

SEQUENCE LISTING

<110> Pieris AG

<120> Muteins of human lipocalin 2 (Lcn2, hNGAL) with affinity for a given target

<130> SG3149A

<150> US 61/267,098

<151> 2009-12-07

<160> 52

<170> PatentIn version 3.3

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<223> NNK oligomer for positions 36, 40, 41, 49, 52

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gcgtattgga agatcaagag catcaagtcg ctaaagaaga aagggaaca cctactactg	4020
atagtatgcc gccattatta cgacaagcta tcgaattatt tgatcaccaa ggtgcagagc	4080
cagccttctt attcggcctt gaattgatca tatgctgatt agaaaaacaa cttaaattgtg	4140
aaagtgggtc ttaaaagcag cataaccttt ttccgtgatg gtaacttcac tagtttaaaa	4200
ggatctaggt gaagatcctt tttgataatc tcatgaccaa aatcccttaa cgtgagtttt	4260
cgttccactg agcgtcagac cccgtagaaa agatcaaagg atcttcttga gatccttttt	4320
ttctgcgct aatctgctgc ttgcaaaca aaaaaccacc gctaccagcg gtggtttgtt	4380
tgccggatca agagctacca actctttttc cgaaggtaac tggcttcagc agagcgcaga	4440
taccaaatac tgtccttcta gtgtagccgt agttaggcca ccacttcaag aactctgtag	4500
caccgcctac atacctcgct ctgctaattc tgttaccagt ggctgctgcc agtggcgata	4560
agtcgtgtct taccgggttg gactcaagac gatagttacc ggataaggcg cagcggtcgg	4620
gctgaacggg gggttcgtgc acacagccca gcttggagcg aacgacctac accgaactga	4680
gatacctaca gcgtgagcta tgagaaagcg ccacgcttcc cgaagggaga aaggcggaca	4740
ggtatccggt aagcggcagg gtcggaacag gagagcgcac gaggagctt ccagggggaa	4800
acgcctggta tctttatagt cctgtcgggt ttcgccacct ctgacttgag cgtcgatttt	4860
tgtgatgctc gtcagggggg cggagcctat ggaaaaacgc cagcaacgcg gcctttttac	4920
ggttcctggc cttttgctgg ccttttgctc acatgacctg aca	4963

<210> 13
 <211> 907
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> XbaI - HindIII cassette; Start-ATG: Position 43; FN7B8:
 recombinant ED-B domain flanked by adjacent type III FN homology
 repeats encoded as a cassette cloned on pASK75

<400> 13

tctagaaata attttgttta actttaagaa ggagatatac atatgccatt gtctccacca	60
acaaacttgc atctggaggc aaaccctgac actggagtgc tcacagtctc ctgggagagg	120

```

agcaccaccc cagacattac tggttataga attaccacaa cccctacaaa cggccagcag 180
ggaaattctt tggaagaagt ggtccatgct gatcagagct cctgcacttt tgataacctg 240
agtcccggcc tggagtacaa tgtcagtgtt tacactgtca aggatgacaa ggaaagtgtc 300
cctatctctg ataccatcat cccagaagtt ccgcagctga cagatctgtc cttcgttgac 360
atcaccgaca gctccatcgg tctgcgttgg accccgctga attcctccac catcatcggg 420
tatcgtatca ccgttggtgc tgctggtgaa gggatcccgga tctttgaaga cttcgttgac 480
tcctccgttg gttactacac cgttaccggt ctggaacccg ggatcgacta cgacatctcc 540
gttatcacc ctgatcaacgg tggatgaatcc gctccgacca ccttaacca gcagaccgcg 600
gttcctctc cactgacct gcgattcacc aacattgggtc cagacaccat gcgtgtcacc 660
tggggtccac ccccatccat tgatttaacc aacttctctg tgcgttactc acctgtgaaa 720
aatgaggaag atgttgcaga gttgtcaatt tctccttcag acaatgcagt ggtcttaaca 780
aatctctctg ctggtacaga atatgtagtg agtgtctcca gtgtctacga acaacatgag 840
agcacacctc ttagaggaag acagaaaaca ggtagcgctc accatcacca tcaccattaa 900
taagctt 907

```

```

<210> 14
<211> 298
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> MISC_FEATURE
<223> XbaI - HindIII cassette; Start-MET: Position 13; FN7B8:
recombinant ED-B domain flanked by adjacent type III FN homology
repeats encoded as a cassette cloned on pASK75

```

```

<400> 14

```

```

Ser Arg Asn Asn Phe Val Leu Glu Gly Asp Ile His Met Pro Leu Ser
1          5          10          15

```

```

Pro Pro Thr Asn Leu His Leu Glu Ala Asn Pro Asp Thr Gly Val Leu
20          25          30

```

```

Thr Val Ser Trp Glu Arg Ser Thr Thr Pro Asp Ile Thr Gly Tyr Arg
35          40          45

```

```

Ile Thr Thr Thr Pro Thr Asn Gly Gln Gln Gly Asn Ser Leu Glu Glu
50          55          60

```

```

Val Val His Ala Asp Gln Ser Ser Cys Thr Phe Asp Asn Leu Ser Pro
65          70          75          80

```

```

Gly Leu Glu Tyr Asn Val Ser Val Tyr Thr Val Lys Asp Asp Lys Glu
85          90          95

```

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

<210> 15
 <211> 379
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> XbaI - HindIII cassette; Start-ATG; Position 43; ED-B:
 Recombinant ED-B domain alone encoded as a cassette cloned on
 pASK75

<400> 15

tctagaaata attttgttta actttaagaa ggagatatat aaatgcgtgg ttccgaagtt 60

ccgcagctga cagatctgtc cttcgttgac atcaccgaca gctccatcgg tctgcgttgg 120
 accccgctga attcctccac catcatcggg tctcgatatca ccgttggtgc tgctggtgaa 180
 gggatcccga tctttgaaga cttcgttgac tcctccggtg gttactacac cgttaccggt 240
 ctggaacccg ggatcgacta cgacatctcc gttatcacc tgatcaacgg tggatgaatcc 300
 gctccgacca ccttaacca gcagaccgct gggagcgctc accatcacca tcaccattaa 360
 gggagccacc cgcaagctt 379

<210> 16
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> XbaI - HindIII cassette; Start-MET: Position 13; ED-B:
 Recombinant ED-B domain alone encoded as a cassette cloned on
 pASK75

