaactttacc
aagctccaca	cccttgggga
1320	
tgctttgctt	ggaaggaggc
aaaatgattc	ccttgataaa
tactactatg	ctctgtacga
1380	
gatgattgtt	cggggaagct
gcttttgcaa	tggccatgct
agcgaatgtc	gccctatgca
1440	

gaagatgcgg	ggagatgttt	tcagccctcc	tggaatgggt	cacggtcagt	gtgtgtgtca	1500
gcacaataca	gatggtccga	actgtgagag	atgcaaggac	ttcttccagg	atgctccttg	1560
gaggccagct	gcagacctcc	aggacaacgc	ttgcagatcg	tgcagctgta	acagccactc	1620
cagccgctgt	cactttgaca	tgactacgta	cctggcaagc	ggtggcctca	gcgggggcgt	1680
gtgtgaagac	tgccagcaca	acactgaggg	gcagcactgc	gaccgctgca	gacccctctt	1740
ctacagggac	ccgctcaaga	ccatctcaga	tccttacgcg	tgcattcctt	gtgaatgtga	1800
ccccgatggg	accatatctg	gtggcatttg	tgtgagccac	tctgatcctg	ccttaggggtc	1860
tgtggctggc	cagtgccttt	gtaaagagaa	cgtggaagga	gccaaatgcg	accagtgcaa	1920
acccaaccac	tatggactaa	gcgccaccga	ccccctgggc	tgccagccct	gcgactgtaa	1980
cccccttggg	agtctgccat	tcttgacctg	tgatgtggat	acaggccaat	gcttgtgcct	2040
gtcatatgtc	accggagcac	actgcgaaga	atgcactggt	ggatactggg	gcctgggaaa	2100
tcattctccat	gggtgttctc	cctgtgactg	tgatattgga	ggtgcttatt	ctaactgtgtg	2160
ctcacccaag	aatgggcagt	gtgaatgccg	cccacatgtc	actggccgta	gctgctctga	2220
accagcccct	ggctacttct	ttgctccttt	gaatttctat	ctctacgagg	cagaggaagc	2280
cacaacactc	caaggactgg	cgcctttggg	ctcggagacg	tttggccaga	gtcctgctgt	2340
tcacgttggt	ttaggagagc	cagttcctgg	gaaccctggt	acatggactg	gacctggatt	2400
tgccaggggt	ctccctgggg	ctggcttgag	atttgctgtc	aacaacattc	cctttcctgt	2460
ggacttcacc	attgccattc	actatgaaac	ccagtctgca	gctgactgga	ctgtccagat	2520
tgtggtgaac	ccccctggag	ggagtgaagc	ctgcataccc	aagactctac	agtcaaagcc	2580
tcagtctttt	gccttaccag	cggctacgag	aatcatgctg	cttcccacac	ccatctgttt	2640
agaaccagat	gtacaatatt	ccatagatgt	ctatttttct	cagcctttgc	aaggagagtc	2700
ccacgctcat	tcacatgtcc	tggtggactc	tcttggcctt	attccccaaa	tcaattcatt	2760
ggagaatttc	tgcaagcagc	aggacttaga	tgagtatcag	cttcacaact	gtgttgaaat	2820
tgctcagca	atgggacctc	aagtgtctcc	gggtgcctgt	gaaaggctga	tcatacagcat	2880
gtctgccaag	ctgcatgatg	gggctgtggc	ctgcaagtgt	cacccccagg	gctcagtcgg	2940
atccagctgc	agccgacttg	gaggccagtg	ccagtgtaaa	cctcttgtgg	tcgggcgctg	3000
ctgtgacagg	tgctcaactg	gaagctatga	tttggggcat	cacggctgtc	acccatgtca	3060
ctgccatcct	caaggatcaa	aggacactgt	atgtgaccaa	gtaacaggac	agtgcccttg	3120
ccatggagag	gtgtctggcc	gccgctgtga	tcgctgcctg	gcaggctact	ttggattttcc	3180
cagctgccac	ccttgccctt	gtaatagggt	tgctgaactt	tgtgatcctg	agacaggggtc	3240
atgcttcaat	tgtggaggct	ttacaactgg	cagaaactgt	gaaagggtga	ttgatggtta	3300
ctatggaaat	ccttcttcag	gacagccctg	tcgtccttgc	ctgtgtccag	atgatccctc	3360
aagcaatcag	tattttgccc	attcctgtta	tcagaatctg	tggagctcag	atgtaatctg	3420
caattgtctt	caaggttata	cgggtactca	gtgtggagaa	tgctctactg	gtttctatgg	3480

aaatccaaga	atttcaggag	caccttgcca	accatgtgcc	tgcaacaaca	acatagatgt	3540
aaccgatcca	gagtcctgca	gccgggtaac	aggggagtg	cttcgatgtt	tgcacaacac	3600
tcagggcgca	aactgccagc	tctgcaaacc	aggtcactat	ggatcagccc	tcaatcagac	3660
ctgcagaaga	tgctcctgcc	atgcttccgg	cgtgagtc	atggagtgtc	cccctggtgg	3720
gggagcttgc	ctctgtgacc	ctgtcactgg	tgcattgtct	tgtctgccga	atgtcacagg	3780
cctggcctgt	gaccgttgtg	ctgatggata	ctggaatctg	gtccctggca	gaggatgtca	3840
gtcatgtgac	tgtgacccta	ggacctctca	aagtagccac	tgtgaccagc	ttacaggcca	3900
gtgtccgtgt	aaattaggtt	acggcgggaa	acgttgacgt	gagtgccagg	aaaattatta	3960
tggtgatcca	cctgggcat	gcattccatg	tgattgtaac	agggcaggta	cccagaagcc	4020
catctgtgat	ccagacacag	gcattgtgcc	ctgccgggag	ggtgtcagcg	gccagagatg	4080
tgatcgctgt	gcccggggac	acagccagga	attccctact	tgtcttcaat	gtcacttgtg	4140
ctttgatcag	tgggaccaca	ccatttcttc	cctctccaaa	gcggtgcaag	ggttaatgag	4200
actggctgct	aacatggaag	ataaaagaga	gaccctgcct	gtctgtgagg	cagacttcaa	4260
agacctcaga	gggaacgtgt	ctgaaataga	aaggattttg	aaacatcctg	ttttcccatc	4320
tgggaaattc	ttaaaagtca	aggattatca	tgactctgtt	agaagacaaa	tcattgcagct	4380
aaatgaacaa	ctgaaagcag	tgtatgaatt	tcaagatctg	aaagatacaa	tagaaagagc	4440
aaagaatgaa	gcagacctct	tacttgaaga	ccttcaggaa	gaaattgatt	tgcaatccag	4500
tgtccttaat	gcaagcattg	cggactcctc	agaaaacatc	aagaaatatt	atcacatatc	4560
atcatctgct	gaaaagaaaa	ttaatgaaac	tagttccacc	attaatacct	ctgcaaatac	4620
aaggaatgac	ttacttacca	tcttagatac	actaacctca	aaaggaaact	tgtcattgga	4680
aagattaaag	cagattaaga	taccagatat	ccaaatattg	aatgaaaagg	tgtgcggaga	4740
tccaggaaat	gtgccatgtg	tgcccttgcc	ctgtggcggt	gctctctgca	cgggccggaa	4800
ggggcacagg	aagtgtaggg	gtcccggctg	tcacggctcc	ctgaccctct	caacgaatgc	4860
cctccaaaaa	gcccaggaag	caaaatccat	tattcgtaat	ttggacaaac	aggttcgtgg	4920
gttgaaaaat	cagatcgaaa	gtataagtga	acaggcagaa	gtctccaaaa	acaatgcctt	4980
acagctgagg	gaaaaactgg	gaaatataag	aaaccaaagt	gactctgaag	aagaaaacat	5040
caatcttttc	atcaaaaaag	tgaaaaactt	tttgttagag	gaaaacgtgc	ctccagaaga	5100
catcgagaag	gttgcgaaat	gtgtgcttga	cattcaccta	ccaattccat	cccaaatctt	5160
aaccgatgaa	cttgtcaaaa	tacagaaaca	tatgcaactc	tgtgaggatt	acaggacaga	5220
tgaaaacagg	ttaaatgaag	aagcagatgg	agcccaaaag	cttttggtga	aggccaaagc	5280
agctgagaaa	gcagcaaata	ttctattaaa	tcttgacaaa	acattgaacc	agttacaaca	5340
agctcaaatc	actcaaggac	gggcaaactc	taccattaca	cagctgactg	ccaatataac	5400
aaaaataaaa	aagaatgtgc	tgagggtga	aaatcaaacc	agggaaatga	agagtgaagt	5460
ggagttagca	aagcagcgat	cagggtgga	ggatggactt	tccctgctgc	agaccaagtt	5520

gcaaaggcat	caagaccacg	ctgtcaatgc	gaaagttcag	gctgaatctg	cccaacacca	5580
ggctgggagt	cttgagaagg	aatttgttga	gctgaaaaaa	caatatgcta	ttctccaacg	5640
taagacaagc	actacaggac	taacaaagga	gacattagga	aaagttaaac	agctaaaaga	5700
tgcggcagaa	aaattggctg	gagatacaga	ggccaagata	agaagaataa	cagatttaga	5760
aaggaaaatc	caagatttga	atctaagtag	acaagcaaaa	gctgatcaac	tgagaatatt	5820
ggaagatcaa	gttgttgcc	ttaaaaatga	aattgttgaa	caagaaaaaa	aatatgctag	5880
gtgctatagc	tagctcgagc	accaccatca	ccatcaccat	cactaagtga	ttaacctcag	5940
gtgcaggctg	cctatcagaa	ggtggtggct	ggtgtggcca	atgccctggc	tcacaaatac	6000
cactgagatc	gatctttttc	cctctgccaa	aaattatggg	gacatcatga	agccccttga	6060
gcatctgact	tctggcta	aaaggaaatt	tattttcatt	gcaatagtgt	gttggaattt	6120
tttgtgtctc	tcactcgaa	ggacatatgg	gagggcaaat	cattttaa	atcagaatga	6180
gtatttggtt	tagagtttgg	caacatatgc	ccatatgtaa	ctagcataac	cccttggggc	6240
ctctaaacgg	gtcttgaggg	gttttttgct	gaaagcatgc	ggaggaaatt	ctccttgaag	6300
tttccctggg	gttcaaagta	aaggagtttg	caccagacgc	acctctgttc	actggtccgg	6360
cgtattaaaa	cacgatacat	tgttattagt	acatttatta	agcgctagat	tctgtgcgtt	6420
gttgatttac	agacaattgt	tgtacgtatt	ttaataattc	attaaattta	taatctttag	6480
ggtggtatgt	tagagcgaaa	atcaa	atgat	tttcagcgtc	tttatatctg	6540
ttaaatcctc	aatagatttg	taaaataggt	ttcgattagt	ttcaaacaag	ggttggtttt	6600
ccgaaccgat	ggctggacta	tcta	atggat	tttcgctcaa	cgccacaaaa	6660
cttgtagcag	caatctagct	ttgtcgatat	tcgtttgtgt	tttgttttgt	aataaaggtt	6720
cgacgtcgtt	caaaatatta	tgcgcttttg	tatttctttc	atcactgtcg	ttagtgtaca	6780
attgactcga	cgtaa	acacg	attagag	cttggacata	tttaacatcg	6840
ctttattagg	ccgattatcg	tcgtcgtccc	aaccctcgtc	gttagaagtt	gcttccgaag	6900
acgattttgc	catagccaca	cgacgcctat	taattgtgtc	ggctaacacg	tccgcgatca	6960
aattttagt	tgagcttttt	ggaattattt	ctgattgcgg	gcgtttttgg	gcgggtttca	7020
atctaactgt	gcccgatttt	aattcagaca	acacgttaga	aagcgatggt	gcaggcggtg	7080
gtaacatttc	agacggcaaa	tctactaatg	gcggcggtgg	tggagctgat	gataaatcta	7140
ccatcggtgg	aggcgaggc	ggggctggcg	gcggaggcg	aggcgagggt	ggtggcggtg	7200
atgcagacgg	cggtttaggc	tcaa	atgtct	ctttaggcaa	cacagtcggc	7260
ttgtactggg	ttcgggcgcc	gtttttggtt	tgaccggtct	gagacgagt	cgattttttt	7320
cgtttcta	agcttccaac	aattgttgtc	tgtcgtctaa	aggtgcagcg	ggttgagggt	7380
ccgtcggcat	tgggtggagcg	ggcggcaatt	cagacatcga	tgggtggtggt	ggtggtggag	7440
gcgctggaat	gttaggcacg	ggagaaggtg	gtggcggcgg	tgccgccggt	ataatttgtt	7500
ctggtttagt	ttgttcgcgc	acgattgtgg	gcaccggcgc	aggcgccgct	ggctgcacaa	7560

