

[illegible]

```

1  CCAATTCCAATGGGAAATGGTATGTCTGTGGGCGnnnGCCGAAATnnnnnnCTGCGTGAGGATAAGGATCCGnnnAAAAATGnnnGCGACCAT 90
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GGTTAAGGTACCCCTTTACCAATACAGCACCGGACCGGCCCTTTACGGTAAGACGCACTCCCTATTCCCTAGGCGTCTTTTACATACGCTGGTA
GlnPheHisGlyLysTrpTyrValValGlyXaaAlaGlyAsnXaaXaaLeuArgGluAspLysAspProXaaLysMetXaaAlaThrIle
8      12 13      21      24
21  24

91  TTACGAGTTGAAAGAAGATAAAATCATATAACGTCAACnnnGTGnnnTTTnnnnnnAAGAAATGCnnnTACnnnATnnnACCTTTGTGCC 180
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
AATGCTCAACTTTCTTCTATTAGTATATTGCAGTGGAGGCACAACAAGCGTCTTTCTTTACGCTGATGACCTAAGCATGGAAACACGGG
TyrGluLeuLysGluAspLysSerTyrAsnValThrXaaValXaaPheXaaXaaLysLysCysXaaTyrXaaIleXaaThrPheValPro
40  42  44  45      49  51  53

181 GGGAGCCAGCCGGCGAGTTACTTTAGGCGnnnATTAAAGTnnnCCGGGCGnnnACATCAnnnTTGGTCCGCGTGTGAGCACCAACTA 270
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CCCCTCGGTCGGCCCCGCTCAAAATGAAATCCGTTGTAAATTTTCAATGGGCCCGGACTGTAGTATGAACAGCGCGCAGCACTCGTGGTTGAT
GlySerGlnProGlyGluPheThrLeuGlyXaaIleLysSerXaaProGlyXaaThrSerXaaLeuValArgValValSerThrAsnTyr
68      72      75      78

271 CAACCAGCATGCCATGGTGTCTTCAAGnnnGTGnnnCAGAACCCGCGAGnnnTTTnnnATCACACTGTACGGGCGCACGAAAGAACTGAC 360
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GTTGGTCGTACGGTACCACAAGAAGTTCTTTACAGGGTCTTTGGCGCTCATGAAATTTCTAGTGTGACATGCCCGCGTCTTTCTTGACTG
AsnGlnHisAlaMetValPhePheLysXaaValXaaGlnAsnArgGluXaaPheXaaIleThrLeuTyrGlyArgThrLysGluLeuThr
97  99      104  106

361 AAGCGAGCTGAAGGAAATTTTATCCGCTTTTCCAAATCTCTGG 404
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TTCGCTCGACTTCCTTTTAAATAGCGGAAAGGTTTAGAGACC
SerGluLeuLysGluAsnPheIleArgPheSerLysSerLeu