<400> 16

Ser Arg Asn Asn Phe Val Leu Glu Gly Asp Ile Gln Met Arg Gly Ser
 1 5 10 15

Glu Val Pro Gln Leu Thr Asp Leu Ser Phe Val Asp Ile Thr Asp Ser
 20 25 30

Ser Ile Gly Leu Arg Trp Thr Pro Leu Asn Ser Ser Thr Ile Ile Gly
 35 40 45

Tyr Arg Ile Thr Val Val Ala Ala Gly Glu Gly Ile Pro Ile Phe Glu
 50 55 60

Asp Phe Val Asp Ser Ser Val Gly Tyr Tyr Thr Val Thr Gly Leu Glu
 65 70 75 80

Pro Gly Ile Asp Tyr Asp Ile Ser Val Ile Thr Leu Ile Asn Gly Gly
 85 90 95

Glu Ser Ala Pro Thr Thr Leu Thr Gln Gln Thr Ala Gly Ser Ala His
 100 105 110

His His His His His Gly Ser His Pro Gln Ala
 115 120

<210> 17
 <211> 904
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature
 <223> XbaI - HindIII cassette; Start-ATG: Position 43; FN789:
 recombinant Type III FN homology repeats without ED-B encoded as
 a cassette cloned on pASK75

<400> 17

```
tctagaaata attttgttta actttaagaa ggagatatac atatgccatt gtctccacca      60
acaaacttgc atctggaggc aaaccctgac actggagtgct tcacagtctc ctgggagagg    120
agcaccaccc cagacattac tggttataga attaccacaa cccctacaaa cggccagcag    180
ggaaattctt tggaagaagt ggtccatgct gatcagagct cctgcacttt tgataacctg    240
agtcccggcc tggagtacaa tgcagtggt tacactgtca aggatgacaa ggaaagtgtc    300
cctatctctg ataccatcat ccagctggt cctcctccca ctgacctgcg attcaccaac    360
attggtccag acaccatgcg tgcacctgg gctccacccc catccattga tttaaccaac    420
ttcctggtgc gttactcacc tgtgaaaaat gaggaagatg ttgcagagtt gtcaatttct    480
ccttcagaca atgcagtggc cttacaaaat ctctgcctg gtacagaata tgtagtgagt    540
gtctccagtg tctacgaaca acatgagagc acacctctta gaggaagaca gaaaacaggt    600
cttgattccc caactggcat tgacttttct gatattactg ccaactcttt tactgtgcac    660
tggattgctc ctcgagccac catcactggc tacaggatcc gccatcatcc cgagcacttc    720
agtgggagac ctcgagaaga tcgggtgccc cactctcgga attccatcac ctcaccaac    780
ctcactccag gcacagagta tgggtcagc atcggtgctc ttaatggcag agaggaaagt    840
cccttattga ttggccaaca atcaacagtt agcgctcacc atcaccatca ccattaataa    900
gctt                                     904
```

<210> 18
 <211> 297
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> XbaI - HindIII cassette; Start-MET: Position 13; FN789:
 recombinant Type III FN homology repeats without ED-B encoded as
 a cassette cloned on pASK75

<400> 18

Ser Arg Asn Asn Phe Val Leu Glu Gly Asp Ile His Met Pro Leu Ser
 1 5 10 15

Pro Pro Thr Asn Leu His Leu Glu Ala Asn Pro Asp Thr Gly Val Leu
 20 25 30

Thr Val Ser Trp Glu Arg Ser Thr Thr Pro Asp Ile Thr Gly Tyr Arg
 35 40 45

Ile Thr Thr Thr Pro Thr Asn Gly Gln Gln Gly Asn Ser Leu Glu Glu

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

<210> 19
 <211> 534
 <212> DNA
 <213> Artificial

<220>
 <223> N7A: Mutein of hNGAL specific for ED-B of fibronectin
 cloned on pHNGAL98

<400> 19

caggactcca cctcagacct gatcccagcc ccacctctga gcaagggtccc tctgcagcag	60
aacttccagg acaaccaatt ccatgggaaa tggatatgtcg tgggcaaagc cggaatcac	120
gacctgcgtg aggataagga tccgcgtaaa atgcaagcga ccatttacga gttgaaagaa	180
gataaatcat ataacgtcac caatgtgcgt tttgttcaca agaaatgcaa ttaccgtatt	240
tggacctttg tgccggggag ccagccgggc gagtttactt taggcaatat taaaagttgg	300
ccgggcctga catcatgggtt ggtccgcgtc gtgagcacca actacaacca gcatgccatg	360
gtgtttcttca agcgtgtgta ccagaaccgc gagctgtttg agatcacact gtacgggcgc	420
acgaaagaac tgacaaacga gctgaaggaa aattttatcc gcttttccaa atctctgggc	480
ctccctgaaa accacatcgt cttccctgtc ccaatcgacc agtgtatcga cggc	534

<210> 20
 <211> 178
 <212> PRT
 <213> Artificial

<220>
 <223> N7A: Mutein of hNGAL specific for ED-B of fibronectin
 cloned on pHNGAL98

<400> 20

Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val	1 5 10 15
Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe His Gly Lys Trp Tyr	20 25 30
Val Val Gly Lys Ala Gly Asn His Asp Leu Arg Glu Asp Lys Asp Pro	35 40 45
Arg Lys Met Gln Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr	50 55 60
Asn Val Thr Asn Val Arg Phe Val His Lys Lys Cys Asn Tyr Arg Ile	65 70 75 80
Trp Thr Phe Val Pro Gly Ser Gln Pro Gly Glu Phe Thr Leu Gly Asn	85 90 95
Ile Lys Ser Trp Pro Gly Leu Thr Ser Trp Leu Val Arg Val Val Ser	100 105 110

Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys Arg Val Tyr Gln
115 120 125

Asn Arg Glu Leu Phe Glu Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu
130 135 140

Thr Asn Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly
145 150 155 160

Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile
165 170 175

Asp Gly

<210> 21
<211> 534
<212> DNA
<213> Artificial

<220>
<223> N7E: Mutein of hNGAL specific for ED-B of fibronectin
cloned on pHNGAL98