cggaaggtcg	tctgcttcga	ggcagcgctt	ggggtggtgg	caattcaata	ttataattgg	7620
aatacaaadc	gtaaaaatct	gctataagca	ttgtaatttc	gctatcgttt	accgtgccga	7680
tatttaacaa	ccgctcaatg	taagcaattg	tattgtaaag	agattgtctc	aagctcgga	7740
cgctgcgctc	ggtcgttcgg	ctgcggcgag	cggtatcagc	tcactcaaag	gcggtataac	7800
ggttatccac	agaatcaggg	gataacgcag	gaaagaacat	gtgagcaaaa	ggccagcaaa	7860
aggccaggaa	ccgtaaaaag	gccgcgttgc	tggcgttttt	ccataggctc	cgccccctg	7920
acgagcatca	caaaaatcga	cgctcaagtc	agaggtggcg	aaacccgaca	ggactataaa	7980
gataaccaggc	gtttccccct	ggaagctccc	tcgtgcgctc	tcctgtttcg	accctgccgc	8040
ttaccggata	cctgtccgcc	tttctccctt	cggaagcgt	ggcgctttct	caatgctcac	8100
gctgtaggta	tctcagttcg	gtgtaggctg	ttcgtccaa	gctgggctgt	gtgcacgaac	8160
ccccggttca	gcccgaaccg	tgcgccttat	ccgtaacta	tcgtcttgag	tccaacccgg	8220
taagacacga	cttatcgcca	ctggcagcag	ccactggtaa	caggattagc	agagcgaggt	8280
atgtaggcgg	tgctacagag	ttcttgaagt	ggtggcctaa	ctacggctac	actagaagga	8340
cagtatttgg	tatctgcgct	ctgctgaagc	cagttacctt	cggaaaaaga	gttggtagct	8400
cttgatccgg	caaacaaacc	accgctggta	gcggtggttt	ttttgtttgc	aagcagcaga	8460
ttacgcgcag	aaaaaaagga	tctcaagaag	atcctttgtt	accaatgctt	aatcagtgag	8520
gcacctatct	cagcgatctg	tctatttctg	tcattccatag	ttgcctgact	ccccgtcgtg	8580
tagataacta	cgatacggga	gggcttacca	tctggcccca	gtgctgcaat	gataaccgca	8640
gaccacgcgt	caccggctcc	agatttatca	gcaataaacc	agccagccgg	aagggccgag	8700
cgcagaagtg	gtcctgcaac	tttatccgcc	tccatccagt	ctattaattg	ttgccgggaa	8760
gctagagtaa	gtagttcgcc	agttaatagt	ttgcgcaacg	ttgttgccat	tgctacaggc	8820
atcgtggtgt	cacgctcgtc	gtttggtatg	gcttcattca	gctccggttc	ccaacgatca	8880
aggcgagtta	catgatcccc	catgttgtgc	aaaaaagcgg	ttagctcctt	cggtcctccg	8940
atcgttgtca	gaagtaagtt	ggccgcagtg	ttatcactca	tggttatggc	agcactgcat	9000
aattctctta	ctgtcatgcc	atccgtaaga	tgcttttctg	tgactggtga	gtactcaacc	9060
aagtcattct	gagaatagt	tatgcggcga	ccgagttgct	cttgcccggc	gtcaatacgg	9120
gataataccg	cgccacatag	cagaacttta	aaagtgtca	tcattggaaa	acgttcttcg	9180
ggcgcaaaac	tctcaaggat	cttaccgctg	ttgagatcca	gttcgatgta	accactcgt	9240
gcaccaact	gatcttcagc	atcttttact	ttcaccagcg	tttctgggtg	agcaaaaaca	9300
ggaaggcaaa	atgccgcaaa	aaagggaata	agggcgacac	ggaaatgttg	aataactcata	9360
ctcttccttt	ttcaatatta	ttgaagcatt	tatcagggtt	attgtctcat	gtccgcgcgt	9420
ttcctgcatc	ttttaatcaa	atcccaagat	gtgtataaac	caccaaactg	ccaaaaaatg	9480
aaaactgtcg	acaagctctg	tccgtttgct	ggcaactgca	agggctctca	tcctatttgt	9540
aattattgaa	taataaaaaca	attataaatg	tcaaatgtgt	tttttattaa	cgatacaaac	9600

```

caaacgcaac aagaacattt gtagtattat ctataattga aaacgcgtag ttataatcgc      9660
tgaggtaata tttaaaatca ttttcaaagc attcacagtt aatttgcgac aatataattt      9720
tattttcaca taaactagac gccttgtcgt cttcttcttc gtattccttc tctttttcat      9780
ttttctcttc ataaaaatta acatagttat tatcgtatcc atatatgtat ctatcgtata      9840
gagtaaattt tttgttgtca taaatatata tgtctttttt aatgggggtgt atagtaccgc      9900
tgcgcatagt ttttctgtaa tttaacaacg tgctattttc tggtagttct tcggagtgtg      9960
ttgctttaat tattaaattt atataatcaa tgaatttggg atcgtcgggt ttgtacaata     10020
tgttgccggc atagtacgca gcttcttcta gttcaattac accatttttt agcagcaccg     10080
gattaacata actttccaaa atgttgtacg aaccgttaaa caaaaacagt tcacctccct     10140
tttctatact attgtctgcg agcagttgtt tgttgttaaa aataacagcc attgtaatga     10200
gacgcacaaa ctaatatcac aaactggaaa tgtctatcaa tatatagttg ctctagttat     10260
taatagtaat caattacggg gtcattagtt catagcccat atatggagtt ccgcggttaca     10320
taacttacgg taaatggccc gcctggctga ccgccaacg acccccgcgc attgacgtca     10380
ataatgacgt atgttcccat agtaacgcca atagggactt tccattgacg tcaatgggtg     10440
gactatttac ggtaaactgc ccacttgcca gtacatcaag tgtatcatat gccaagtacg     10500
ccccctattg acgtcaatga cggtaaattg cccgcctggc attatgcca gtacatgacc     10560
ttatgggact ttcctacttg gcagtacatc tacgtattag tcatcgctat taccatgcat     10620
ggtcgaggtg agccccacgt tctgcttcac tctccccatc tccccccct cccaccccc     10680
aattttgtat ttatttattt ttttaattatt ttgtgcagcg atgggggcg gggggggggg     10740
ggggcgcgcg ccaggcgggg cggggcgggg cgaggggcg ggcggggcg ggcggagagg     10800
tgcggcggca gccaatcaga gcggcgcgct ccgaaagttt ctttttatgg cgaggcgggc     10860
gcggcgggcg ccctataaaa agcgaagcgc gcggcgggcg                               10900

```

```

<210> 7
<211> 1771
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> LAMB4-His

```

```

<400> 7

```

```

Met Gln Phe Gln Leu Thr Leu Phe Leu His Leu Gly Trp Leu Ser Tyr
1           5           10           15

```

```

Ser Lys Ala Gln Asp Asp Cys Asn Arg Gly Ala Cys His Pro Thr Thr
          20           25           30

```

```

Gly Asp Leu Leu Val Gly Arg Asn Thr Gln Leu Met Ala Ser Ser Thr
          35           40           45

```

Cys Gly Leu Ser Arg Ala Gln Lys Tyr Cys Ile Leu Ser Tyr Leu Glu
 50 55 60

Gly Glu Gln Lys Cys Phe Ile Cys Asp Ser Arg Phe Pro Tyr Asp Pro
 65 70 75 80

Tyr Asp Gln Pro Asn Ser His Thr Ile Glu Asn Val Ile Val Ser Phe
 85 90 95

Glu Pro Asp Arg Glu Lys Lys Trp Trp Gln Ser Glu Asn Gly Leu Asp
 100 105 110

His Val Ser Ile Arg Leu Asp Leu Glu Ala Leu Phe Arg Phe Ser His
 115 120 125

Leu Ile Leu Thr Phe Lys Thr Phe Arg Pro Ala Ala Met Leu Val Glu
 130 135 140

Arg Ser Thr Asp Tyr Gly His Asn Trp Lys Val Phe Lys Tyr Phe Ala
 145 150 155 160

Lys Asp Cys Ala Thr Ser Phe Pro Asn Ile Thr Ser Gly Gln Ala Gln
 165 170 175

Gly Val Gly Asp Ile Val Cys Asp Ser Lys Tyr Ser Asp Ile Glu Pro
 180 185 190

Ser Thr Gly Gly Glu Val Val Leu Lys Val Leu Asp Pro Ser Phe Glu
 195 200 205

Ile Glu Asn Pro Tyr Ser Pro Tyr Ile Gln Asp Leu Val Thr Leu Thr
 210 215 220

Asn Leu Arg Ile Asn Phe Thr Lys Leu His Thr Leu Gly Asp Ala Leu
 225 230 235 240

Leu Gly Arg Arg Gln Asn Asp Ser Leu Asp Lys Tyr Tyr Tyr Ala Leu
 245 250 255

Tyr Glu Met Ile Val Arg Gly Ser Cys Phe Cys Asn Gly His Ala Ser
 260 265 270

Glu Cys Arg Pro Met Gln Lys Met Arg Gly Asp Val Phe Ser Pro Pro
 275 280 285

Gly Met Val His Gly Gln Cys Val Cys Gln His Asn Thr Asp Gly Pro
 290 295 300

Asn Cys Glu Arg Cys Lys Asp Phe Phe Gln Asp Ala Pro Trp Arg Pro
 305 310 315 320

Ala Ala Asp Leu Gln Asp Asn Ala Cys Arg Ser Cys Ser Cys Asn Ser
 325 330 335
 His Ser Ser Arg Cys His Phe Asp Met Thr Thr Tyr Leu Ala Ser Gly
 340 345 350
 Gly Leu Ser Gly Gly Val Cys Glu Asp Cys Gln His Asn Thr Glu Gly
 355 360 365
 Gln His Cys Asp Arg Cys Arg Pro Leu Phe Tyr Arg Asp Pro Leu Lys
 370 375 380
 Thr Ile Ser Asp Pro Tyr Ala Cys Ile Pro Cys Glu Cys Asp Pro Asp
 385 390 395 400
 Gly Thr Ile Ser Gly Gly Ile Cys Val Ser His Ser Asp Pro Ala Leu
 405 410 415
 Gly Ser Val Ala Gly Gln Cys Leu Cys Lys Glu Asn Val Glu Gly Ala
 420 425 430
 Lys Cys Asp Gln Cys Lys Pro Asn His Tyr Gly Leu Ser Ala Thr Asp
 435 440 445
 Pro Leu Gly Cys Gln Pro Cys Asp Cys Asn Pro Leu Gly Ser Leu Pro
 450 455 460
 Phe Leu Thr Cys Asp Val Asp Thr Gly Gln Cys Leu Cys Leu Ser Tyr
 465 470 475 480
 Val Thr Gly Ala His Cys Glu Glu Cys Thr Val Gly Tyr Trp Gly Leu
 485 490 495
 Gly Asn His Leu His Gly Cys Ser Pro Cys Asp Cys Asp Ile Gly Gly
 500 505 510
 Ala Tyr Ser Asn Val Cys Ser Pro Lys Asn Gly Gln Cys Glu Cys Arg
 515 520 525
 Pro His Val Thr Gly Arg Ser Cys Ser Glu Pro Ala Pro Gly Tyr Phe
 530 535 540
 Phe Ala Pro Leu Asn Phe Tyr Leu Tyr Glu Ala Glu Glu Ala Thr Thr
 545 550 555 560
 Leu Gln Gly Leu Ala Pro Leu Gly Ser Glu Thr Phe Gly Gln Ser Pro
 565 570 575
 Ala Val His Val Val Leu Gly Glu Pro Val Pro Gly Asn Pro Val Thr
 580 585 590