```

FIG. 2

FIG. 3

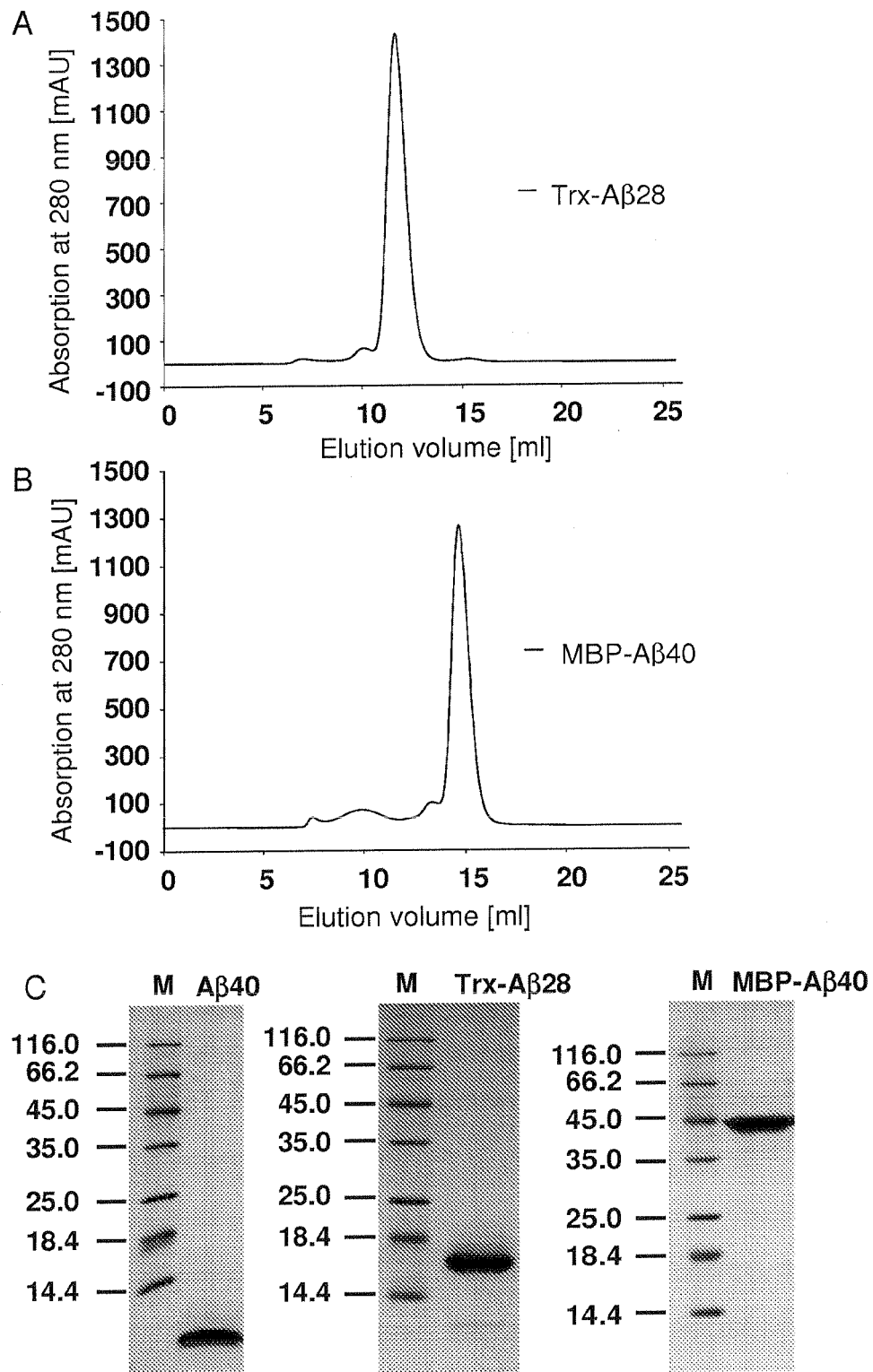


FIG. 4

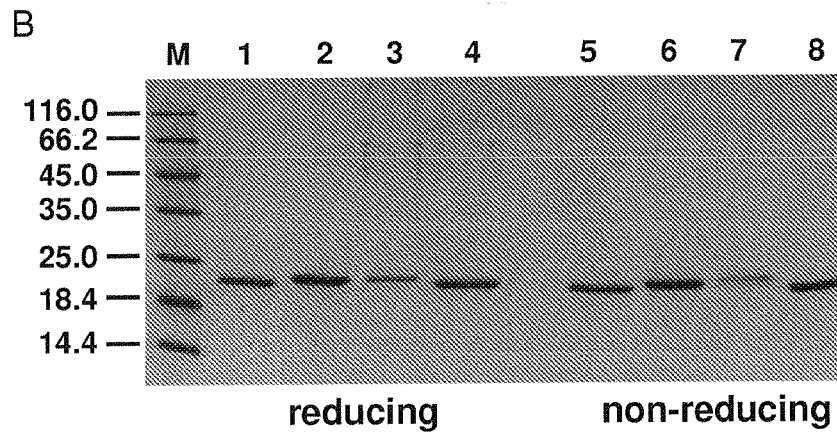
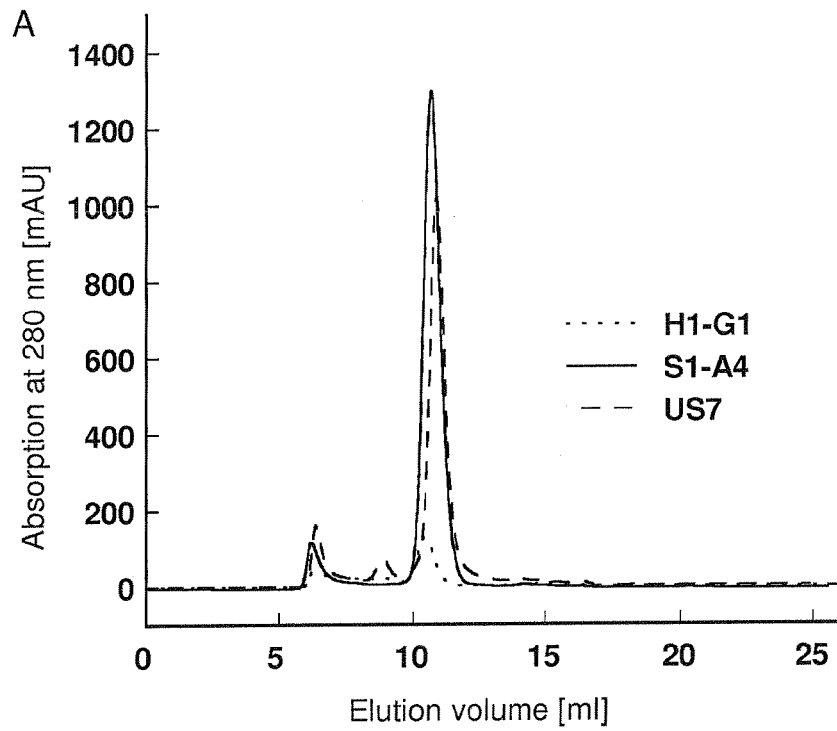