<400> 21
caggactcca cctcagacct gatcccagcc ccacctctga gcaagggtccc tctgcagcag 60
aactttccagg acaaccaatt ccatgggaaa tggatatgtcg tgggcgaggc cggaatatagc 120
ctgctgctg aggataagga tccgcgtaaa atgtacgcga ccattttacga gttgaaagaa 180
gataaatcat ataacgtcac cagcggtgcgt tttcgtagca agaaatgccca ctacctgatt 240
cgtacctttg tgccgggggag ccagccggggc gagttttactt taggcctgat taaaagtaaa 300
ccggggccaca catcattctt ggtccgcggt gtgagcacca actacaacca gcatgccatg 360
gtgtttcttca agaccgtggc acagaaccgc gagtactttt tcatcacact gtacggggcgc 420
acgaaagaac tgacaagcga gctgaaggaa aatttttatcc gctttttcaa atctctgggc 480
ctccctgaaa accacatcgt cttccctgtc ccaatcgacc agtgtatcga cggc 534

<210> 22
<211> 178
<212> PRT
<213> Artificial

<220>
<223> N7E: Mutein of hNGAL specific for ED-B of fibronectin
cloned on pHNGAL98

<400> 22

Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val
1 5 10 15

Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe His Gly Lys Trp Tyr
 20 25 30
 Val Val Gly Glu Ala Gly Asn Ser Leu Leu Arg Glu Asp Lys Asp Pro
 35 40 45
 Arg Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr
 50 55 60
 Asn Val Thr Ser Val Arg Phe Arg Ser Lys Lys Cys His Tyr Leu Ile
 65 70 75 80
 Arg Thr Phe Val Pro Gly Ser Gln Pro Gly Glu Phe Thr Leu Gly Leu
 85 90 95
 Ile Lys Ser Lys Pro Gly His Thr Ser Phe Leu Val Arg Val Val Ser
 100 105 110
 Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys Thr Val Ala Gln
 115 120 125
 Asn Arg Glu Tyr Phe Phe Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu
 130 135 140
 Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly
 145 150 155 160
 Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile
 165 170 175
 Asp Gly

<210> 23
 <211> 534
 <212> DNA
 <213> Artificial

<220>
 <223> N9B: Mutein of hNGAL specific for ED-B of fibronectin
 cloned on pHNGAL98

<400> 23

caggactcca cctcagacct gatcccagcc ccacctctga gcaagggtccc tctgcagcag	60
aacttccagg acaaccaatt ccatgggaaa tggatatgtcg tgggccgtgc cggaaatatg	120
cgtctgcgtg aggataagga tccggcaaaa atggttgcga ccattttacga gttgaaagaa	180
gataaatcat ataacgtcac caaagtgatg tttcaacgta agaaatgcaa atacatgatt	240
aatacctttg tgccgggggag ccagccgggc gagtttactt taggcgcaat taaaagtcct	300
ccggggccta catcaacctt ggtccgcgtc gtgagcacca actacaacca gcatgccatg	360

gtgtttcttca agcacgtgtt ccagaaccgc gagtactttc acatcacact gtacggggcgc 420
acgaaagaac tgacaagcga gctgaaggaa aattttatcc gcttttccaa atctctgggc 480
ctccctgaaa accacatcgt cttccctgtc ccaatcgacc agtgtatcga cggc 534

<210> 24
<211> 178
<212> PRT
<213> Artificial

<220>
<223> N9B: Mutein of hNGAL specific for ED-B of fibronectin
cloned on phNGAL98

<400> 24

Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val
1 5 10 15
Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe His Gly Lys Trp Tyr
20 25 30
Val Val Gly Arg Ala Gly Asn Met Arg Leu Arg Glu Asp Lys Asp Pro
35 40 45
Ala Lys Met Val Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr
50 55 60
Asn Val Thr Lys Val Met Phe Gln Arg Lys Lys Cys Lys Tyr Met Ile
65 70 75 80
Asn Thr Phe Val Pro Gly Ser Gln Pro Gly Glu Phe Thr Leu Gly Ala
85 90 95
Ile Lys Ser Pro Pro Gly Pro Thr Ser Thr Leu Val Arg Val Val Ser
100 105 110
Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys His Val Phe Gln
115 120 125
Asn Arg Glu Tyr Phe His Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu
130 135 140
Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly
145 150 155 160
Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile
165 170 175
Asp Gly

<210> 25
 <211> 534
 <212> DNA
 <213> Artificial

<220>
 <223> N10D: Mutein of hNGAL specific for ED-B of fibronectin
 cloned on pHNGAL98

<400> 25

caggactcca cctcagacct gatcccagcc ccacctctga gcaaggtccc tctgcagcag	60
aacttccagg acaaccaatt ccatgggaaa tggatatgtcg tgggcgcagc cggaataacc	120
tggctgcgtg aggataagga tccgtacaaa atgcaagcga ccatttacga gttgaaagaa	180
gataaatcat ataacgtcac caatgtgctg tttatgagca agaaatgccg ttacatgatt	240
cacacctttg tgccggggag ccagccgggc gagtttactt taggcagcat taaaagttgg	300
ccgggcctga catcatggtt ggtccgcgtc gtgagcacca actacaacca gcatgccatg	360
gtgtttcttca agcgtgtgta ccagaaccgc gagttctttg gaatcacact gtacgggcgc	420
acgaaagaac tgacaagcga gctgaaggaa aattttatcc gcttttccaa atctctgggc	480
ctccctgaaa accacatcgt cttccctgtc ccaatcgacc agtgtatcga cggc	534

<210> 26
 <211> 178
 <212> PRT
 <213> Artificial

<220>
 <223> N10D: Mutein of hNGAL specific for ED-B of fibronectin
 cloned on pHNGAL98

<400> 26

Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val	1 5 10 15
Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe His Gly Lys Trp Tyr	20 25 30
Val Val Gly Ala Ala Gly Asn Thr Trp Leu Arg Glu Asp Lys Asp Pro	35 40 45
Tyr Lys Met Gln Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr	50 55 60
Asn Val Thr Asn Val Leu Phe Met Ser Lys Lys Cys Arg Tyr Met Ile	65 70 75 80
His Thr Phe Val Pro Gly Ser Gln Pro Gly Glu Phe Thr Leu Gly Ser	85 90 95

Ile Lys Ser Trp Pro Gly Leu Thr Ser Trp Leu Val Arg Val Val Ser
100 105 110

Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys Arg Val Tyr Gln
115 120 125

Asn Arg Glu Phe Phe Gly Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu
130 135 140

Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly
145 150 155 160

Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile
165 170 175

Asp Gly

<210> 27
<211> 3745
<212> DNA
<213> Artificial

<220>
<223> Expression vector pHNGAL98 with AmpR encoding wild type Lcn2 with the C-terminal Strep-tagII

<400> 27

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ccatcgaatg gccagatgat taattcctaa tttttgttga cactctatca ttgatagagt      60
tattttacca ctccctatca gtgatagaga aaagtgaaat gaatagttcg acaaaaaatct      120
agataacgag ggcaaaaaat gaaaaagaca gctatcgcgga ttgcagtggc tctggctggc      180
ttcgctaccg tagcgcaggc ccaggactcc acctcagacc tgatcccagc cccacctctg      240
agcaaggtcc ctctgcagca gaacttccag gacaaccaat tccatgggaa gtggtatgtg      300
gtaggtctcg cagggaatgc aattctcaga gaagacaaag acccgcaaaa gatgtatgcc      360
accatctatg agctgaaaga agacaagagc tacaatgtca cctccgtcct gtttaggaaa      420
aagaagtgtg actactggat caggactttt gttccagggt cccagccagg cgagttcacg      480
ctgggcaaca ttaagagtta ccctggatta acgagttacc tcgtccgagt ggtgagcacc      540
aactacaacc agcatgctat ggtgttcttc aagaaagttt ctcaaaacag ggagtacttc      600
aagatcacc cttacgggag aaccaaggag ctgacttcgg aactaaagga gaacttcac      660
```

cgcttctcca aatctctggg cctccctgaa aaccacatcg tcttccctgt cccaatcgac	720
cagtgtatcg acggcagcgc ttggtctcac ccgcagttcg aaaaataata agcttgacct	780
gtgaagtgaa aaatggcgca cattgtgcga catttttttt gtctgccgtt taccgctact	840
gcgtcacgga tctccacgcg ccctgtagcg gcgcattaag cgcggcgggt gtggtgggta	900
cgcgacgcgt gaccgctaca cttgccagcg ccctagcgcc cgctcctttc gctttcttcc	960
cttccctttct cgccacgttc gccggctttc cccgtcaagc tctaaatcgg gggctccctt	1020
tagggttccg atttagtgct ttacggcacc tcgaccccaa aaaacttgat tagggtgatg	1080
gttcacgtag tgggccatcg ccctgataga cggtttttcg ccctttgacg ttggagtcca	1140
cgttctttta tagtggactc ttgttccaaa ctggaacaac actcaaccct atctcgggtct	1200
attcttttga ttataaaggg attttgccga tttcggccta ttgggttaaaa aatgagctga	1260
tttaacaaaa atttaacgcg aattttaaca aaatattaac gtttacaatt tcagggtggca	1320
cttttcgggg aaatgtgcgc ggaaccacct tttgtttatt tttctaaata cattcaaata	1380
tgtatccgct catgagacaa taaccctgat aaatgcttca ataatttga aaaaggaaga	1440
gtatgagtat tcaacatttc cgtgtcgccc ttattccctt ttttgcggca ttttgccttc	1500
ctgtttttgc tcaccagaa acgctgggtga aagtaaaaga tgctgaagat cagttgggtg	1560
cacgagtggg ttacatcgaa ctggatctca acagcggtaa gatccttgag agttttcgcc	1620
ccgaagaacg ttttccaatg atgagcactt ttaaagttct gctatgtggc gcggtattat	1680
cccgtattga cgccgggcaa gagcaactcg gtcgccgat acactattct cagaatgact	1740
tggttgagta ctaccagtc acagaaaagc atcttacgga tggcatgaca gtaagagaat	1800
tatgcagtgc tgccataacc atgagtgata aactgcggc caacttactt ctgacaacga	1860
tcggaggacc gaaggagcta accgcttttt tgcacaacat gggggatcat gtaactcgcc	1920
ttgatcgttg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt gacaccacga	1980

tgctgtagc aatggcaaca acgttgcgca aactattaac tggcgaacta cttactctag	2040
cttcccggca acaattgata gactggatgg aggcggataa agttgcagga ccacttctgc	2100
gctcggccct tccggctggc tggtttattg ctgataaatc tggagccggg gagcgtggct	2160
ctcgcggtat cattgcagca ctggggccag atggtaagcc ctcccgtatc gtagttatct	2220
acacgacggg gagtcaggca actatggatg aacgaaatag acagatcgct gagataggtg	2280
cctcactgat taagcattgg taggaattaa tgatgtctcg tttagataaa agtaaagtga	2340
ttaacagcgc attagagctg cttaatgagg tcggaatcga aggtttaaca acccgtaaac	2400
tcgcccagaa gctaggtgta gagcagccta cattgtattg gcatgtaaaa aataagcggg	2460
ctttgctcga cgccttagcc attgagatgt tagataggca ccatactcac ttttgccctt	2520
tagaagggga aagctggcaa gattttttac gtaataacgc taaaagtttt agatgtgctt	2580
tactaagtca tcgcgatgga gcaaaagtac atttaggtac acggcctaca gaaaaacagt	2640
atgaaactct cgaaaatcaa ttagcctttt tatgccaaaca aggtttttca ctagagaatg	2700
cattatatgc actcagcgca gtggggcatt ttactttagg ttgctgattg gaagatcaag	2760
agcatcaagt cgctaaagaa gaaagggaaa cacctactac tgatagtatg ccgccattat	2820
tacgacaagc tatcgaatta tttgatcacc aaggtgcaga gccagccttc ttattcggcc	2880
ttgaattgat catatgcgga ttagaaaaac aacttaaattg tgaaagtggg tcttaaaagc	2940
agcataacct ttttccgtga tggtaacttc actagtttaa aaggatctag gtgaagatcc	3000
tttttgataa tctcatgacc aaaatccctt aacgtgagtt ttcgttccac tgagcgtcag	3060
accccgtaga aaagatcaaa ggatcttctt gagatccttt ttttctgcgc gtaatctgct	3120