Trp Thr Gly₅₉₅ Pro Gly Phe Ala Arg₆₀₀ Val Leu Pro Gly₆₀₅ Ala Gly Leu Arg
 Phe Ala₆₁₀ Val Asn Asn Ile Pro₆₁₅ Phe Pro Val Asp Phe₆₂₀ Thr Ile Ala Ile
 His₆₂₅ Tyr Glu Thr Gln Ser₆₃₀ Ala Ala Asp Trp Thr₆₃₅ Val Gln Ile Val₆₄₀
 Asn Pro Pro Gly Gly₆₄₅ Ser Glu His Cys Ile₆₅₀ Pro Lys Thr Leu Gln₆₅₅ Ser
 Lys Pro Gln Ser₆₆₀ Phe Ala Leu Pro Ala₆₆₅ Ala Thr Arg Ile Met₆₇₀ Leu Leu
 Pro Thr Pro₆₇₅ Ile Cys Leu Glu Pro₆₈₀ Asp Val Gln Tyr Ser₆₈₅ Ile Asp Val
 Tyr Phe₆₉₀ Ser Gln Pro Leu Gln₆₉₅ Gly Glu Ser His Ala₇₀₀ His Ser His Val
 Leu Val₇₀₅ Asp Ser Leu Gly₇₁₀ Leu Ile Pro Gln Ile₇₁₅ Asn Ser Leu Glu Asn₇₂₀
 Phe Cys Ser Lys Gln₇₂₅ Asp Leu Asp Glu Tyr₇₃₀ Gln Leu His Asn Cys₇₃₅ Val
 Glu Ile Ala Ser₇₄₀ Ala Met Gly Pro Gln₇₄₅ Val Leu Pro Gly Ala₇₅₀ Cys Glu
 Arg Leu Ile₇₅₅ Ile Ser Met Ser Ala₇₆₀ Lys Leu His Asp Gly₇₆₅ Ala Val Ala
 Cys Lys₇₇₀ Cys His Pro Gln Gly₇₇₅ Ser Val Gly Ser Ser₇₈₀ Cys Ser Arg Leu
 Gly₇₈₅ Gly Gln Cys Gln Cys₇₉₀ Lys Pro Leu Val Val₇₉₅ Gly Arg Cys Cys Asp₈₀₀
 Arg Cys Ser Thr Gly₈₀₅ Ser Tyr Asp Leu Gly₈₁₀ His His Gly Cys His₈₁₅ Pro
 Cys His Cys His₈₂₀ Pro Gln Gly Ser Lys₈₂₅ Asp Thr Val Cys Asp₈₃₀ Gln Val
 Thr Gly Gln₈₃₅ Cys Pro Cys His Gly₈₄₀ Glu Val Ser Gly Arg₈₄₅ Arg Cys Asp
 Arg Cys₈₅₀ Leu Ala Gly Tyr Phe₈₅₅ Gly Phe Pro Ser Cys₈₆₀ His Pro Cys Pro

Cys Asn Arg Phe Ala Glu Leu Cys Asp Pro Glu Thr Gly Ser Cys Phe
 865 870 875 880
 Asn Cys Gly Gly Phe Thr Thr Gly Arg Asn Cys Glu Arg Cys Ile Asp
 885 890 895
 Gly Tyr Tyr Gly Asn Pro Ser Ser Gly Gln Pro Cys Arg Pro Cys Leu
 900 905 910
 Cys Pro Asp Asp Pro Ser Ser Asn Gln Tyr Phe Ala His Ser Cys Tyr
 915 920 925
 Gln Asn Leu Trp Ser Ser Asp Val Ile Cys Asn Cys Leu Gln Gly Tyr
 930 935 940
 Thr Gly Thr Gln Cys Gly Glu Cys Ser Thr Gly Phe Tyr Gly Asn Pro
 945 950 955 960
 Arg Ile Ser Gly Ala Pro Cys Gln Pro Cys Ala Cys Asn Asn Asn Ile
 965 970 975
 Asp Val Thr Asp Pro Glu Ser Cys Ser Arg Val Thr Gly Glu Cys Leu
 980 985 990
 Arg Cys Leu His Asn Thr Gln Gly Ala Asn Cys Gln Leu Cys Lys Pro
 995 1000 1005
 Gly His Tyr Gly Ser Ala Leu Asn Gln Thr Cys Arg Arg Cys Ser
 1010 1015 1020
 Cys His Ala Ser Gly Val Ser Pro Met Glu Cys Pro Pro Gly Gly
 1025 1030 1035
 Gly Ala Cys Leu Cys Asp Pro Val Thr Gly Ala Cys Pro Cys Leu
 1040 1045 1050
 Pro Asn Val Thr Gly Leu Ala Cys Asp Arg Cys Ala Asp Gly Tyr
 1055 1060 1065
 Trp Asn Leu Val Pro Gly Arg Gly Cys Gln Ser Cys Asp Cys Asp
 1070 1075 1080
 Pro Arg Thr Ser Gln Ser Ser His Cys Asp Gln Leu Thr Gly Gln
 1085 1090 1095
 Cys Pro Cys Lys Leu Gly Tyr Gly Gly Lys Arg Cys Ser Glu Cys
 1100 1105 1110
 Gln Glu Asn Tyr Tyr Gly Asp Pro Pro Gly Arg Cys Ile Pro Cys
 1115 1120 1125

Asp	Cys 1130	Asn	Arg	Ala	Gly	Thr 1135	Gln	Lys	Pro	Ile	Cys 1140	Asp	Pro	Asp
Thr	Gly 1145	Met	Cys	Arg	Cys	Arg 1150	Glu	Gly	Val	Ser	Gly 1155	Gln	Arg	Cys
Asp	Arg 1160	Cys	Ala	Arg	Gly	His 1165	Ser	Gln	Glu	Phe	Pro 1170	Thr	Cys	Leu
Gln	Cys 1175	His	Leu	Cys	Phe	Asp 1180	Gln	Trp	Asp	His	Thr 1185	Ile	Ser	Ser
Leu	Ser 1190	Lys	Ala	Val	Gln	Gly 1195	Leu	Met	Arg	Leu	Ala 1200	Ala	Asn	Met
Glu	Asp 1205	Lys	Arg	Glu	Thr	Leu 1210	Pro	Val	Cys	Glu	Ala 1215	Asp	Phe	Lys
Asp	Leu 1220	Arg	Gly	Asn	Val	Ser 1225	Glu	Ile	Glu	Arg	Ile 1230	Leu	Lys	His
Pro	Val 1235	Phe	Pro	Ser	Gly	Lys 1240	Phe	Leu	Lys	Val	Lys 1245	Asp	Tyr	His
Asp	Ser 1250	Val	Arg	Arg	Gln	Ile 1255	Met	Gln	Leu	Asn	Glu 1260	Gln	Leu	Lys
Ala	Val 1265	Tyr	Glu	Phe	Gln	Asp 1270	Leu	Lys	Asp	Thr	Ile 1275	Glu	Arg	Ala
Lys	Asn 1280	Glu	Ala	Asp	Leu	Leu 1285	Leu	Glu	Asp	Leu	Gln 1290	Glu	Glu	Ile
Asp	Leu 1295	Gln	Ser	Ser	Val	Leu 1300	Asn	Ala	Ser	Ile	Ala 1305	Asp	Ser	Ser
Glu	Asn 1310	Ile	Lys	Lys	Tyr	Tyr 1315	His	Ile	Ser	Ser	Ser 1320	Ala	Glu	Lys
Lys	Ile 1325	Asn	Glu	Thr	Ser	Ser 1330	Thr	Ile	Asn	Thr	Ser 1335	Ala	Asn	Thr
Arg	Asn 1340	Asp	Leu	Leu	Thr	Ile 1345	Leu	Asp	Thr	Leu	Thr 1350	Ser	Lys	Gly
Asn	Leu 1355	Ser	Leu	Glu	Arg	Leu 1360	Lys	Gln	Ile	Lys	Ile 1365	Pro	Asp	Ile
Gln	Ile 1370	Leu	Asn	Glu	Lys	Val 1375	Cys	Gly	Asp	Pro	Gly 1380	Asn	Val	Pro

Cys	Val 1385	Pro	Leu	Pro	Cys	Gly 1390	Gly	Ala	Leu	Cys	Thr 1395	Gly	Arg	Lys
Gly	His 1400	Arg	Lys	Cys	Arg	Gly 1405	Pro	Gly	Cys	His	Gly 1410	Ser	Leu	Thr
Leu	Ser 1415	Thr	Asn	Ala	Leu	Gln 1420	Lys	Ala	Gln	Glu	Ala 1425	Lys	Ser	Ile
Ile	Arg 1430	Asn	Leu	Asp	Lys	Gln 1435	Val	Arg	Gly	Leu	Lys 1440	Asn	Gln	Ile
Glu	Ser 1445	Ile	Ser	Glu	Gln	Ala 1450	Glu	Val	Ser	Lys	Asn 1455	Asn	Ala	Leu
Gln	Leu 1460	Arg	Glu	Lys	Leu	Gly 1465	Asn	Ile	Arg	Asn	Gln 1470	Ser	Asp	Ser
Glu	Glu 1475	Glu	Asn	Ile	Asn	Leu 1480	Phe	Ile	Lys	Lys	Val 1485	Lys	Asn	Phe
Leu	Leu 1490	Glu	Glu	Asn	Val	Pro 1495	Pro	Glu	Asp	Ile	Glu 1500	Lys	Val	Ala
Asn	Gly 1505	Val	Leu	Asp	Ile	His 1510	Leu	Pro	Ile	Pro	Ser 1515	Gln	Asn	Leu
Thr	Asp 1520	Glu	Leu	Val	Lys	Ile 1525	Gln	Lys	His	Met	Gln 1530	Leu	Cys	Glu
Asp	Tyr 1535	Arg	Thr	Asp	Glu	Asn 1540	Arg	Leu	Asn	Glu	Glu 1545	Ala	Asp	Gly
Ala	Gln 1550	Lys	Leu	Leu	Val	Lys 1555	Ala	Lys	Ala	Ala	Glu 1560	Lys	Ala	Ala
Asn	Ile 1565	Leu	Leu	Asn	Leu	Asp 1570	Lys	Thr	Leu	Asn	Gln 1575	Leu	Gln	Gln
Ala	Gln 1580	Ile	Thr	Gln	Gly	Arg 1585	Ala	Asn	Ser	Thr	Ile 1590	Thr	Gln	Leu
Thr	Ala 1595	Asn	Ile	Thr	Lys	Ile 1600	Lys	Lys	Asn	Val	Leu 1605	Gln	Ala	Glu
Asn	Gln 1610	Thr	Arg	Glu	Met	Lys 1615	Ser	Glu	Leu	Glu	Leu 1620	Ala	Lys	Gln
Arg	Ser 1625	Gly	Leu	Glu	Asp	Gly 1630	Leu	Ser	Leu	Leu	Gln 1635	Thr	Lys	Leu