FIG. 5

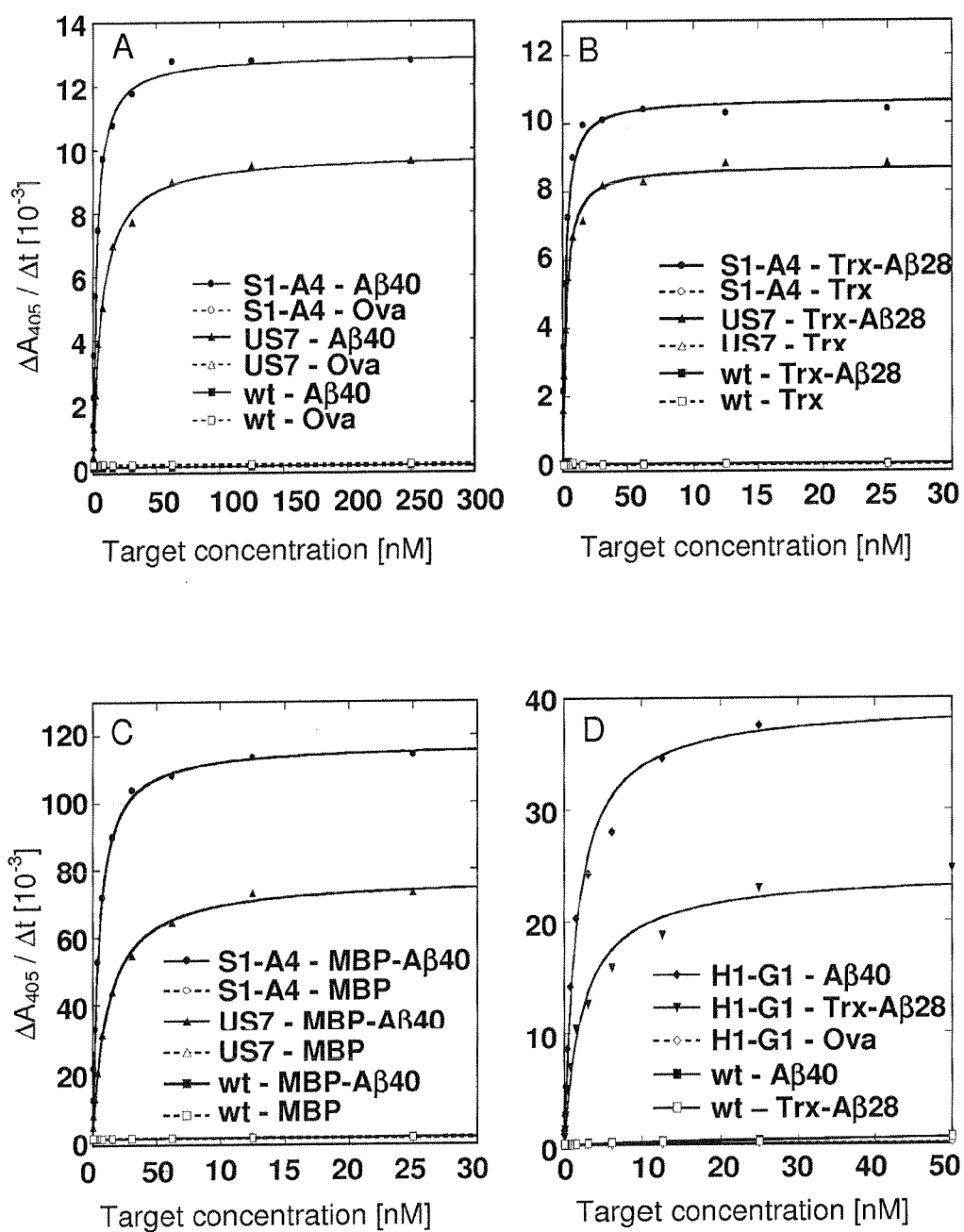


FIG. 6

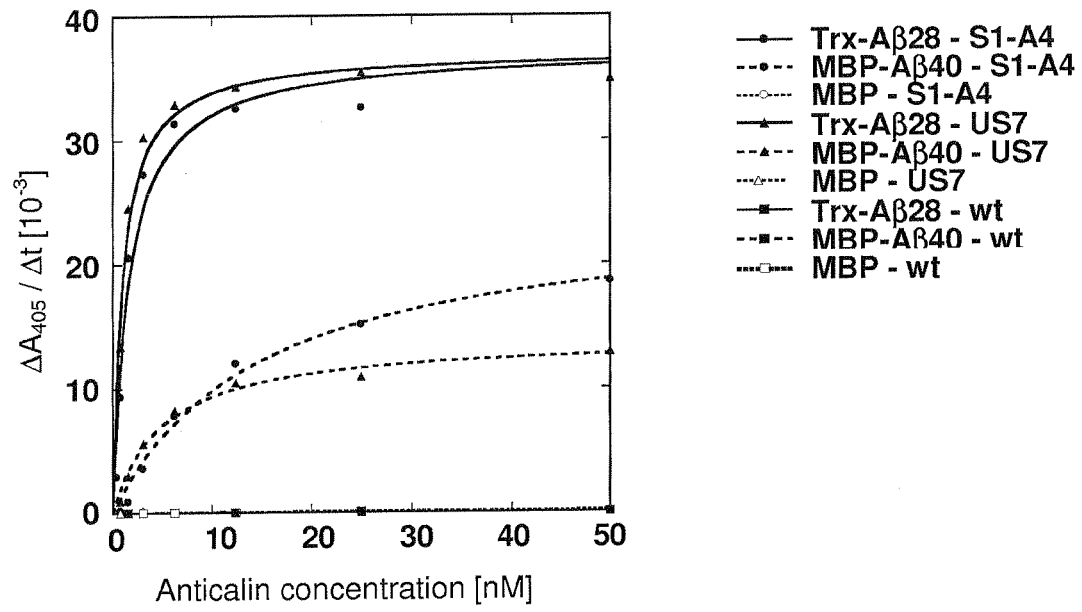


FIG. 7