gcttgcaaac aaaaaaacca ccgctaccag cggtggtttg tttgccggat caagagctac	3180
caactctttt tccgaaggta actggcttca gcagagcgca gataccaaat actgtccttc	3240
tagttagacc gtagttaggc caccacttca agaactctgt agcaccgcct acatacctcg	3300
ctctgctaatt cctgttacca gtggctgctg ccagtgccga taagtcgtgt cttaccgggt	3360

tggactcaag acgatagtta ccggataagg cgcagcggtc gggctgaacg gggggttcgt 3420
 gcacacagcc cagcttgag cgaacgacct acaccgaact gagataccta cagcgtgagc 3480
 tatgagaaag cgccacgctt cccgaaggga gaaaggcgga caggtatccg gtaagcggca 3540
 gggtcggaac aggagagcgc acgagggagc ttccaggggg aaacgcctgg tatctttata 3600
 gtcctgtcgg gtttcgccac ctctgacttg agcgtcgatt tttgtgatgc tcgtcagggg 3660
 ggcggagcct atggaaaaac gccagcaacg cggccttttt acggttcctg gccttttgct 3720
 ggccttttgc tcacatgacc cgaca 3745

<210> 28
 <211> 178
 <212> PRT
 <213> Artificial

<220>
 <223> wild type Lcn2 cloned on pHNGAL98 without OmpA signal peptide and Strep-tagII

<400> 28

Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val
 1 5 10 15

Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe His Gly Lys Trp Tyr
 20 25 30

Val Val Gly Leu Ala Gly Asn Ala Ile Leu Arg Glu Asp Lys Asp Pro
 35 40 45

Gln Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr
 50 55 60

Asn Val Thr Ser Val Leu Phe Arg Lys Lys Lys Cys Asp Tyr Trp Ile
 65 70 75 80

Arg Thr Phe Val Pro Gly Ser Gln Pro Gly Glu Phe Thr Leu Gly Asn
 85 90 95

Ile Lys Ser Tyr Pro Gly Leu Thr Ser Tyr Leu Val Arg Val Val Ser
 100 105 110

Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys Lys Val Ser Gln
 115 120 125

Asn Arg Glu Tyr Phe Lys Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu

130 135 140

Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly
 145 150 155 160

Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile
 165 170 175

Asp Gly

<210> 29
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> peptide sequence of A beta 40

<400> 29

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
 1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
 20 25 30

Gly Leu Met Val Gly Gly Val Val
 35 40

<210> 30
 <211> 11
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> peptide sequence of A beta 1-11

<400> 30

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu
 1 5 10

<210> 31
 <211> 12
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> peptide sequence of A beta 16-27

<400> 31

Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn
 1 5 10

<210> 32
 <211> 1182
 <212> DNA
 <213> Artificial

<220>
 <223> XbaI HindIII DNA restriction fragment of pMBP-His. Reading frame starts at position 27 with atg

<220>
 <221> misc_feature
 <222> (34)..(34)
 <223> c can be t

<220>
 <221> misc_feature
 <222> (35)..(35)
 <223> t can be c

<400> 32
 tctagaacca acaaggacca tagcatatga aaactgaaga aggtaaactg gtaatctgga 60
 ttaacggcga taaaggctat aacgggtctcg ctgaagtcgg taagaaattc gagaaagata 120
 ccggaattaa agtcaccgtt gagcatccgg ataaactgga agagaaattc ccacaggttg 180
 cggcaactgg cgatggccct gacattatct tctgggcaca cgaccgcttt ggtggctacg 240
 ctcaatctgg cctgttggct gaaatcacc cggacaaagc gttccaggac aagctgtatc 300
 cgtttacctg ggatgccgta cgttacaacg gcaagctgat tgcttaccg atcgctgttg 360
 aagcgttatc gctgatttat acaaagatc tgctgccgaa cccgccaaaa acctgggaag 420
 agatcccggc gctggataaa gaactgaaag cgaaaggtaa gagcgcgctg atgttcaacc 480
 tgcaagaacc gtacttcacc tggccgctga ttgctgctga cgggggttat gcgttcaagt 540
 atgaaaacgg caagtacgac attaaagacg tgggcgtgga taacgctggc gcgaaagcgg 600
 gtctgacctt cctggttgac ctgattaaaa acaaacacat gaatgcagac accgattact 660
 ccatcgcaga agctgccttt aataaaggcg aaacagcgat gaccatcaac ggcccgtggg 720
 catggtccaa catcgacacc agcaaagtga attatggtgt aacgggtactg ccgaccttca 780
 agggtaacc atccaaaccg ttcgttggcg tgctgagcgc aggtattaac gccgccagtc 840
 cgaacaaaga gctggcgaaa gagttcctcg aaaactatct gctgactgat gaaggtctgg 900
 aagcggttaa taaagacaaa ccgctgggtg ccgtagcgct gaagtcttac gaggaagagt 960
 tggcgaaaga tccacgtatt gccgccacca tggaaaacgc ccagaaaggc gaaatcatgc 1020
 cgaacatccc gcagatgtcc gctttctggt atgccgtgcy tactgcggtg atcaacgccg 1080
 ccagcggctg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt atcaccagg 1140
 gatccctcga gatcaaacat caccaccatc accattaagc tt 1182