Gln Arg His Gln Asp His Ala Val Asn Ala Lys Val Gln Ala Glu
 1640 1645 1650
 Ser Ala Gln His Gln Ala Gly Ser Leu Glu Lys Glu Phe Val Glu
 1655 1660 1665
 Leu Lys Lys Gln Tyr Ala Ile Leu Gln Arg Lys Thr Ser Thr Thr
 1670 1675 1680
 Gly Leu Thr Lys Glu Thr Leu Gly Lys Val Lys Gln Leu Lys Asp
 1685 1690 1695
 Ala Ala Glu Lys Leu Ala Gly Asp Thr Glu Ala Lys Ile Arg Arg
 1700 1705 1710
 Ile Thr Asp Leu Glu Arg Lys Ile Gln Asp Leu Asn Leu Ser Arg
 1715 1720 1725
 Gln Ala Lys Ala Asp Gln Leu Arg Ile Leu Glu Asp Gln Val Val
 1730 1735 1740
 Ala Ile Lys Asn Glu Ile Val Glu Gln Glu Lys Lys Tyr Ala Arg
 1745 1750 1755
 Cys Tyr Ser Leu Glu His His His His His His His
 1760 1765 1770

<210> 8
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Autoantikörper Epitop 1
 <400> 8

Glu Phe Gln Asp Leu
 1 5

<210> 9
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Autoantikörper-Epitop 2
 <400> 9

Ala Asp Leu Leu Leu Glu Asp Leu Gln Glu
 1 5 10

<210> 10
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Autoantikörper-Epitop 3
 <400> 10
 Ala Asp Leu Leu Leu Glu Asp Leu Gln Glu Glu Ile Asp Leu Gln Ser
 1 5 10 15

<210> 11
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Autoantikörper-Epitop 4
 <400> 11

Asp Leu Leu Thr Ile Leu Asp Thr Leu Thr Ser Lys
 1 5 10

<210> 12
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Autoantikörper-Epitop 5
 <400> 12

Gln Ile Lys Ile Pro Asp Ile Gln Ile Leu Asn Glu Lys
 1 5 10

<210> 13
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Autoantikörper-Epitop 6
 <400> 13

Val Arg Gly Leu Lys Asn Gln Ile Glu Ser Ile Ser Glu
 1 5 10

<210> 14
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Autoantikörper-Epitop 7
 <400> 14