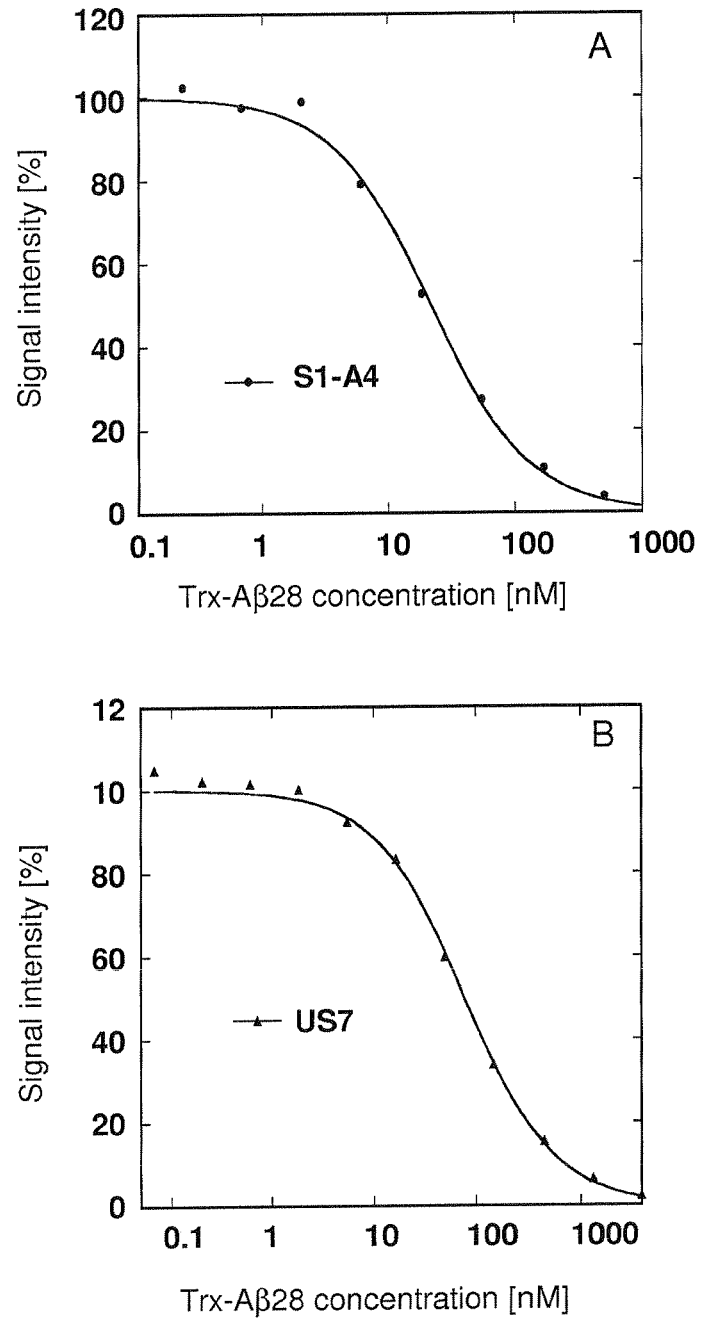


FIG. 8

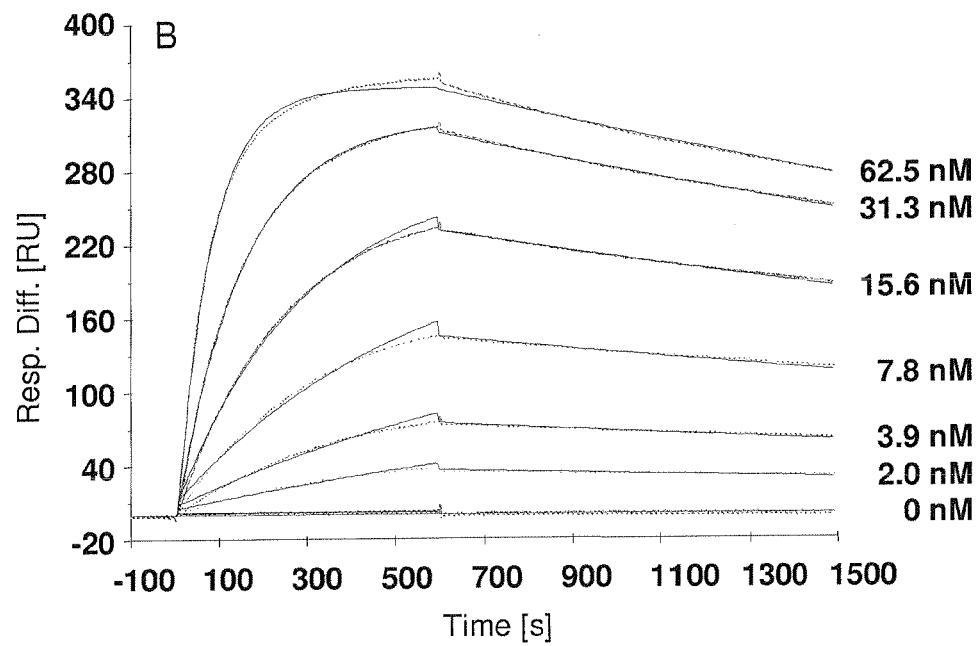
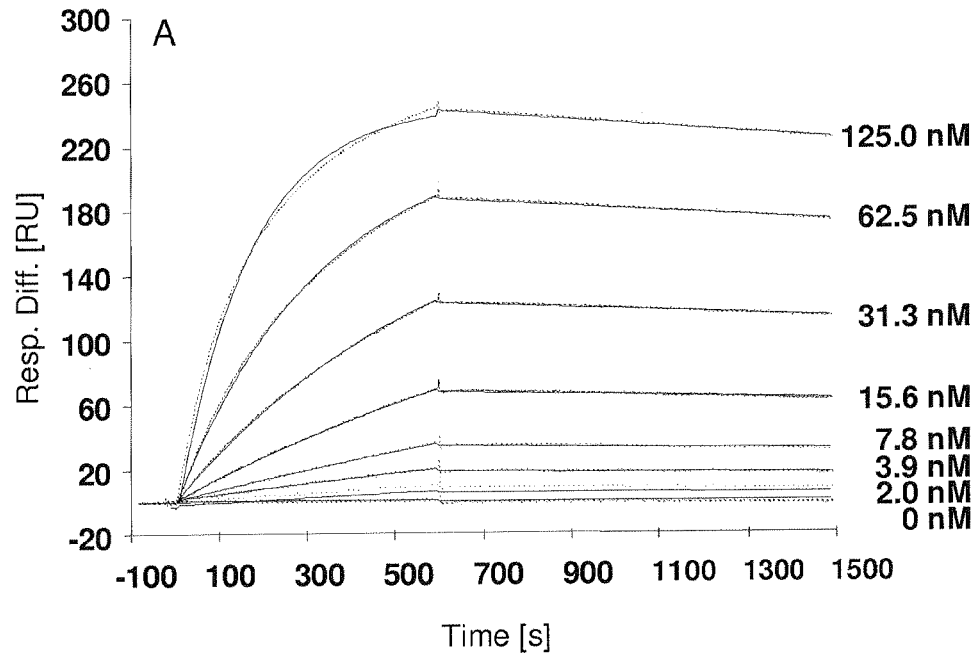