```

<210> 33
<211> 1308
<212> DNA
<213> Artificial

<220>
<223> XbaI HindIII DNA restriction fragment pASK75-MBP-Abeta40. Reading
      frame starts at position 27 with atg

<220>
<221> misc_feature
<222> (34)..(34)
<223> c can be t

<220>
<221> misc_feature
<222> (35)..(35)
<223> t can be c

<400> 33

tctagaacca acaaggacca tagcatatga aaactgaaga aggtaaactg gtaatctgga      60
ttaacggcga taaaggctat aacggtctcg ctgaagtcgg taagaaattc gagaaagata      120
ccggaattaa agtcaccgtt gagcatccgg ataaactgga agagaaattc ccacaggttg      180
cggcaactgg cgatggccct gacattatct tctgggcaca cgaccgcttt ggtggctacg      240
ctcaatctgg cctgttggct gaaatcaccc cggacaaagc gttccaggac aagctgtatc      300
cgtttacctg ggatgccgta cgttacaacg gcaagctgat tgcttaccg atcgctgttg      360
aagcgttatc gctgatttat acaaagatc tgctgccgaa cccgccaaaa acctgggaag      420
agatccgggc gctggataaa gaactgaaag cgaaaggtaa gagcgcgctg atgttcaacc      480
tgcaagaacc gtacttcacc tggccgctga ttgctgctga cgggggttat gcgttcaagt      540
atgaaaacgg caagtacgac attaaagacg tgggcgtgga taacgctggc gcgaaagcgg      600
gtctgacctt cctggttgac ctgattaaaa acaaacacat gaatgcagac accgattact      660
ccatcgcaga agctgccttt aataaaggcg aaacagcgat gaccatcaac ggcccgtggg      720
catggtccaa catcgacacc agcaaagtga attatggtgt aacggtactg ccgaccttca      780
agggtcaacc atccaaaccg ttcgttggcg tgctgagcgc aggtattaac gccgccagtc      840
cgaacaaaga gctggcgaaa gagttcctcg aaaactatct gctgactgat gaaggctctgg      900
aagcggttaa taaagacaaa ccgctgggtg ccgtagcgct gaagtcttac gaggaagagt      960
tggcgaaaga tccacgtatt gccgccacca tggaaaacgc ccagaaagggt gaaatcatgc     1020
cgaacatccc gcagatgtcc gctttctggt atgccgtgcg tactgcggtg atcaacgccg     1080
ccagcggtcg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt atcaccaggg     1140
gatcccatca ccaccatcat caccagaact tgtacttcca ggacgctgaa ttccgtcacg     1200
actccggtta cgaagttcac caccagaagc tggttttctt cgctgaagac gttggttcca     1260
acaaagggtg tatcatcggt ctgatggttg gtggtgttgt ttaagctt                    1308

```

<210> 34
 <211> 488
 <212> DNA
 <213> Artificial

<220>
 <223> XbaI HindIII DNA restriction fragment of pASK75-TrxABeta28H6.
 Reading frame starts at position 23 with atg

<400> 34

tctagatact gtggagttat atatgagcga taaaattatt cacctgactg acgacagttt	60
tgacacggat gtactcaaag cggacggggc gatcctcgtc gatttctggg cagagtgggtg	120
cgggtccgggt ggtggtgacg ctgaattccg tcacgactcc ggttacgaag ttcaccacca	180
gaaactgggtg ttcttcgctg aagacgttgg ttccaacaaa ggtggcggtc cgtgcaaaat	240
gatcgccccg attctggatg aaatcgctga cgaatatcag ggcaaaactga ccgttgcaaa	300
actgaacatc gatcaaaacc ctggcactgc gccgaaatat ggcatccgtg gtatcccgac	360
tctgctgctg ttcaaaaacg gtgaagtggc ggcaaccaaa gtgggtgcac tgtctaaagg	420
tcagttgaaa gagttcctcg acgctaacct ggccagcgct caccatcacc atcaccatta	480
ataagctt	488

<210> 35
 <211> 383
 <212> DNA
 <213> Artificial

<220>
 <223> XbaI HindIII DNA restriction fragment of pASK75-TrxH6. Reading
 frame starts at position 23 with atg

<400> 35

tctagatact gtggagttat atatgagcga taaaattatt cacctgactg acgacagttt	60
tgacacggat gtactcaaag cggacggggc gatcctcgtc gatttctggg cagagtgggtg	120
cgggtccgtgc aaaatgatcg ccccgattct ggatgaaatc gctgacgaat atcagggcaa	180
actgaccgtt gcaaaaactga acatcgatca aaaccctggc actgcgccga aatatggcat	240
ccgtgggtatc ccgactctgc tgctgttcaa aaacggtgaa gtggcggcaa ccaaagtggg	300
tgcactgtct aaagggtcagt tgaaagagtt cctcgacgct aacctggcca gcgctcacca	360
tcaccatcac cattaataag ctt	383

<210> 36
 <211> 534
 <212> DNA
 <213> Artificial

<220>
 <223> DNA sequence for the mature protein wt Lcn2 without Strep-tag II.
 Reading frame starts with the first nucleotide of the following
 sequence

<400> 36

caggactcca cctcagacct gatcccagcc ccacctctga gcaagggtccc tctgcagcag	60
aacttccagg acaaccaatt ccatgggaag tggatatgtg taggtctcgc agggaaatgca	120
attctcagag aagacaaaga cccgcaaaag atgtatgcca ccatctatga gctgaaagaa	180
gacaagagct acaatgtcac ctccgtcctg tttaggaaaa agaagtgtga ctactggatc	240