Leu Leu Glu Glu Asn Val Pro Pro Glu Asp Ile
 1 5 10

<210> 15
 <211> 300

<212> PRT
<213> Artificial Sequence

<220>
<223> Teilfragment 1

<400> 15

Met Gln Asp Asp Cys Asn Arg Gly Ala Cys His Pro Thr Thr Gly Asp
1 5 10 15

Leu Leu Val Gly Arg Asn Thr Gln Leu Met Ala Ser Ser Thr Cys Gly
20 25 30

Leu Ser Arg Ala Gln Lys Tyr Cys Ile Leu Ser Tyr Leu Glu Gly Glu
35 40 45

Gln Lys Cys Phe Ile Cys Asp Ser Arg Phe Pro Tyr Asp Pro Tyr Asp
50 55 60

Gln Pro Asn Ser His Thr Ile Glu Asn Val Ile Val Ser Phe Glu Pro
65 70 75 80

Asp Arg Glu Lys Lys Trp Trp Gln Ser Glu Asn Gly Leu Asp His Val
85 90 95

Ser Ile Arg Leu Asp Leu Glu Ala Leu Phe Arg Phe Ser His Leu Ile
100 105 110

Leu Thr Phe Lys Thr Phe Arg Pro Ala Ala Met Leu Val Glu Arg Ser
115 120 125

Thr Asp Tyr Gly His Asn Trp Lys Val Phe Lys Tyr Phe Ala Lys Asp
130 135 140

Cys Ala Thr Ser Phe Pro Asn Ile Thr Ser Gly Gln Ala Gln Gly Val
145 150 155 160

Gly Asp Ile Val Cys Asp Ser Lys Tyr Ser Asp Ile Glu Pro Ser Thr
165 170 175

Gly Gly Glu Val Val Leu Lys Val Leu Asp Pro Ser Phe Glu Ile Glu
180 185 190

Asn Pro Tyr Ser Pro Tyr Ile Gln Asp Leu Val Thr Leu Thr Asn Leu
195 200 205

Arg Ile Asn Phe Thr Lys Leu His Thr Leu Gly Asp Ala Leu Leu Gly
210 215 220

Arg Arg Gln Asn Asp Ser Leu Asp Lys Tyr Tyr Tyr Ala Leu Tyr Glu
225 230 235 240

Met Ile Val Arg Gly Ser Cys Phe Cys Asn Gly His Ala Ser Glu Cys
245 250 255

Arg Pro Met Gln Lys Met Arg Gly Asp Val Phe Ser Pro Pro Gly Met
260 265 270

Val His Gly Gln Cys Val Cys Gln His Asn Thr Asp Gly Pro Asn Cys
275 280 285

Glu Arg Cys Lys Asp Phe Phe Gln Asp Ala Pro Trp
290 295 300

<210> 16
<211> 301
<212> PRT
<213> Artificial Sequence

<220>
<223> Teilfragment 2

<400> 16

Met Pro Asn Cys Glu Arg Cys Lys Asp Phe Phe Gln Asp Ala Pro Trp
1 5 10 15

Arg Pro Ala Ala Asp Leu Gln Asp Asn Ala Cys Arg Ser Cys Ser Cys
20 25 30

Asn Ser His Ser Ser Arg Cys His Phe Asp Met Thr Thr Tyr Leu Ala
35 40 45

Ser Gly Gly Leu Ser Gly Gly Val Cys Glu Asp Cys Gln His Asn Thr
50 55 60

Glu Gly Gln His Cys Asp Arg Cys Arg Pro Leu Phe Tyr Arg Asp Pro
65 70 75 80

Leu Lys Thr Ile Ser Asp Pro Tyr Ala Cys Ile Pro Cys Glu Cys Asp
85 90 95

Pro Asp Gly Thr Ile Ser Gly Gly Ile Cys Val Ser His Ser Asp Pro
100 105 110

Ala Leu Gly Ser Val Ala Gly Gln Cys Leu Cys Lys Glu Asn Val Glu
115 120 125

Gly Ala Lys Cys Asp Gln Cys Lys Pro Asn His Tyr Gly Leu Ser Ala
130 135 140

Thr Asp Pro Leu Gly Cys Gln Pro Cys Asp Cys Asn Pro Leu Gly Ser
145 150 155 160

Leu Pro Phe Leu Thr Cys Asp Val Asp Thr Gly Gln Cys Leu Cys Leu
165 170 175

Ser Tyr Val Thr Gly Ala His Cys Glu Glu Cys Thr Val Gly Tyr Trp
180 185 190

Gly Leu Gly Asn His Leu His Gly Cys Ser Pro Cys Asp Cys Asp Ile
195 200 205

Gly Gly Ala Tyr Ser Asn Val Cys Ser Pro Lys Asn Gly Gln Cys Glu
210 215 220

Cys Arg Pro His Val Thr Gly Arg Ser Cys Ser Glu Pro Ala Pro Gly
225 230 235 240

Tyr Phe Phe Ala Pro Leu Asn Phe Tyr Leu Tyr Glu Ala Glu Glu Ala
245 250 255

Thr Thr Leu Gln Gly Leu Ala Pro Leu Gly Ser Glu Thr Phe Gly Gln
260 265 270

Ser Pro Ala Val His Val Val Leu Gly Glu Pro Val Pro Gly Asn Pro
275 280 285

Val Thr Trp Thr Gly Pro Gly Phe Ala Arg Val Leu Trp
290 295 300

<210> 17
<211> 318
<212> PRT
<213> Artificial Sequence

<220>
<223> Teilfragment 3

<400> 17

Met Gly Asn Pro Val Thr Trp Thr Gly Pro Gly Phe Ala Arg Val Leu
1 5 10 15

Pro Gly Ala Gly Leu Arg Phe Ala Val Asn Asn Ile Pro Phe Pro Val
20 25 30

Asp Phe Thr Ile Ala Ile His Tyr Glu Thr Gln Ser Ala Ala Asp Trp
35 40 45

Thr Val Gln Ile Val Val Asn Pro Pro Gly Gly Ser Glu His Cys Ile
50 55 60

Pro Lys Thr Leu Gln Ser Lys Pro Gln Ser Phe Ala Leu Pro Ala Ala
65 70 75 80

Thr Arg Ile Met Leu Leu Pro Thr Pro Ile Cys Leu Glu Pro Asp Val
85 90 95

Gln Tyr Ser Ile Asp Val Tyr Phe Ser Gln Pro Leu Gln Gly Glu Ser
100 105 110

His Ala His Ser His Val Leu Val Asp Ser Leu Gly Leu Ile Pro Gln
115 120 125

Ile Asn Ser Leu Glu Asn Phe Cys Ser Lys Gln Asp Leu Asp Glu Tyr
130 135 140

Gln Leu His Asn Cys Val Glu Ile Ala Ser Ala Met Gly Pro Gln Val
145 150 155 160

Leu Pro Gly Ala Cys Glu Arg Leu Ile Ile Ser Met Ser Ala Lys Leu
165 170 175

His Asp Gly Ala Val Ala Cys Lys Cys His Pro Gln Gly Ser Val Gly
180 185 190

Ser Ser Cys Ser Arg Leu Gly Gly Gln Cys Gln Cys Lys Pro Leu Val
195 200 205

Val Gly Arg Cys Cys Asp Arg Cys Ser Thr Gly Ser Tyr Asp Leu Gly
210 215 220

His His Gly Cys His Pro Cys His Cys His Pro Gln Gly Ser Lys Asp
225 230 235 240

Thr Val Cys Asp Gln Val Thr Gly Gln Cys Pro Cys His Gly Glu Val
245 250 255

Ser Gly Arg Arg Cys Asp Arg Cys Leu Ala Gly Tyr Phe Gly Phe Pro
260 265 270

Ser Cys His Pro Cys Pro Cys Asn Arg Phe Ala Glu Leu Cys Asp Pro
275 280 285

Glu Thr Gly Ser Cys Phe Asn Cys Gly Gly Phe Thr Thr Gly Arg Asn
290 295 300

Cys Glu Arg Cys Ile Asp Gly Tyr Tyr Gly Asn Trp Gly Trp
305 310 315

<210> 18
<211> 286
<212> PRT
<213> Artificial Sequence

<220>
<223> Teilfragment 4

<400> 18

Met Thr Gly Arg Asn Cys Glu Arg Cys Ile Asp Gly Tyr Tyr Gly Asn
1 5 10 15

Pro Ser Ser Gly Gln Pro Cys Arg Pro Cys Leu Cys Pro Asp Asp Pro
 20 25 30
 Ser Ser Asn Gln Tyr Phe Ala His Ser Cys Tyr Gln Asn Leu Trp Ser
 35 40 45
 Ser Asp Val Ile Cys Asn Cys Leu Gln Gly Tyr Thr Gly Thr Gln Cys
 50 55 60
 Gly Glu Cys Ser Thr Gly Phe Tyr Gly Asn Pro Arg Ile Ser Gly Ala
 65 70 75 80
 Pro Cys Gln Pro Cys Ala Cys Asn Asn Asn Ile Asp Val Thr Asp Pro
 85 90 95
 Glu Ser Cys Ser Arg Val Thr Gly Glu Cys Leu Arg Cys Leu His Asn
 100 105 110
 Thr Gln Gly Ala Asn Cys Gln Leu Cys Lys Pro Gly His Tyr Gly Ser
 115 120 125
 Ala Leu Asn Gln Thr Cys Arg Arg Cys Ser Cys His Ala Ser Gly Val
 130 135 140
 Ser Pro Met Glu Cys Pro Pro Gly Gly Gly Ala Cys Leu Cys Asp Pro
 145 150 155 160
 Val Thr Gly Ala Cys Pro Cys Leu Pro Asn Val Thr Gly Leu Ala Cys
 165 170 175
 Asp Arg Cys Ala Asp Gly Tyr Trp Asn Leu Val Pro Gly Arg Gly Cys
 180 185 190
 Gln Ser Cys Asp Cys Asp Pro Arg Thr Ser Gln Ser Ser His Cys Asp
 195 200 205
 Gln Leu Thr Gly Gln Cys Pro Cys Lys Leu Gly Tyr Gly Gly Lys Arg
 210 215 220
 Cys Ser Glu Cys Gln Glu Asn Tyr Tyr Gly Asp Pro Pro Gly Arg Cys
 225 230 235 240
 Ile Pro Cys Asp Cys Asn Arg Ala Gly Thr Gln Lys Pro Ile Cys Asp
 245 250 255
 Pro Asp Thr Gly Met Cys Arg Cys Arg Glu Gly Val Ser Gly Gln Arg
 260 265 270
 Cys Asp Arg Cys Ala Arg Gly His Ser Gln Glu Trp Gly Trp
 275 280 285

<210> 19
 <211> 320
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Teilfragment 5

<400> 19

Met Ser Gly Gln Arg Cys Asp Arg Cys Ala Arg Gly His Ser Gln Glu
 1 5 10 15

Phe Pro Thr Cys Leu Gln Cys His Leu Cys Phe Asp Gln Trp Asp His
 20 25 30

Thr Ile Ser Ser Leu Ser Lys Ala Val Gln Gly Leu Met Arg Leu Ala
 35 40 45

Ala Asn Met Glu Asp Lys Arg Glu Thr Leu Pro Val Cys Glu Ala Asp
 50 55 60

Phe Lys Asp Leu Arg Gly Asn Val Ser Glu Ile Glu Arg Ile Leu Lys
 65 70 75 80

His Pro Val Phe Pro Ser Gly Lys Phe Leu Lys Val Lys Asp Tyr His
 85 90 95

Asp Ser Val Arg Arg Gln Ile Met Gln Leu Asn Glu Gln Leu Lys Ala
 100 105 110

Val Tyr Glu Phe Gln Asp Leu Lys Asp Thr Ile Glu Arg Ala Lys Asn
 115 120 125

Glu Ala Asp Leu Leu Leu Glu Asp Leu Gln Glu Glu Ile Asp Leu Gln
 130 135 140

Ser Ser Val Leu Asn Ala Ser Ile Ala Asp Ser Ser Glu Asn Ile Lys
 145 150 155 160

Lys Tyr Tyr His Ile Ser Ser Ser Ala Glu Lys Lys Ile Asn Glu Thr
 165 170 175

Ser Ser Thr Ile Asn Thr Ser Ala Asn Thr Arg Asn Asp Leu Leu Thr
 180 185 190

Ile Leu Asp Thr Leu Thr Ser Lys Gly Asn Leu Ser Leu Glu Arg Leu
 195 200 205

Lys Gln Ile Lys Ile Pro Asp Ile Gln Ile Leu Asn Glu Lys Val Cys
 210 215 220

Gly Asp Pro Gly Asn Val Pro Cys Val Pro Leu Pro Cys Gly Gly Ala
225 230 235 240

Leu Cys Thr Gly Arg Lys Gly His Arg Lys Cys Arg Gly Pro Gly Cys
245 250 255

His Gly Ser Leu Thr Leu Ser Thr Asn Ala Leu Gln Lys Ala Gln Glu
260 265 270

Ala Lys Ser Ile Ile Arg Asn Leu Asp Lys Gln Val Arg Gly Leu Lys
275 280 285

Asn Gln Ile Glu Ser Ile Ser Glu Gln Ala Glu Val Ser Lys Asn Asn
290 295 300

Ala Leu Gln Leu Arg Glu Lys Leu Gly Asn Ile Trp Gly Trp Gly Trp
305 310 315 320

<210> 20
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> Teilfragment 6

<400> 20

Met Ser Lys Asn Asn Ala Leu Gln Leu Arg Glu Lys Leu Gly Asn Ile
1 5 10 15

Arg Asn Gln Ser Asp Ser Glu Glu Glu Asn Ile Asn Leu Phe Ile Lys
20 25 30

Lys Val Lys Asn Phe Leu Leu Glu Glu Asn Val Pro Pro Glu Asp Ile
35 40 45

Glu Lys Val Ala Asn Gly Val Leu Asp Ile His Leu Pro Ile Pro Ser
50 55 60

Gln Asn Leu Thr Asp Glu Leu Val Lys Ile Gln Lys His Met Gln Leu
65 70 75 80

Cys Glu Asp Tyr Arg Thr Asp Glu Asn Arg Leu Asn Glu Glu Ala Asp
85 90 95

Gly Ala Gln Lys Leu Leu Val Lys Ala Lys Ala Ala Glu Lys Ala Ala
100 105 110

Asn Ile Leu Leu Asn Leu Asp Lys Thr Leu Asn Gln Leu Gln Gln Ala
115 120 125

Gln Ile Thr Gln Gly Arg Ala Asn Ser Thr Ile Thr Gln Leu Thr Ala
130 135 140

Asn Ile Thr Lys Ile Lys Lys Asn Val Leu Gln Ala Glu Asn Gln Thr
145 150 155 160

Arg Glu Met Lys Ser Glu Leu Glu Leu Ala Lys Gln Arg Ser Gly Leu
165 170 175

Glu Asp Gly Leu Ser Leu Leu Gln Thr Lys Leu Gln Arg His Gln Asp
180 185 190

His Ala Val Asn Ala Lys Val Gln Ala Glu Ser Ala Gln His Gln Ala
195 200 205

Gly Ser Leu Glu Lys Glu Phe Val Glu Leu Lys Lys Gln Tyr Ala Ile
210 215 220

Leu Gln Arg Lys Thr Ser Thr Thr Gly Leu Thr Lys Glu Thr Leu Gly
225 230 235 240

Lys Val Lys Gln Leu Lys Asp Ala Ala Glu Lys Leu Ala Gly Asp Thr
245 250 255

Glu Ala Lys Ile Arg Arg Ile Thr Asp Leu Glu Arg Lys Ile Gln Asp
260 265 270

Leu Asn Leu Ser Arg Gln Ala Lys Ala Asp Gln Leu Arg Ile Leu Glu
275 280 285

Asp Gln Val Val Ala Ile Lys Asn Glu Ile Val Glu Gln Glu Lys Lys
290 295 300

Tyr Ala Arg Cys Tyr Ser Trp Gly Trp Gly Trp Gly Trp
305 310 315

<210> 21
<211> 308
<212> PRT
<213> Artificial Sequence

<220>
<223> Teilfragment 1, mit vier Tryptophanen und C-terminalem His-Tag
(AMB4-TF1-4W-His)

<400> 21

Met Gln Asp Asp Cys Asn Arg Gly Ala Cys His Pro Thr Thr Gly Asp
1 5 10 15

Leu Leu Val Gly Arg Asn Thr Gln Leu Met Ala Ser Ser Thr Cys Gly
20 25 30

Leu Ser Arg Ala Gln Lys Tyr Cys Ile Leu Ser Tyr Leu Glu Gly Glu
35 40 45

Gln Lys Cys Phe Ile Cys Asp Ser Arg Phe Pro Tyr Asp Pro Tyr Asp
 50 55 60
 Gln Pro Asn Ser His Thr Ile Glu Asn Val Ile Val Ser Phe Glu Pro
 65 70 75 80
 Asp Arg Glu Lys Lys Trp Trp Gln Ser Glu Asn Gly Leu Asp His Val
 85 90 95
 Ser Ile Arg Leu Asp Leu Glu Ala Leu Phe Arg Phe Ser His Leu Ile
 100 105 110
 Leu Thr Phe Lys Thr Phe Arg Pro Ala Ala Met Leu Val Glu Arg Ser
 115 120 125
 Thr Asp Tyr Gly His Asn Trp Lys Val Phe Lys Tyr Phe Ala Lys Asp
 130 135 140
 Cys Ala Thr Ser Phe Pro Asn Ile Thr Ser Gly Gln Ala Gln Gly Val
 145 150 155 160
 Gly Asp Ile Val Cys Asp Ser Lys Tyr Ser Asp Ile Glu Pro Ser Thr
 165 170 175
 Gly Gly Glu Val Val Leu Lys Val Leu Asp Pro Ser Phe Glu Ile Glu
 180 185 190
 Asn Pro Tyr Ser Pro Tyr Ile Gln Asp Leu Val Thr Leu Thr Asn Leu
 195 200 205
 Arg Ile Asn Phe Thr Lys Leu His Thr Leu Gly Asp Ala Leu Leu Gly
 210 215 220
 Arg Arg Gln Asn Asp Ser Leu Asp Lys Tyr Tyr Tyr Ala Leu Tyr Glu
 225 230 235 240
 Met Ile Val Arg Gly Ser Cys Phe Cys Asn Gly His Ala Ser Glu Cys
 245 250 255
 Arg Pro Met Gln Lys Met Arg Gly Asp Val Phe Ser Pro Pro Gly Met
 260 265 270
 Val His Gly Gln Cys Val Cys Gln His Asn Thr Asp Gly Pro Asn Cys
 275 280 285
 Glu Arg Cys Lys Asp Phe Phe Gln Asp Ala Pro Trp Leu Glu His His
 290 295 300
 His His His His
 305

<210> 22
 <211> 309
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Teilfragment 2, mit vier Tryptophanen und C-terminalem His-Tag
 (LAMB4-TF2-4W-His)