FIG. 9

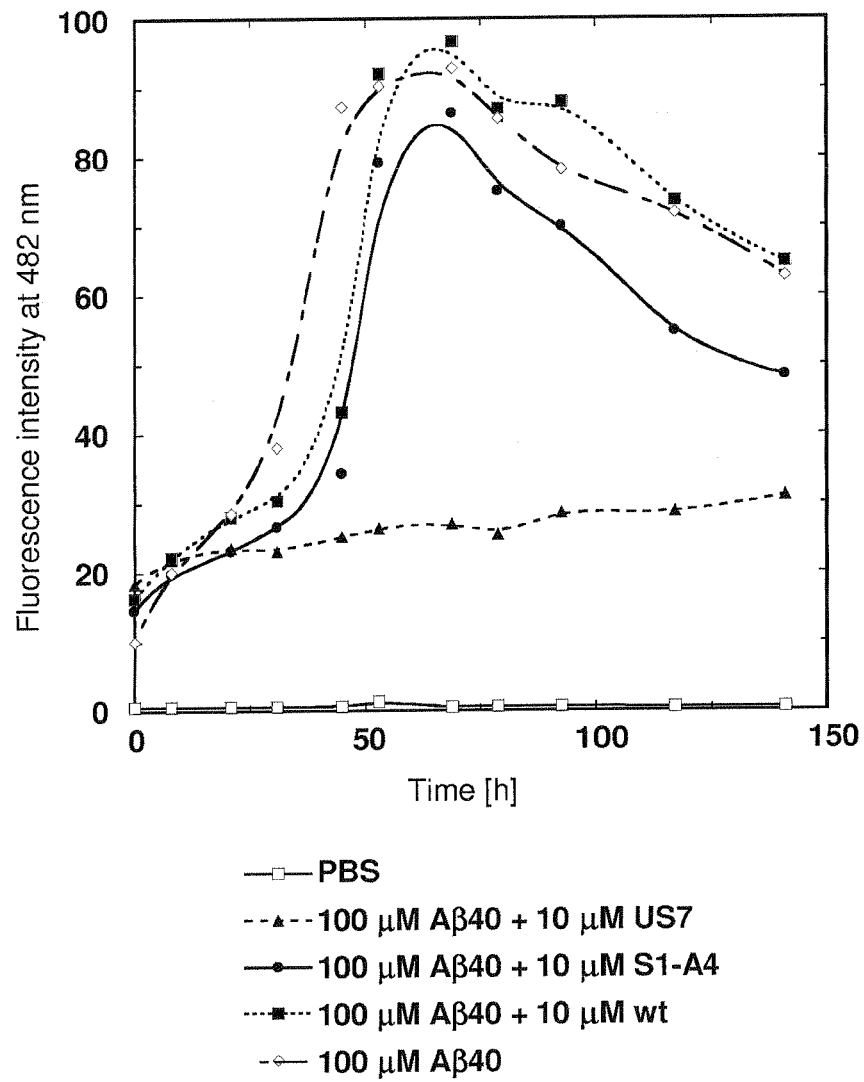


FIG. 10

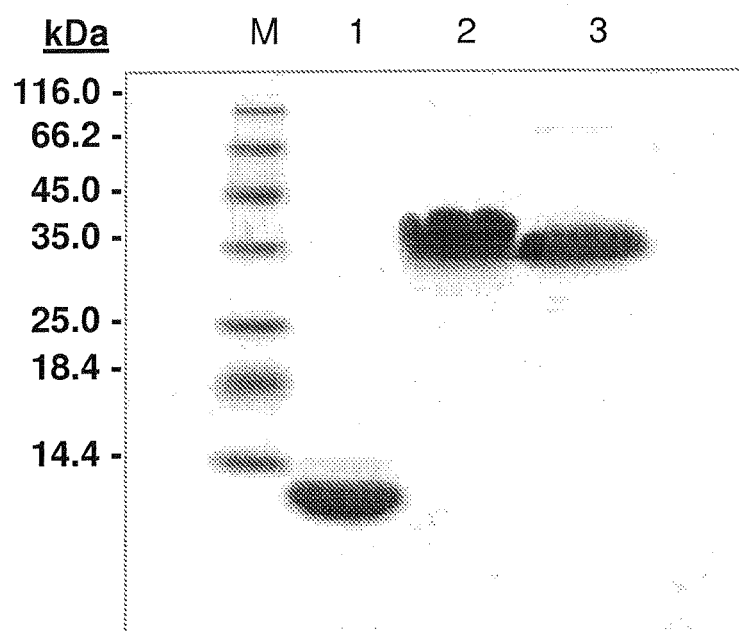


FIG. 11

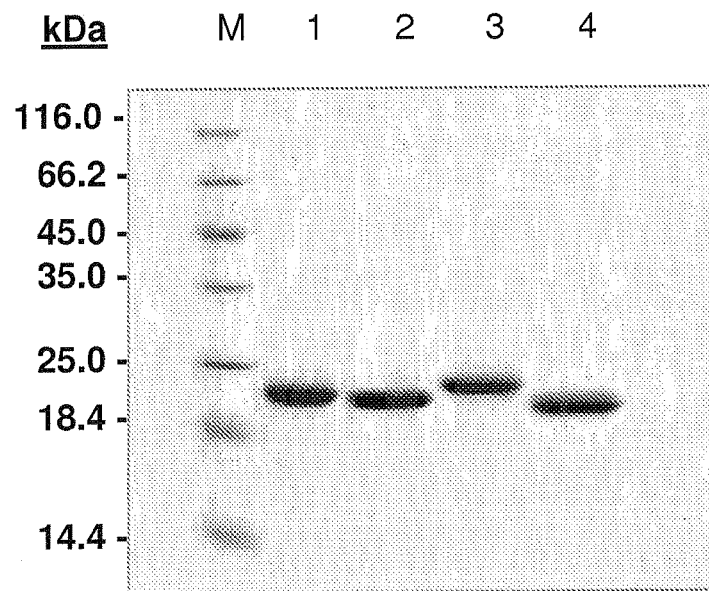


FIG. 12

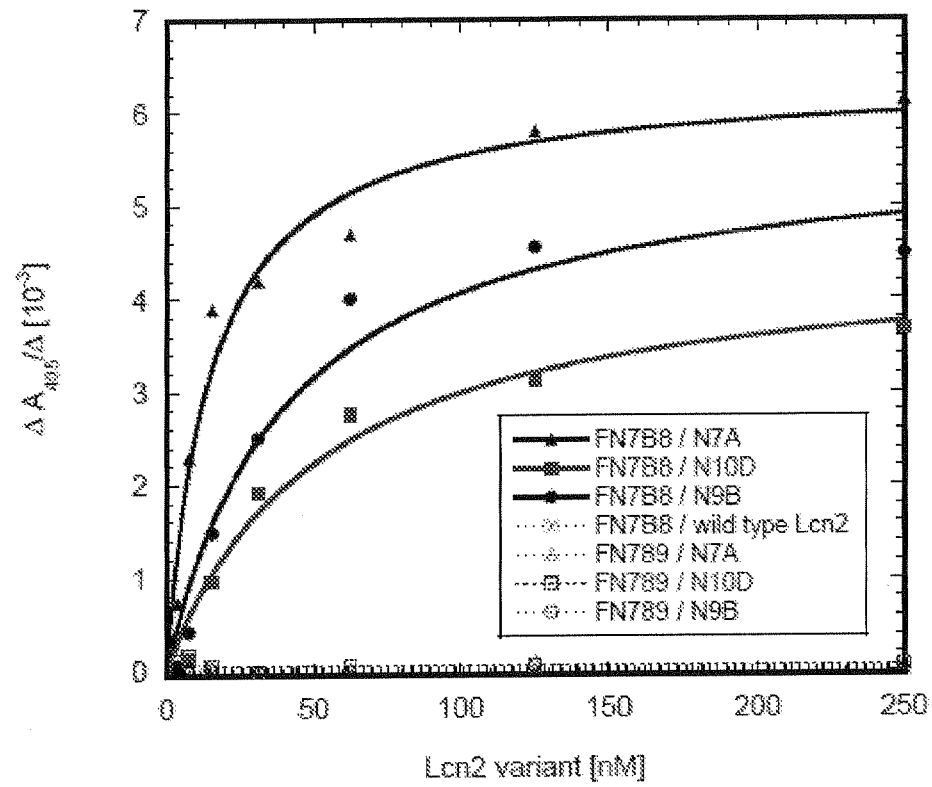


FIG. 13

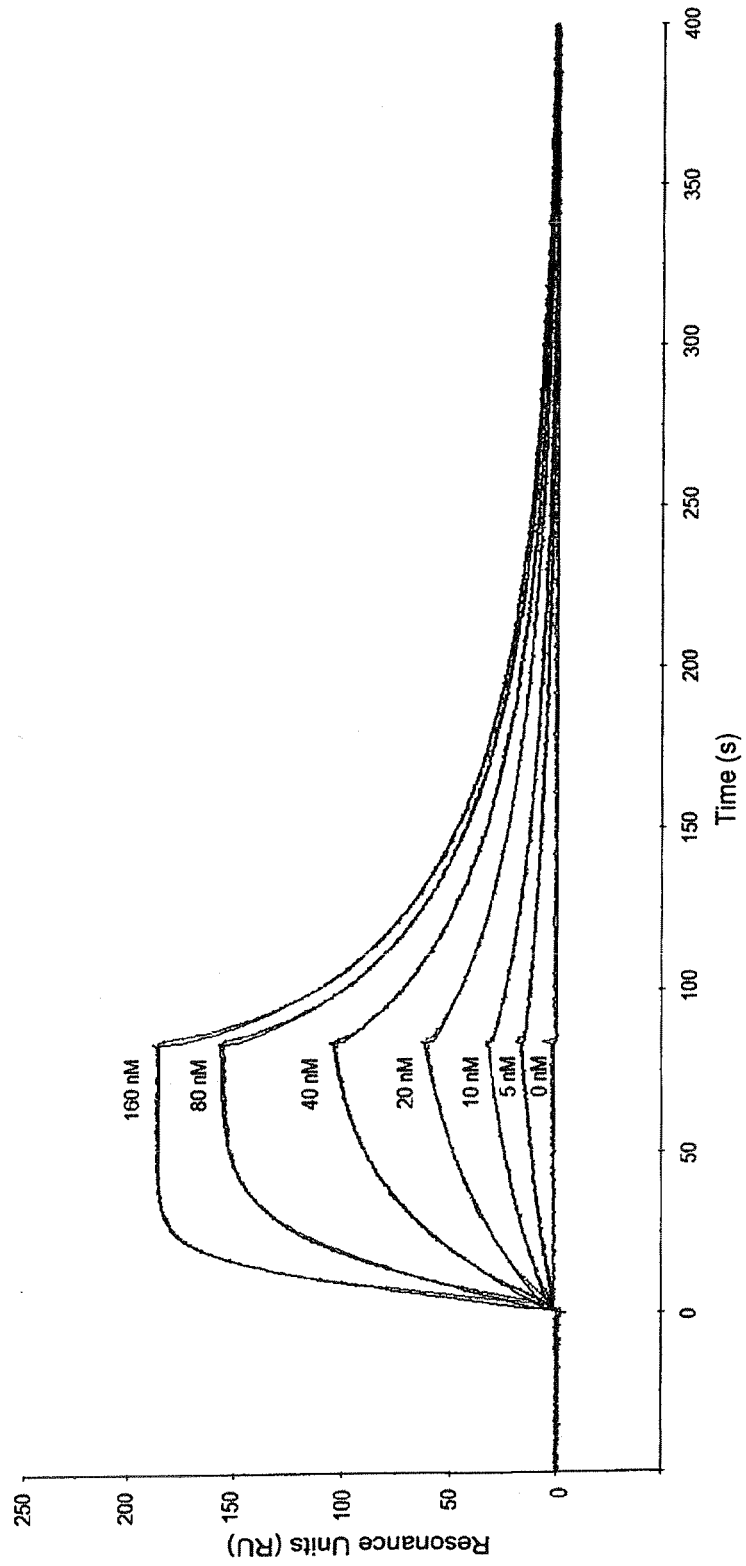


FIG. 14

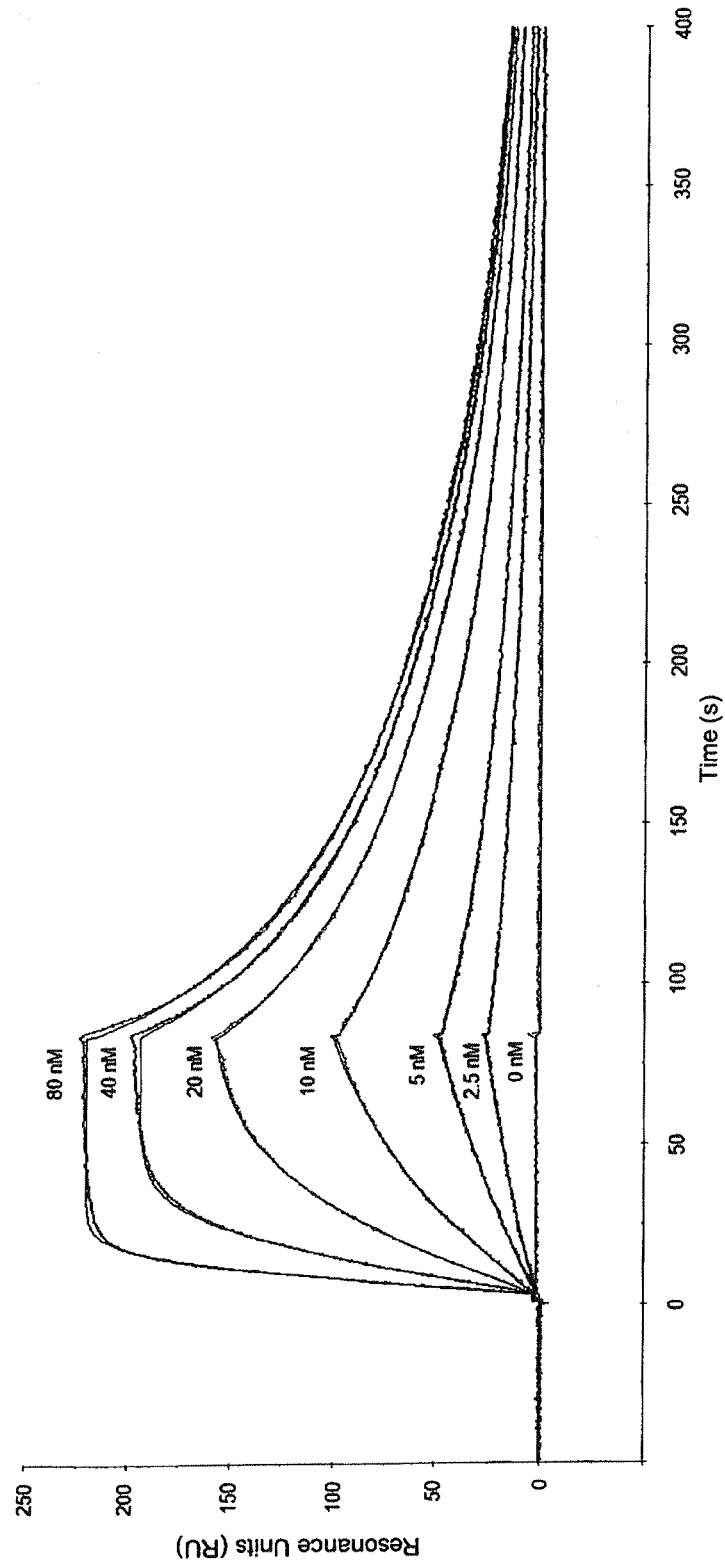


FIG. 15

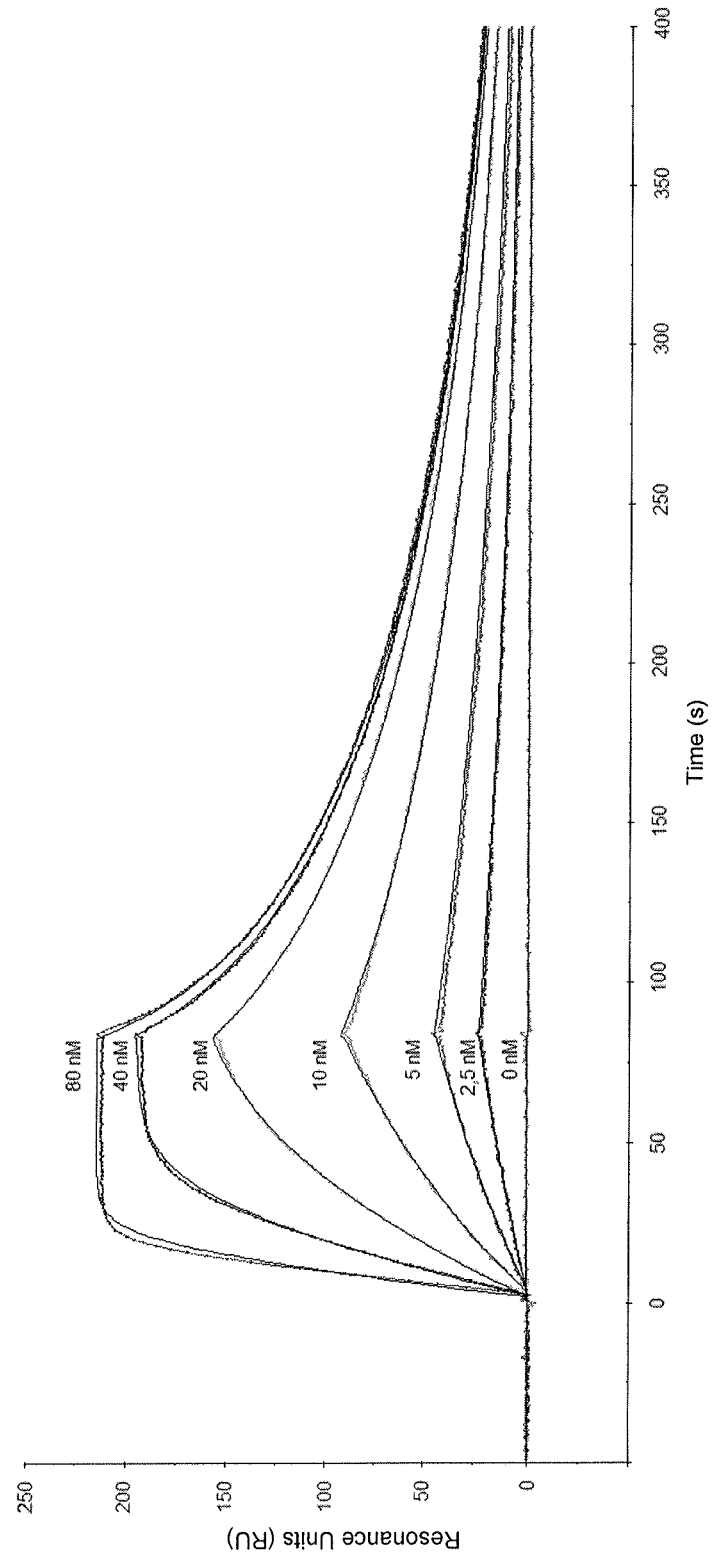
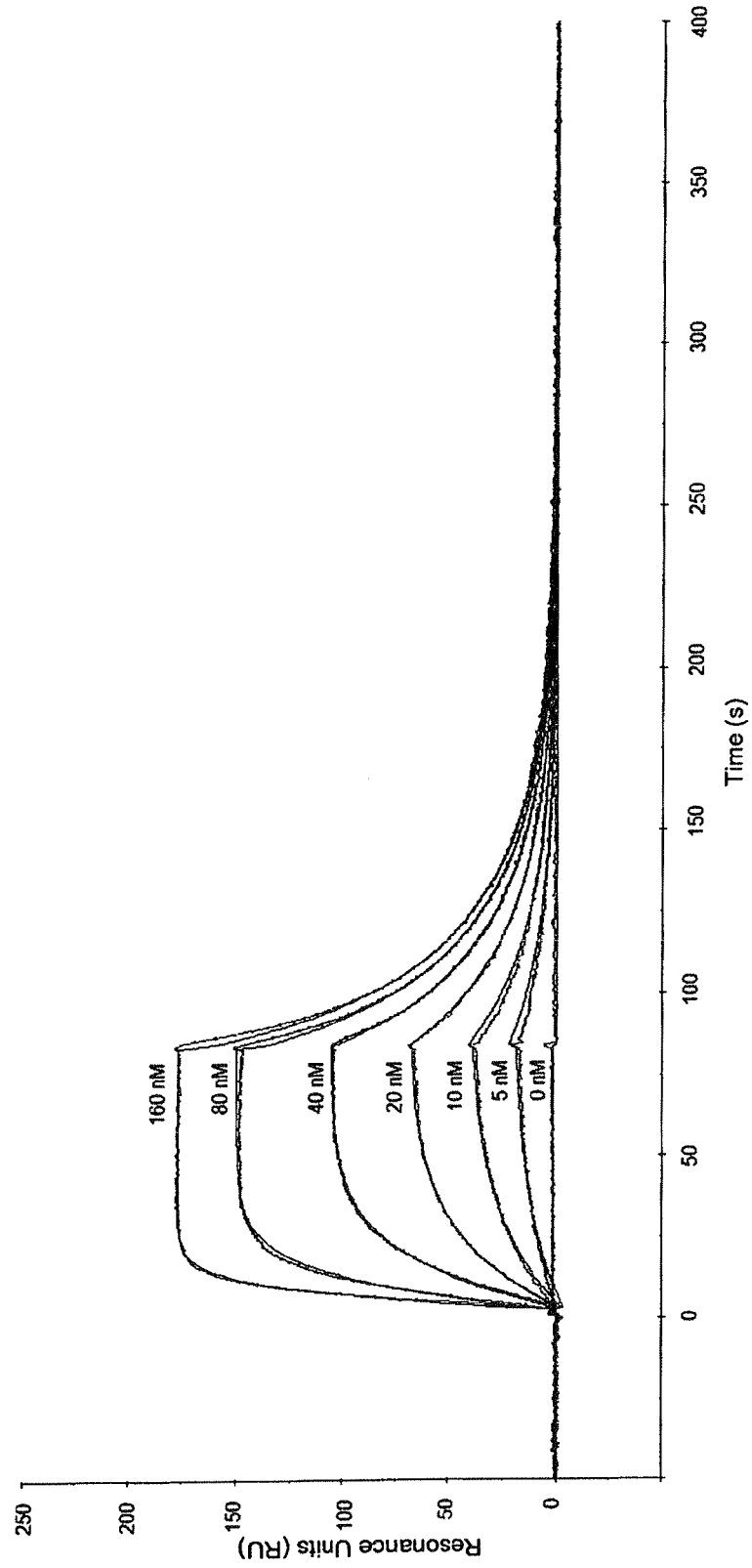


FIG. 16



```

1      10      20      30      40      50      60      70      80      90
Len2  QDSTDLIPAPPLSKVPLQQNFQDNQFQGRKVVVGLAGNAILREDKDPQKMYATIYELKEDKSYNVTSLFRKKKCDYWIRTFVPGCQPG
Lib    .....h.....x.....x.....x.....x.....x.....x.....x.....x.....x.....s...
S1-A4 (Abeta) .....h.....h.....h.....h.....h.....h.....h.....h.....h.....h.....s...
US7 (Abeta) .....h.....h.....h.....h.....h.....h.....h.....h.....h.....h.....s...
H1-G1 (Abeta) .....h.....h.....h.....h.....h.....h.....h.....h.....h.....h.....s...
N7A (ED-B) .....h.....h.....h.....h.....h.....h.....h.....h.....h.....h.....s...
N7E (ED-B) .....h.....h.....h.....h.....h.....h.....h.....h.....h.....h.....s...
N9B (ED-B) .....h.....h.....h.....h.....h.....h.....h.....h.....h.....h.....s...
N10D (ED-B) .....h.....h.....h.....h.....h.....h.....h.....h.....h.....h.....s...

====A=====1-----#1-----#2-----#3-----#4-----#5=====D===