aggacttttg ttccagggtc ccagccaggc gagttcacgc tgggcaacat taagagttac	300
cctggattaa cgagttacct cgtccgagtg gtgagcacca actacaacca gcatgctatg	360
gtgttcttca agaaagtttc tcaaaacagg gagtacttca agatcacccct ctacgggaga	420
accaaggagc tgacttcgga actaaaggag aacttcatcc gcttctccaa atctctgggc	480
ctccctgaaa accacatcgt cttccctgtc ccaatcgacc agtgtatcga cggc	534

<210> 37
 <211> 534
 <212> DNA
 <213> Artificial

<220>
 <223> DNA sequence for the mature protein H1-G1 without Strep-tag II.
 Reading frame starts with the first nucleotide of the following
 sequence

<400> 37

caggactcca cctcagacct gatcccagcc ccacctctga gcaagggtccc tctgcagcag	60
aacttccagg acaaccaatt ccatgggaag tggatatgtg taggttgtgc agggaaatgtg	120
ttgctcagag aagacaaaga cccgcttaag atgtatgcca ccatctatga gctgaaagaa	180
gacaagagct acaatgtcac cagtgtcggg tttgatgata agaagtgttt gtacaagatc	240
cggacttttg ttccagggtc ccagccaggc gagttcacgc tgggcaggat taagagttag	300
cctggaggta cgagttggct cgtccgagtg gtgagcacca actacaacca gcatgctatg	360
gtgttcttca aggaggttgc gcaaaacagg gagacgttca atatcacccct ctacgggaga	420
accaaggagc tgacttcgga actaaaggag aacttcatcc gcttctccaa atctctgggc	480
ctccctgaaa accacatcgt cttccctgtc ccaatcgacc agtgtatcga cggc	534

<210> 38
 <211> 534
 <212> DNA
 <213> Artificial

<220>
 <223> DNA sequence for the mature protein S1-A4 without Strep-tag II.
 Reading frame starts with the first nucleotide of the following
 sequence

<400> 38

caggactcca cctcagacct gatcccagcc ccacctctga gcaagggtccc tctgcagcag	60
aacttccagg acaaccaatt ccatgggaag tggatatgtg taggtgttgc agggaaattat	120

acgctcagag aagacaaaga cccgctgaag atgtatgcca ccatctatga gctgaaagaa 180
gacaagagct acaatgtcac cagtgtcggg tttaggttga agaagtgtaa ttacaagatc 240
cggacttttg ttccagggtc ccagccaggc gagttcacgc tgggcattat taagagtcag 300
cctggaatga cgagttatct cgtccgagtg gtgagcacca actacaacca gcatgctatg 360
gtgttcttca agacggttgg gcaaaacagg gagatgttca atatcacct ctacgggaga 420
accaaggagc tgacttcgga actaaaggag aacttcatcc gcttctccaa atctctgggc 480
ctccctgaaa accacatcgt cttccctgtc ccaatcgacc agtgtatcga cggc 534

<210> 39
<211> 178
<212> PRT
<213> Artificial

<220>
<223> S1-A4 (Abeta)

<400> 39

Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val
1 5 10 15

Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe His Gly Lys Trp Tyr
20 25 30

Val Val Gly Val Ala Gly Asn Tyr Thr Leu Arg Glu Asp Lys Asp Pro
35 40 45

Leu Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr
50 55 60

Asn Val Thr Ser Val Gly Phe Arg Leu Lys Lys Cys Asn Tyr Lys Ile
65 70 75 80

Arg Thr Phe Val Pro Gly Ser Gln Pro Gly Glu Phe Thr Leu Gly Ile
85 90 95

Ile Lys Ser Gln Pro Gly Met Thr Ser Tyr Leu Val Arg Val Val Ser
100 105 110

Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys Thr Val Gly Gln
115 120 125

Asn Arg Glu Met Phe Asn Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu
130 135 140

Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly
145 150 155 160

Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile
165 170 175

Asp Gly

<210> 40
<211> 534
<212> DNA
<213> Artificial

<220>
<223> DNA sequence for the mature protein US7 without Strep-tag II.
Reading frame starts with the first nucleotide of the following
sequence

<400> 40

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caggactcca cctcagacct gatcccagcc ccacctctga gcaaggtccc tctgcagcag      60
aacttccagg acaaccaatt ccatgggaag tggatatgtg taggtgttgc agggaataag     120
tctctcagag aagacaaaga cccgtggaag atgtatgccca ccatctatga gctgaaagaa     180
gacaagagct acaatgtcac ctcggtcggg tttgggacta agaagtgta ttacaagatc     240
aggacttttg ttccaggttc ccagccaggc gagttcacgc tgggcaggat taagagtcgg     300
cctggaagga cgagtgtctt cgtccgagtg gtgagcacca actacaacca gcatgctatg     360
gtgtttcttca aggtggttca gcaaaacagg gagtcgttca atatcaccct ctacgggaga     420
accaaggagc tgacttcgga actaaaggag aacttcatcc gcttctccaa atctctgggc     480
ctccctgaaa accacatcgt cttccctgtc ccaatcgacc agtgtatcga cggc          534
```