<400> 22

Met Pro Asn Cys Glu Arg Cys Lys Asp Phe Phe Gln Asp Ala Pro Trp
 1 5 10 15

Arg Pro Ala Ala Asp Leu Gln Asp Asn Ala Cys Arg Ser Cys Ser Cys
 20 25 30

Asn Ser His Ser Ser Arg Cys His Phe Asp Met Thr Thr Tyr Leu Ala
 35 40 45

Ser Gly Gly Leu Ser Gly Gly Val Cys Glu Asp Cys Gln His Asn Thr
 50 55 60

Glu Gly Gln His Cys Asp Arg Cys Arg Pro Leu Phe Tyr Arg Asp Pro
 65 70 75 80

Leu Lys Thr Ile Ser Asp Pro Tyr Ala Cys Ile Pro Cys Glu Cys Asp
 85 90 95

Pro Asp Gly Thr Ile Ser Gly Gly Ile Cys Val Ser His Ser Asp Pro
 100 105 110

Ala Leu Gly Ser Val Ala Gly Gln Cys Leu Cys Lys Glu Asn Val Glu
 115 120 125

Gly Ala Lys Cys Asp Gln Cys Lys Pro Asn His Tyr Gly Leu Ser Ala
 130 135 140

Thr Asp Pro Leu Gly Cys Gln Pro Cys Asp Cys Asn Pro Leu Gly Ser
 145 150 155 160

Leu Pro Phe Leu Thr Cys Asp Val Asp Thr Gly Gln Cys Leu Cys Leu
 165 170 175

Ser Tyr Val Thr Gly Ala His Cys Glu Glu Cys Thr Val Gly Tyr Trp
 180 185 190

Gly Leu Gly Asn His Leu His Gly Cys Ser Pro Cys Asp Cys Asp Ile
 195 200 205

Gly Gly Ala Tyr Ser Asn Val Cys Ser Pro Lys Asn Gly Gln Cys Glu
 210 215 220

Cys Arg Pro His Val Thr Gly Arg Ser Cys Ser Glu Pro Ala Pro Gly
225 230 235 240

Tyr Phe Phe Ala Pro Leu Asn Phe Tyr Leu Tyr Glu Ala Glu Glu Ala
245 250 255

Thr Thr Leu Gln Gly Leu Ala Pro Leu Gly Ser Glu Thr Phe Gly Gln
260 265 270

Ser Pro Ala Val His Val Val Leu Gly Glu Pro Val Pro Gly Asn Pro
275 280 285

Val Thr Trp Thr Gly Pro Gly Phe Ala Arg Val Leu Trp Leu Glu His
290 295 300

His His His His His
305

<210> 23
<211> 326
<212> PRT
<213> Artificial Sequence

<220>
<223> Teilfragment 3, mit vier Tryptophanen und C-terminalem His-Tag
(LAMB4-TF3-4W-His)

<400> 23

Met Gly Asn Pro Val Thr Trp Thr Gly Pro Gly Phe Ala Arg Val Leu
1 5 10 15

Pro Gly Ala Gly Leu Arg Phe Ala Val Asn Asn Ile Pro Phe Pro Val
20 25 30

Asp Phe Thr Ile Ala Ile His Tyr Glu Thr Gln Ser Ala Ala Asp Trp
35 40 45

Thr Val Gln Ile Val Val Asn Pro Pro Gly Gly Ser Glu His Cys Ile
50 55 60

Pro Lys Thr Leu Gln Ser Lys Pro Gln Ser Phe Ala Leu Pro Ala Ala
65 70 75 80

Thr Arg Ile Met Leu Leu Pro Thr Pro Ile Cys Leu Glu Pro Asp Val
85 90 95

Gln Tyr Ser Ile Asp Val Tyr Phe Ser Gln Pro Leu Gln Gly Glu Ser
100 105 110

His Ala His Ser His Val Leu Val Asp Ser Leu Gly Leu Ile Pro Gln
115 120 125

Ile Asn Ser Leu Glu Asn Phe Cys Ser Lys Gln Asp Leu Asp Glu Tyr
130 135 140

Gln Leu His Asn Cys Val Glu Ile Ala Ser Ala Met Gly Pro Gln Val
145 150 155 160

Leu Pro Gly Ala Cys Glu Arg Leu Ile Ile Ser Met Ser Ala Lys Leu
165 170 175

His Asp Gly Ala Val Ala Cys Lys Cys His Pro Gln Gly Ser Val Gly
180 185 190

Ser Ser Cys Ser Arg Leu Gly Gly Gln Cys Gln Cys Lys Pro Leu Val
195 200 205

Val Gly Arg Cys Cys Asp Arg Cys Ser Thr Gly Ser Tyr Asp Leu Gly
210 215 220

His His Gly Cys His Pro Cys His Cys His Pro Gln Gly Ser Lys Asp
225 230 235 240

Thr Val Cys Asp Gln Val Thr Gly Gln Cys Pro Cys His Gly Glu Val
245 250 255

Ser Gly Arg Arg Cys Asp Arg Cys Leu Ala Gly Tyr Phe Gly Phe Pro
260 265 270

Ser Cys His Pro Cys Pro Cys Asn Arg Phe Ala Glu Leu Cys Asp Pro
275 280 285

Glu Thr Gly Ser Cys Phe Asn Cys Gly Gly Phe Thr Thr Gly Arg Asn
290 295 300

Cys Glu Arg Cys Ile Asp Gly Tyr Tyr Gly Asn Trp Gly Trp Leu Glu
305 310 315 320

His His His His His His
325

<210> 24

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> Teilfragment 4, mit vier Tryptophanen und C-terminalem His-Tag
(LAMB4-TF4-4W-His)

<400> 24

Met Thr Gly Arg Asn Cys Glu Arg Cys Ile Asp Gly Tyr Tyr Gly Asn
1 5 10 15

Pro Ser Ser Gly Gln Pro Cys Arg Pro Cys Leu Cys Pro Asp Asp Pro
 20 25 30
 Ser Ser Asn Gln Tyr Phe Ala His Ser Cys Tyr Gln Asn Leu Trp Ser
 35 40 45
 Ser Asp Val Ile Cys Asn Cys Leu Gln Gly Tyr Thr Gly Thr Gln Cys
 50 55 60
 Gly Glu Cys Ser Thr Gly Phe Tyr Gly Asn Pro Arg Ile Ser Gly Ala
 65 70 75 80
 Pro Cys Gln Pro Cys Ala Cys Asn Asn Asn Ile Asp Val Thr Asp Pro
 85 90 95
 Glu Ser Cys Ser Arg Val Thr Gly Glu Cys Leu Arg Cys Leu His Asn
 100 105 110
 Thr Gln Gly Ala Asn Cys Gln Leu Cys Lys Pro Gly His Tyr Gly Ser
 115 120 125
 Ala Leu Asn Gln Thr Cys Arg Arg Cys Ser Cys His Ala Ser Gly Val
 130 135 140
 Ser Pro Met Glu Cys Pro Pro Gly Gly Gly Ala Cys Leu Cys Asp Pro
 145 150 155 160
 Val Thr Gly Ala Cys Pro Cys Leu Pro Asn Val Thr Gly Leu Ala Cys
 165 170 175
 Asp Arg Cys Ala Asp Gly Tyr Trp Asn Leu Val Pro Gly Arg Gly Cys
 180 185 190
 Gln Ser Cys Asp Cys Asp Pro Arg Thr Ser Gln Ser Ser His Cys Asp
 195 200 205
 Gln Leu Thr Gly Gln Cys Pro Cys Lys Leu Gly Tyr Gly Gly Lys Arg
 210 215 220
 Cys Ser Glu Cys Gln Glu Asn Tyr Tyr Gly Asp Pro Pro Gly Arg Cys
 225 230 235 240
 Ile Pro Cys Asp Cys Asn Arg Ala Gly Thr Gln Lys Pro Ile Cys Asp
 245 250 255
 Pro Asp Thr Gly Met Cys Arg Cys Arg Glu Gly Val Ser Gly Gln Arg
 260 265 270
 Cys Asp Arg Cys Ala Arg Gly His Ser Gln Glu Trp Gly Trp Leu Glu
 275 280 285

His His His His His His
290

<210> 25
<211> 328
<212> PRT
<213> Artificial Sequence

<220>
<223> Teilfragment 5, mit vier Tryptophanen und C-terminalem His-Tag
(LAMB4-TF5-4W-His)

<400> 25

Met Ser Gly Gln Arg Cys Asp Arg Cys Ala Arg Gly His Ser Gln Glu
1 5 10 15

Phe Pro Thr Cys Leu Gln Cys His Leu Cys Phe Asp Gln Trp Asp His
20 25 30

Thr Ile Ser Ser Leu Ser Lys Ala Val Gln Gly Leu Met Arg Leu Ala
35 40 45

Ala Asn Met Glu Asp Lys Arg Glu Thr Leu Pro Val Cys Glu Ala Asp
50 55 60

Phe Lys Asp Leu Arg Gly Asn Val Ser Glu Ile Glu Arg Ile Leu Lys
65 70 75 80

His Pro Val Phe Pro Ser Gly Lys Phe Leu Lys Val Lys Asp Tyr His
85 90 95

Asp Ser Val Arg Arg Gln Ile Met Gln Leu Asn Glu Gln Leu Lys Ala
100 105 110

Val Tyr Glu Phe Gln Asp Leu Lys Asp Thr Ile Glu Arg Ala Lys Asn
115 120 125

Glu Ala Asp Leu Leu Leu Glu Asp Leu Gln Glu Glu Ile Asp Leu Gln
130 135 140

Ser Ser Val Leu Asn Ala Ser Ile Ala Asp Ser Ser Glu Asn Ile Lys
145 150 155 160

Lys Tyr Tyr His Ile Ser Ser Ser Ala Glu Lys Lys Ile Asn Glu Thr
165 170 175

Ser Ser Thr Ile Asn Thr Ser Ala Asn Thr Arg Asn Asp Leu Leu Thr
180 185 190

Ile Leu Asp Thr Leu Thr Ser Lys Gly Asn Leu Ser Leu Glu Arg Leu
195 200 205

Lys Gln Ile Lys Ile Pro Asp Ile Gln Ile Leu Asn Glu Lys Val Cys
210 215 220

Gly Asp Pro Gly Asn Val Pro Cys Val Pro Leu Pro Cys Gly Gly Ala
225 230 235 240

Leu Cys Thr Gly Arg Lys Gly His Arg Lys Cys Arg Gly Pro Gly Cys
245 250 255

His Gly Ser Leu Thr Leu Ser Thr Asn Ala Leu Gln Lys Ala Gln Glu
260 265 270

Ala Lys Ser Ile Ile Arg Asn Leu Asp Lys Gln Val Arg Gly Leu Lys
275 280 285

Asn Gln Ile Glu Ser Ile Ser Glu Gln Ala Glu Val Ser Lys Asn Asn
290 295 300

Ala Leu Gln Leu Arg Glu Lys Leu Gly Asn Ile Trp Gly Trp Gly Trp
305 310 315 320

Leu Glu His His His His His His
325

<210> 26

<211> 325

<212> PRT

<213> Artificial Sequence

<220>

<223> Teilfragment 6, mit vier Tryptophanen und C-terminalem His-Tag

(LAMB4-TF6-4W-His)

<400> 26

Met Ser Lys Asn Asn Ala Leu Gln Leu Arg Glu Lys Leu Gly Asn Ile
1 5 10 15

Arg Asn Gln Ser Asp Ser Glu Glu Glu Asn Ile Asn Leu Phe Ile Lys
20 25 30

Lys Val Lys Asn Phe Leu Leu Glu Glu Asn Val Pro Pro Glu Asp Ile
35 40 45

Glu Lys Val Ala Asn Gly Val Leu Asp Ile His Leu Pro Ile Pro Ser
50 55 60

Gln Asn Leu Thr Asp Glu Leu Val Lys Ile Gln Lys His Met Gln Leu
65 70 75 80

Cys Glu Asp Tyr Arg Thr Asp Glu Asn Arg Leu Asn Glu Glu Ala Asp
85 90 95

Gly Ala Gln Lys₁₀₀ Leu Leu Val Lys₁₀₅ Ala Lys Ala Ala Glu Lys₁₁₀ Ala Ala

Asn Ile Leu₁₁₅ Leu Asn Leu Asp Lys₁₂₀ Thr Leu Asn Gln Leu₁₂₅ Gln Gln Ala

Gln Ile Thr Gln Gly Arg Ala₁₃₅ Asn Ser Thr Ile Thr₁₄₀ Gln Leu Thr Ala

Asn Ile Thr Lys Ile Lys₁₅₀ Lys Asn Val Leu Gln₁₅₅ Ala Glu Asn Gln Thr₁₆₀

Arg Glu Met Lys Ser₁₆₅ Glu Leu Glu Leu Ala₁₇₀ Lys Gln Arg Ser Gly₁₇₅ Leu

Glu Asp Gly Leu₁₈₀ Ser Leu Leu Gln Thr₁₈₅ Lys Leu Gln Arg His₁₉₀ Gln Asp

His Ala Val₁₉₅ Asn Ala Lys Val Gln₂₀₀ Ala Glu Ser Ala Gln₂₀₅ His Gln Ala

Gly Ser₂₁₀ Leu Glu Lys Glu Phe₂₁₅ Val Glu Leu Lys Lys₂₂₀ Gln Tyr Ala Ile

Leu Gln Arg Lys Thr Ser₂₃₀ Thr Thr Gly Leu Thr₂₃₅ Lys Glu Thr Leu Gly₂₄₀

Lys Val Lys Gln Leu₂₄₅ Lys Asp Ala Ala Glu₂₅₀ Lys Leu Ala Gly Asp₂₅₅ Thr

Glu Ala Lys Ile₂₆₀ Arg Arg Ile Thr Asp₂₆₅ Leu Glu Arg Lys Ile₂₇₀ Gln Asp

Leu Asn Leu₂₇₅ Ser Arg Gln Ala Lys₂₈₀ Ala Asp Gln Leu Arg₂₈₅ Ile Leu Glu

Asp Gln Val Val Ala Ile Lys₂₉₅ Asn Glu Ile Val Glu₃₀₀ Gln Glu Lys Lys

Tyr Ala Arg Cys Tyr Ser₃₁₀ Trp Gly Trp Gly Trp₃₁₅ Gly Trp Leu Glu His₃₂₀

His His His His His₃₂₅

<210> 27
<211> 1761
<212> PRT
<213> Homo sapiens

<400> 27

Met Gln Phe Gln Leu Thr Leu Phe Leu His Leu Gly Trp Leu Ser Tyr

1					5					10					15				
Ser	Lys	Ala	Gln 20	Asp	Asp	Cys	Asn	Arg 25	Gly	Ala	Cys	His	Pro 30	Thr	Thr				
Gly	Asp	Leu 35	Leu	Val	Gly	Arg	Asn 40	Thr	Gln	Leu	Met	Ala 45	Ser	Ser	Thr				
Cys	Gly 50	Leu	Ser	Arg	Ala	Gln 55	Lys	Tyr	Cys	Ile	Leu 60	Ser	Tyr	Leu	Glu				
Gly 65	Glu	Gln	Lys	Cys	Phe 70	Ile	Cys	Asp	Ser	Arg 75	Phe	Pro	Tyr	Asp	Pro 80				
Tyr	Asp	Gln	Pro	Asn 85	Ser	His	Thr	Ile	Glu 90	Asn	Val	Ile	Val	Ser 95	Phe				
Glu	Pro	Asp	Arg 100	Glu	Lys	Lys	Trp	Trp 105	Gln	Ser	Glu	Asn	Gly 110	Leu	Asp				
His	Val	Ser 115	Ile	Arg	Leu	Asp	Leu 120	Glu	Ala	Leu	Phe	Arg 125	Phe	Ser	His				
Leu	Ile 130	Leu	Thr	Phe	Lys	Thr 135	Phe	Arg	Pro	Ala	Ala 140	Met	Leu	Val	Glu				
Arg 145	Ser	Thr	Asp	Tyr	Gly 150	His	Asn	Trp	Lys	Val 155	Phe	Lys	Tyr	Phe	Ala 160				
Lys	Asp	Cys	Ala	Thr 165	Ser	Phe	Pro	Asn	Ile 170	Thr	Ser	Gly	Gln	Ala 175	Gln				
Gly	Val	Gly	Asp 180	Ile	Val	Cys	Asp	Ser 185	Lys	Tyr	Ser	Asp	Ile 190	Glu	Pro				
Ser	Thr	Gly 195	Gly	Glu	Val	Val	Leu 200	Lys	Val	Leu	Asp	Pro 205	Ser	Phe	Glu				
Ile	Glu 210	Asn	Pro	Tyr	Ser	Pro 215	Tyr	Ile	Gln	Asp	Leu 220	Val	Thr	Leu	Thr				
Asn 225	Leu	Arg	Ile	Asn	Phe 230	Thr	Lys	Leu	His	Thr 235	Leu	Gly	Asp	Ala	Leu 240				
Leu	Gly	Arg	Arg	Gln 245	Asn	Asp	Ser	Leu	Asp 250	Lys	Tyr	Tyr	Tyr	Ala 255	Leu				
Tyr	Glu	Met	Ile 260	Val	Arg	Gly	Ser	Cys 265	Phe	Cys	Asn	Gly	His 270	Ala	Ser				
Glu	Cys	Arg	Pro	Met	Gln	Lys	Met	Arg	Gly	Asp	Val	Phe	Ser	Pro	Pro				

275							280						285			
Gly	Met	Val	His	Gly	Gln	Cys	Val	Cys	Gln	His	Asn	Thr	Asp	Gly	Pro	
	290					295					300					
Asn	Cys	Glu	Arg	Cys	Lys	Asp	Phe	Phe	Gln	Asp	Ala	Pro	Trp	Arg	Pro	
305					310					315					320	
Ala	Ala	Asp	Leu	Gln	Asp	Asn	Ala	Cys	Arg	Ser	Cys	Ser	Cys	Asn	Ser	
				325					330					335		
His	Ser	Ser	Arg	Cys	His	Phe	Asp	Met	Thr	Thr	Tyr	Leu	Ala	Ser	Gly	
			340					345					350			
Gly	Leu	Ser	Gly	Gly	Val	Cys	Glu	Asp	Cys	Gln	His	Asn	Thr	Glu	Gly	
		355					360					365				
Gln	His	Cys	Asp	Arg	Cys	Arg	Pro	Leu	Phe	Tyr	Arg	Asp	Pro	Leu	Lys	
	370					375					380					
Thr	Ile	Ser	Asp	Pro	Tyr	Ala	Cys	Ile	Pro	Cys	Glu	Cys	Asp	Pro	Asp	
385					390					395					400	
Gly	Thr	Ile	Ser	Gly	Gly	Ile	Cys	Val	Ser	His	Ser	Asp	Pro	Ala	Leu	
				405					410					415		
Gly	Ser	Val	Ala	Gly	Gln	Cys	Leu	Cys	Lys	Glu	Asn	Val	Glu	Gly	Ala	
			420					425					430			
Lys	Cys	Asp	Gln	Cys	Lys	Pro	Asn	His	Tyr	Gly	Leu	Ser	Ala	Thr	Asp	
		435					440					445				
Pro	Leu	Gly	Cys	Gln	Pro	Cys	Asp	Cys	Asn	Pro	Leu	Gly	Ser	Leu	Pro	
	450					455					460					
Phe	Leu	Thr	Cys	Asp	Val	Asp	Thr	Gly	Gln	Cys	Leu	Cys	Leu	Ser	Tyr	
465					470					475					480	
Val	Thr	Gly	Ala	His	Cys	Glu	Glu	Cys	Thr	Val	Gly	Tyr	Trp	Gly	Leu	
				485					490					495		
Gly	Asn	His	Leu	His	Gly	Cys	Ser	Pro	Cys	Asp	Cys	Asp	Ile	Gly	Gly	
			500					505					510			
Ala	Tyr	Ser	Asn	Val	Cys	Ser	Pro	Lys	Asn	Gly	Gln	Cys	Glu	Cys	Arg	
		515					520					525				
Pro	His	Val	Thr	Gly	Arg	Ser	Cys	Ser	Glu	Pro	Ala	Pro	Gly	Tyr	Phe	
	530					535					540					
Phe	Ala	Pro	Leu	Asn	Phe	Tyr	Leu	Tyr	Glu	Ala	Glu	Glu	Ala	Thr	Thr	

545 550 555 560
 Leu Gln Gly Leu Ala Pro Leu Gly Ser Glu Thr Phe Gly Gln Ser Pro
 565 570 575
 Ala Val His Val Val Leu Gly Glu Pro Val Pro Gly Asn Pro Val Thr
 580 585 590
 Trp Thr Gly Pro Gly Phe Ala Arg Val Leu Pro Gly Ala Gly Leu Arg
 595 600 605
 Phe Ala Val Asn Asn Ile Pro Phe Pro Val Asp Phe Thr Ile Ala Ile
 610 615 620
 His Tyr Glu Thr Gln Ser Ala Ala Asp Trp Thr Val Gln Ile Val Val
 625 630 635 640
 Asn Pro Pro Gly Gly Ser Glu His Cys Ile Pro Lys Thr Leu Gln Ser
 645 650 655
 Lys Pro Gln Ser Phe Ala Leu Pro Ala Ala Thr Arg Ile Met Leu Leu
 660 665
 Pro Thr Pro Ile Cys Leu Glu Pro Asp Val Gln Tyr Ser Ile Asp Val
 675 680 685
 Tyr Phe Ser Gln Pro Leu Gln Gly Glu Ser His Ala His Ser His Val
 690 695 700
 Leu Val Asp Ser Leu Gly Leu Ile Pro Gln Ile Asn Ser Leu Glu Asn
 705 710 715 720
 Phe Cys Ser Lys Gln Asp Leu Asp Glu Tyr Gln Leu His Asn Cys Val
 725 730
 Glu Ile Ala Ser Ala Met Gly Pro Gln Val Leu Pro Gly Ala Cys Glu
 740 745 750
 Arg Leu Ile Ile Ser Met Ser Ala Lys Leu His Asp Gly Ala Val Ala
 755 760 765
 Cys Lys Cys His Pro Gln Gly Ser Val Gly Ser Ser Cys Ser Arg Leu
 770 775 780
 Gly Gly Gln Cys Gln Cys Lys Pro Leu Val Val Gly Arg Cys Cys Asp
 785 790 795 800
 Arg Cys Ser Thr Gly Ser Tyr Asp Leu Gly His His Gly Cys His Pro
 805 810 815
 Cys His Cys His Pro Gln Gly Ser Lys Asp Thr Val Cys Asp Gln Val