<210> 41
<211> 178
<212> PRT
<213> Artificial

<220>
<223> US7 (Abeta)

<400> 41

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Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val
1          5          10          15

Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe His Gly Lys Trp Tyr
20          25          30

Val Val Gly Val Ala Gly Asn Lys Ser Leu Arg Glu Asp Lys Asp Pro
35          40          45

Trp Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr
50          55          60

Asn Val Thr Ser Val Gly Phe Gly Thr Lys Lys Cys His Tyr Lys Ile
65          70          75          80
```

Arg Thr Phe Val Pro Gly Ser Gln Pro Gly Glu Phe Thr Leu Gly Arg
85 90 95

Ile Lys Ser Arg Pro Gly Arg Thr Ser Ala Leu Val Arg Val Val Ser
100 105 110

Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys Val Val Gln Gln
115 120 125

Asn Arg Glu Ser Phe Asn Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu
130 135 140

Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly
145 150 155 160

Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile
165 170 175

Asp Gly

<210> 42
<211> 805
<212> DNA
<213> Artificial

<220>
<223> XbaI/HindIII restriction fragment of pHNGAL124, which encodes wild type Lcn2 as fusion with the albumin-binding domain cloned on pASK75. Reading frame starts at position 22 with atg

<400> 42

tctagataac gagggcaaaa aatgaaaaag acagctatcg cgattgcagt ggctctggct	60
ggcttcgcta ccgtagcgca ggcccaggac tccacctcag acctgatccc agccccacct	120
ctgagcaagg tccctctgca gcagaacttc caggacaacc aattccatgg gaagtgggtat	180
gtggtaggtc tcgcagggaa tgcaattctc agagaagaca aagacccgca aaagatgtat	240
gccaccatct atgagctgaa agaagacaag agctacaatg tcacctccgt cctgttttagg	300
aaaaagaagt gtgactactg gatcaggact tttgttccag gttcccagcc aggcgagttc	360
acgctgggca acattaagag ttaccctgga ttaacgagtt acctcgtccg agtggtgagc	420
accaactaca accagcatgc tatggtgttc ttcaagaaag tttctcaaaa caggaggtac	480
ttcaagatca ccctctacgg gagaaccaag gagctgactt cggaactaaa ggagaacttc	540
atccgcttct ccaaattctt gggcctccct gaaaaccaca tcgtcttccc tgtcccaatc	600
gaccagtgta tcgacggcag cgcttggtcc caccgcgagt tcgaaaaata ggcccacctg	660
gctgaagcta aagttctggc taaccgtgaa ctggacaaat acggtgtttc cgactactac	720
aaaaacctca tcaacaacgc taaaaccgtt gaaggtgtta aagctctgat cgacgaaatt	780
ctcgcagcac tgccgtaata agctt	805

<210> 43
 <211> 178
 <212> PRT
 <213> Artificial

<220>
 <223> H1-G1 (Abeta)

<400> 43

Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val
 1 5 10 15

Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe His Gly Lys Trp Tyr
 20 25 30

Val Val Gly Cys Ala Gly Asn Val Leu Leu Arg Glu Asp Lys Asp Pro
 35 40 45

Leu Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr
 50 55 60

Asn Val Thr Ser Val Gly Phe Asp Asp Lys Lys Cys Leu Tyr Lys Ile
 65 70 75 80

Arg Thr Phe Val Pro Gly Ser Gln Pro Gly Glu Phe Thr Leu Gly Arg
 85 90 95

Ile Lys Ser Glu Pro Gly Gly Thr Ser Trp Leu Val Arg Val Val Ser
 100 105 110

Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys Glu Val Ala Gln
 115 120 125

Asn Arg Glu Thr Phe Asn Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu
 130 135 140

Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly
 145 150 155 160

Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile
 165 170 175

Asp Gly

<210> 44
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> wt Lcn2

<400> 44

Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val
1 5 10 15

Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe His Gly Lys Trp Tyr
20 25 30

Val Val Gly Leu Ala Gly Asn Ala Ile Leu Arg Glu Asp Lys Asp Pro
35 40 45

Gln Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr
50 55 60

Asn Val Thr Ser Val Leu Phe Arg Lys Lys Lys Cys Asp Tyr Trp Ile
65 70 75 80

Arg Thr Phe Val Pro Gly Ser Gln Pro Gly Glu Phe Thr Leu Gly Asn
85 90 95

Ile Lys Ser Tyr Pro Gly Leu Thr Ser Tyr Leu Val Arg Val Val Ser
100 105 110

Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys Lys Val Ser Gln
115 120 125

Asn Arg Glu Tyr Phe Lys Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu
130 135 140

Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly
145 150 155 160

Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile
165 170 175

Asp Gly

<210> 45

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 45

cccaggactc cacctcagac c

21

<210> 46

<211> 27
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer

 <400> 46
 actgcggggtg ggaccaagcg ctgccgt 27

<210> 47
 <211> 58
 <212> DNA
 <213> Artificial

 <220>
 <223> degenerate oligonucleotide DH-4

<220>
 <221> misc_feature
 <222> (39)..(39)
 <223> y i s c o r t

<400> 47
 ggacaaccaa ttccatggga agtggtatgt ggtaggtgyt gcagggaatg tgttgctc 58

<210> 48
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer J08rev

<400> 48
 gctgccgtcg atacactg 18

<210> 49
 <211> 534
 <212> DNA
 <213> Artificial

<220>
 <223> DNA sequence for the mature protein H1GA without Strep-tag II.
 Reading frame starts with the first nucleotide of the following
 sequence

<400> 49
 caggactcca cctcagacct gatcccagcc ccacctctga gcaagggtccc tctgcagcag 60
 aacttccagg acaaccaatt ccatgggaag tggatatgtg taggtgctgc agggaaatgtg 120
 ttgctcagag aagacaaaga cccgcttaag atgtatgccca ccatctatga gctgaaagaa 180
 gacaagagct acaatgtcac cagtgtcggg tttgatgata agaagtgttt gtacaagatc 240
 cggacttttg ttccagggttc ccagccaggc gagttcacgc tgggcaggat taagagttag 300

cctggaggta cgagttggct cgtccgagtg gtgagcacca actacaacca gcatgctatg 360
 gtgtttcttca aggaggttgc gcaaaacagg gagacgttca atatcacct ctacggggaga 420
 accaaggagc tgacttcgga actaaaggag aacttcatcc gcttctccaa atctctgggc 480
 ctccctgaaa accacatcgt cttccctgtc ccaatcgacc agtgtatcga cggc 534

<210> 50
 <211> 178
 <212> PRT
 <213> Artificial

<220>
 <223> H1GA (Abeta)
 <400> 50

Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val
 1 5 10 15
 Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe His Gly Lys Trp Tyr
 20 25 30
 Val Val Gly Ala Ala Gly Asn Val Leu Leu Arg Glu Asp Lys Asp Pro
 35 40 45
 Leu Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr
 50 55 60
 Asn Val Thr Ser Val Gly Phe Asp Asp Lys Lys Cys Leu Tyr Lys Ile
 65 70 75 80
 Arg Thr Phe Val Pro Gly Ser Gln Pro Gly Glu Phe Thr Leu Gly Arg
 85 90 95
 Ile Lys Ser Glu Pro Gly Gly Thr Ser Trp Leu Val Arg Val Val Ser
 100 105 110
 Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys Glu Val Ala Gln
 115 120 125
 Asn Arg Glu Thr Phe Asn Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu
 130 135 140
 Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly
 145 150 155 160
 Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile
 165 170 175
 Asp Gly

<210> 51
 <211> 534
 <212> DNA
 <213> Artificial

 <220>
 <223> DNA sequence for the mature protein H1GV without Strep-tag II.
 Reading frame starts with the first nucleotide of the following
 sequence

 <400> 51
 caggactcca cctcagacct gatcccagcc ccacctctga gcaagggtccc tctgcagcag 60
 aacttccagg acaaccaatt ccatgggaag tggatatgtg taggtgttgc agggaatgtg 120
 ttgctcagag aagacaaaga cccgcttaag atgtatgcca ccatctatga gctgaaagaa 180
 gacaagagct acaatgtcac cagtgtcggg ttgatgata agaagtgttt gtacaagatc 240
 cggacttttg ttccagggtc ccagccaggc gagttcacgc tgggcaggat taagagtgag 300
 cctggaggta cgagttggct cgtccgagtg gtgagcacca actacaacca gcatgctatg 360
 gtgttcttca aggaggttgc gcaaaacagg gagacgttca atatcaccct ctacgggaga 420
 accaaggagc tgacttcgga actaaaggag aacttcatcc gcttctccaa atctctgggc 480
 ctccctgaaa accacatcgt cttccctgtc ccaatcgacc agtgtatcga cggc 534

<210> 52
 <211> 178
 <212> PRT
 <213> Artificial

 <220>
 <223> H1GV (A beta)

 <400> 52
 Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val
 1 5 10 15

 Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe His Gly Lys Trp Tyr
 20 25 30

 Val Val Gly Val Ala Gly Asn Val Leu Leu Arg Glu Asp Lys Asp Pro
 35 40 45

 Leu Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr
 50 55 60

 Asn Val Thr Ser Val Gly Phe Asp Asp Lys Lys Cys Leu Tyr Lys Ile
 65 70 75 80

 Arg Thr Phe Val Pro Gly Ser Gln Pro Gly Glu Phe Thr Leu Gly Arg
 85 90 95

 Ile Lys Ser Glu Pro Gly Gly Thr Ser Trp Leu Val Arg Val Val Ser
 100 105 110

Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys Glu Val Ala Gln
115 120 125

Asn Arg Glu Thr Phe Asn Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu
130 135 140

Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly
145 150 155 160

Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile
165 170 175

Asp Gly