1085					1090					1095				
Cys	Pro	Cys	Lys	Leu	Gly	Tyr	Gly	Gly	Lys	Arg	Cys	Ser	Glu	Cys
	1100					1105					1110			
Gln	Glu	Asn	Tyr	Tyr	Gly	Asp	Pro	Pro	Gly	Arg	Cys	Ile	Pro	Cys
	1115					1120					1125			
Asp	Cys	Asn	Arg	Ala	Gly	Thr	Gln	Lys	Pro	Ile	Cys	Asp	Pro	Asp
	1130					1135					1140			
Thr	Gly	Met	Cys	Arg	Cys	Arg	Glu	Gly	Val	Ser	Gly	Gln	Arg	Cys
	1145					1150					1155			
Asp	Arg	Cys	Ala	Arg	Gly	His	Ser	Gln	Glu	Phe	Pro	Thr	Cys	Leu
	1160					1165					1170			
Gln	Cys	His	Leu	Cys	Phe	Asp	Gln	Trp	Asp	His	Thr	Ile	Ser	Ser
	1175					1180					1185			
Leu	Ser	Lys	Ala	Val	Gln	Gly	Leu	Met	Arg	Leu	Ala	Ala	Asn	Met
	1190					1195					1200			
Glu	Asp	Lys	Arg	Glu	Thr	Leu	Pro	Val	Cys	Glu	Ala	Asp	Phe	Lys
	1205					1210					1215			
Asp	Leu	Arg	Gly	Asn	Val	Ser	Glu	Ile	Glu	Arg	Ile	Leu	Lys	His
	1220					1225					1230			
Pro	Val	Phe	Pro	Ser	Gly	Lys	Phe	Leu	Lys	Val	Lys	Asp	Tyr	His
	1235					1240					1245			
Asp	Ser	Val	Arg	Arg	Gln	Ile	Met	Gln	Leu	Asn	Glu	Gln	Leu	Lys
	1250					1255					1260			
Ala	Val	Tyr	Glu	Phe	Gln	Asp	Leu	Lys	Asp	Thr	Ile	Glu	Arg	Ala
	1265					1270					1275			
Lys	Asn	Glu	Ala	Asp	Leu	Leu	Leu	Glu	Asp	Leu	Gln	Glu	Glu	Ile
	1280					1285					1290			
Asp	Leu	Gln	Ser	Ser	Val	Leu	Asn	Ala	Ser	Ile	Ala	Asp	Ser	Ser
	1295					1300					1305			
Glu	Asn	Ile	Lys	Lys	Tyr	Tyr	His	Ile	Ser	Ser	Ser	Ala	Glu	Lys
	1310					1315					1320			
Lys	Ile	Asn	Glu	Thr	Ser	Ser	Thr	Ile	Asn	Thr	Ser	Ala	Asn	Thr
	1325					1330					1335			
Arg	Asn	Asp	Leu	Leu	Thr	Ile	Leu	Asp	Thr	Leu	Thr	Ser	Lys	Gly

1340	1345	1350
Asn Leu Ser Leu Glu Arg Leu Lys Gln Ile Lys Ile Pro Asp Ile 1355 1360 1365		
Gln Ile Leu Asn Glu Lys Val Cys Gly Asp Pro Gly Asn Val Pro 1370 1375 1380		
Cys Val Pro Leu Pro Cys Gly Gly Ala Leu Cys Thr Gly Arg Lys 1385 1390 1395		
Gly His Arg Lys Cys Arg Gly Pro Gly Cys His Gly Ser Leu Thr 1400 1405 1410		
Leu Ser Thr Asn Ala Leu Gln Lys Ala Gln Glu Ala Lys Ser Ile 1415 1420 1425		
Ile Arg Asn Leu Asp Lys Gln Val Arg Gly Leu Lys Asn Gln Ile 1430 1435 1440		
Glu Ser Ile Ser Glu Gln Ala Glu Val Ser Lys Asn Asn Ala Leu 1445 1450 1455		
Gln Leu Arg Glu Lys Leu Gly Asn Ile Arg Asn Gln Ser Asp Ser 1460 1465 1470		
Glu Glu Glu Asn Ile Asn Leu Phe Ile Lys Lys Val Lys Asn Phe 1475 1480 1485		
Leu Leu Glu Glu Asn Val Pro Pro Glu Asp Ile Glu Lys Val Ala 1490 1495 1500		
Asn Gly Val Leu Asp Ile His Leu Pro Ile Pro Ser Gln Asn Leu 1505 1510 1515		
Thr Asp Glu Leu Val Lys Ile Gln Lys His Met Gln Leu Cys Glu 1520 1525 1530		
Asp Tyr Arg Thr Asp Glu Asn Arg Leu Asn Glu Glu Ala Asp Gly 1535 1540 1545		
Ala Gln Lys Leu Leu Val Lys Ala Lys Ala Ala Glu Lys Ala Ala 1550 1555 1560		
Asn Ile Leu Leu Asn Leu Asp Lys Thr Leu Asn Gln Leu Gln Gln 1565 1570 1575		
Ala Gln Ile Thr Gln Gly Arg Ala Asn Ser Thr Ile Thr Gln Leu 1580 1585 1590		
Thr Ala Asn Ile Thr Lys Ile Lys Lys Asn Val Leu Gln Ala Glu		

Glu Glu Lys Trp Gln His Arg Val Val Glu Gln Ile Pro Lys Glu Val
 50 55 60
 Gln Phe Gln Pro Pro Gly Ala Pro Leu Glu Lys Glu Lys Ser Gln Gln
 65 70 75 80
 Cys Tyr Ser Glu Tyr Phe Ser Gln Thr Ser Thr Glu Leu Gln Ile Thr
 85 90 95
 Phe Asp Glu Thr Asn Pro Ile Thr Arg Leu Ser Glu Ile Glu Lys Ile
 100 105 110
 Arg Asp Gln Ala Leu Asn Asn Ser Arg Pro Pro Val Arg Tyr Gln Asp
 115 120 125
 Asn Ala Cys Glu Met Glu Leu Val Lys Val Leu Thr Pro Leu Glu Ile
 130 135 140
 Ala Lys Asn Lys Gln Tyr Asp Met His Thr Glu Val Thr Thr Leu Lys
 145 150 155 160
 Gln Glu Lys Asn Pro Val Pro Ser Ala Glu Glu Trp Met Leu Glu Gly
 165 170 175
 Cys Arg Ala Ser Gly Gly Leu Lys Lys Gly Asp Phe Leu Lys Lys Gly
 180 185 190
 Leu Glu Pro Glu Thr Phe Gln Asn Phe Asp Gly Asp His Ala Cys Ser
 195 200 205
 Val Arg Asp Asp Glu Phe Lys Phe Gln Gly Leu Arg His Thr Val Thr
 210 215 220
 Ala Arg Gln Leu Val Glu Ala Lys Leu Leu Asp Met Arg Thr Ile Glu
 225 230 235 240
 Gln Leu Arg Leu Gly Leu Lys Thr Val Glu Glu Val Gln Lys Thr Leu
 245 250 255
 Asn Lys Phe Leu Thr Lys Ala Thr Ser Ile Ala Gly Leu Tyr Leu Glu
 260 265 270
 Ser Thr Lys Glu Lys Ile Ser Phe Ala Ser Ala Ala Glu Arg Ile Ile
 275 280 285
 Ile Asp Lys Met Val Ala Leu Ala Phe Leu Glu Ala Gln Ala Ala Thr
 290 295 300
 Gly Phe Ile Ile Asp Pro Ile Ser Gly Gln Thr Tyr Ser Val Glu Asp
 305 310 315 320

Ala Val Leu Lys Gly Val Val Asp Pro Glu Phe Arg Ile Arg Leu Leu
 325 330 335
 Glu Ala Glu Lys Ala Ala Val Gly Tyr Ser Tyr Ser Ser Lys Thr Leu
 340 345 350
 Ser Val Phe Gln Ala Met Glu Asn Arg Met Leu Asp Arg Gln Lys Gly
 355 360 365
 Lys His Ile Leu Glu Ala Gln Ile Ala Ser Gly Gly Val Ile Asp Pro
 370 375 380
 Val Arg Gly Ile Arg Val Pro Pro Glu Ile Ala Leu Gln Gln Gly Leu
 385 390 395 400
 Leu Asn Asn Ala Ile Leu Gln Phe Leu His Glu Pro Ser Ser Asn Thr
 405 410 415
 Arg Val Phe Pro Asn Pro Asn Asn Lys Gln Ala Leu Tyr Tyr Ser Glu
 420 425 430
 Leu Leu Arg Met Cys Val Phe Asp Val Glu Ser Gln Cys Phe Leu Phe
 435 440 445
 Pro Phe Gly Glu Arg Asn Ile Ser Asn Leu Asn Val Lys Lys Thr His
 450 455 460
 Arg Ile Ser Val Val Asp Thr Lys Thr Gly Ser Glu Leu Thr Val Tyr
 465 470 475 480
 Glu Ala Phe Gln Arg Asn Leu Ile Glu Lys Ser Ile Tyr Leu Glu Leu
 485 490 495
 Ser Gly Gln Gln Tyr Gln Trp Lys Glu Ala Met Phe Phe Glu Ser Tyr
 500 505 510
 Gly His Ser Ser His Met Leu Thr Asp Thr Lys Thr Gly Leu His Phe
 515 520 525
 Asn Ile Asn Glu Ala Ile Glu Gln Gly Thr Ile Asp Lys Ala Leu Val
 530 535 540
 Lys Lys Tyr Gln Glu Gly Leu Ile Thr Leu Thr Glu Leu Ala Asp Ser
 545 550 555 560
 Leu Leu Ser Arg Leu Val Pro Lys Lys Asp Leu His Ser Pro Val Ala
 565 570 575
 Gly Tyr Trp Leu Thr Ala Ser Gly Glu Arg Ile Ser Val Leu Lys Ala
 580 585 590

Ser Arg Arg Asn Leu Val Asp Arg Ile Thr Ala Leu Arg Cys Leu Glu
595 600 605

Ala Gln Val Ser Thr Gly Gly Ile Ile Asp Pro Leu Thr Gly Lys Lys
610 615 620

Tyr Arg Val Ala Glu Ala Leu His Arg Gly Leu Val Asp Glu Gly Phe
625 630 635 640

Ala Gln Gln Leu Arg Gln Cys Glu Leu Val Ile Thr Gly Ile Gly His
645 650 655

Pro Ile Thr Asn Lys Met Met Ser Val Val Glu Ala Val Asn Ala Asn
660 665 670

Ile Ile Asn Lys Glu Met Gly Ile Arg Cys Leu Glu Phe Gln Tyr Leu
675 680 685

Thr Gly Gly Leu Ile Glu Pro Gln Val His Ser Arg Leu Ser Ile Glu
690 695 700

Glu Ala Leu Gln Val Gly Ile Ile Asp Val Leu Ile Ala Thr Lys Leu
705 710 715 720

Lys Asp Gln Lys Ser Tyr Val Arg Asn Ile Ile Cys Pro Gln Thr Lys
725 730 735

Arg Lys Leu Thr Tyr Lys Glu Ala Leu Glu Lys Ala Asp Phe Asp Phe
740 745 750

His Thr Gly Leu Lys Leu Leu Glu Val Ser Glu Pro Leu Met Thr Gly
755 760 765

Ile Ser Ser Leu Tyr Tyr Ser Ser Leu Leu Glu
770 775

<210> 29
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Gliadin Peptid

<400> 29

Leu Gly Gln Gln Gln Pro Phe Pro Pro Gln Gln Pro Tyr Pro Gln Pro
1 5 10 15

Gln Pro Phe Pro Ser Gln Gln Pro Tyr
20 25

<210> 30

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Gliadin Peptid

<400> 30

Gln Leu Gln Pro Phe Pro Gln Pro Glu Leu Pro Tyr Pro Gln Pro Gln
1 5 10 15

Ser

<210> 31
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Gliadin Peptid

<400> 31

Gln Gln Leu Pro Gln Pro Glu Gln Pro Gln Gln Ser Phe Pro Glu Gln
1 5 10 15

Glu Arg Pro Phe
20