```

```

100      110      120      130      140      150      160      170
Len2  EFTLGNIKSYPGLTSLYLRVVSTNYNQHAMVFFKKVSONREYFKITLYGRTKELTSELKENFIRFSKSLGLPENHIVFPIDQCIDG
Lib    .....x.....x.....x.....x.....x.....x.....x.....x.....x.....x.....s...
S1-A4 .....I.....Q.....M.....Y.....T.....G.....M.....N.....S.....N.....s...
US7    .....R.....R.....R.....A.....V.....Q.....S.....N.....s...
H1-G1 .....R.....E.....G.....W.....E.....A.....T.....N.....s...
N7A    .....N.....W.....L.....W.....R.....Y.....L.....E.....N.....s...
N7E    .....L.....K.....H.....F.....T.....A.....Y.....F.....s...
N9B    .....A.....P.....P.....T.....H.....F.....Y.....H.....s...
N10D   .....S.....W.....L.....W.....R.....Y.....F.....G.....s...

==E=====3-----#3-----#4-----#5=====H===

```

FIG. 17

FIG. 18

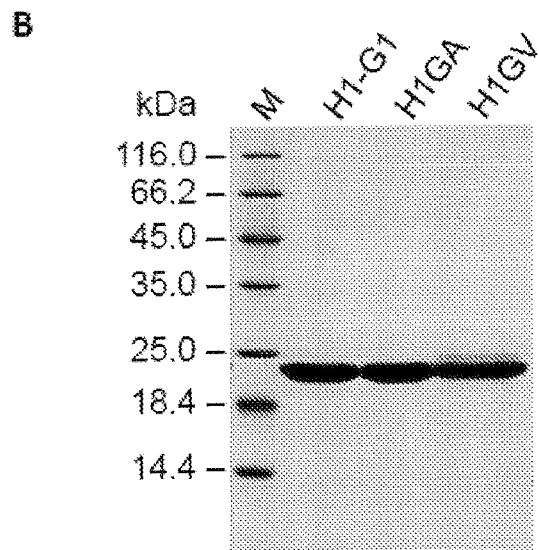
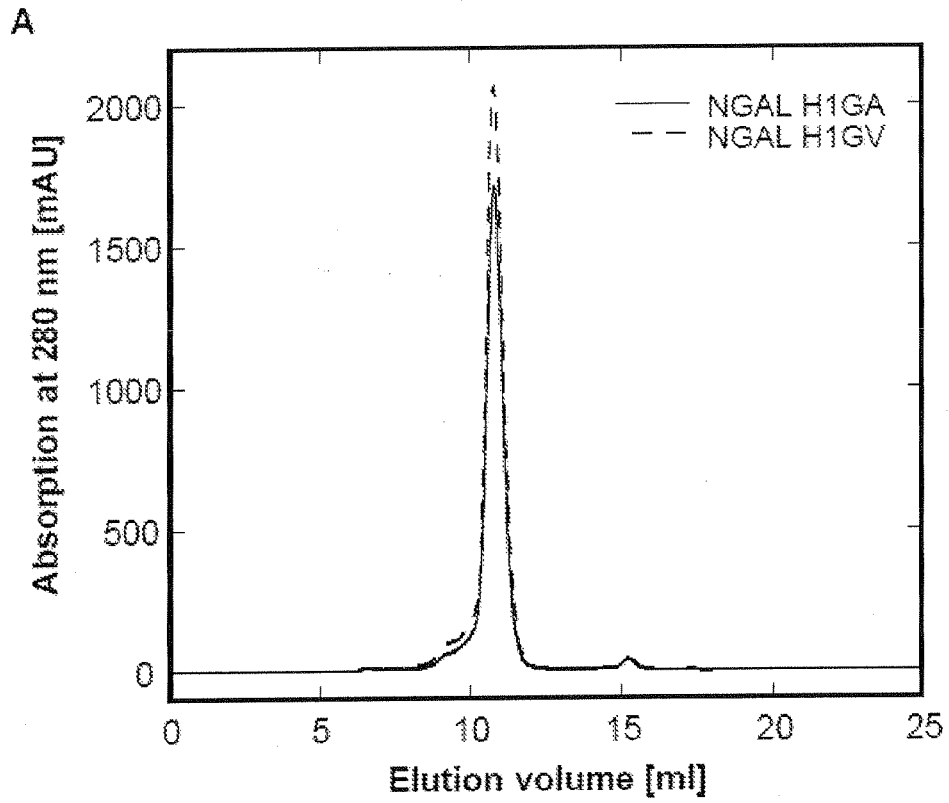


FIG. 19

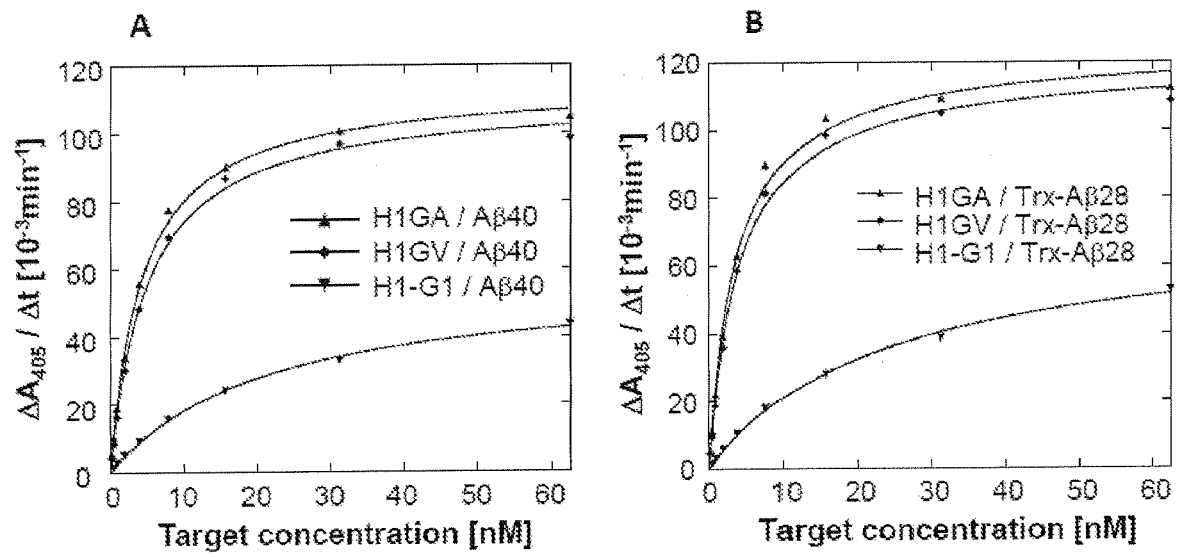


FIG. 20

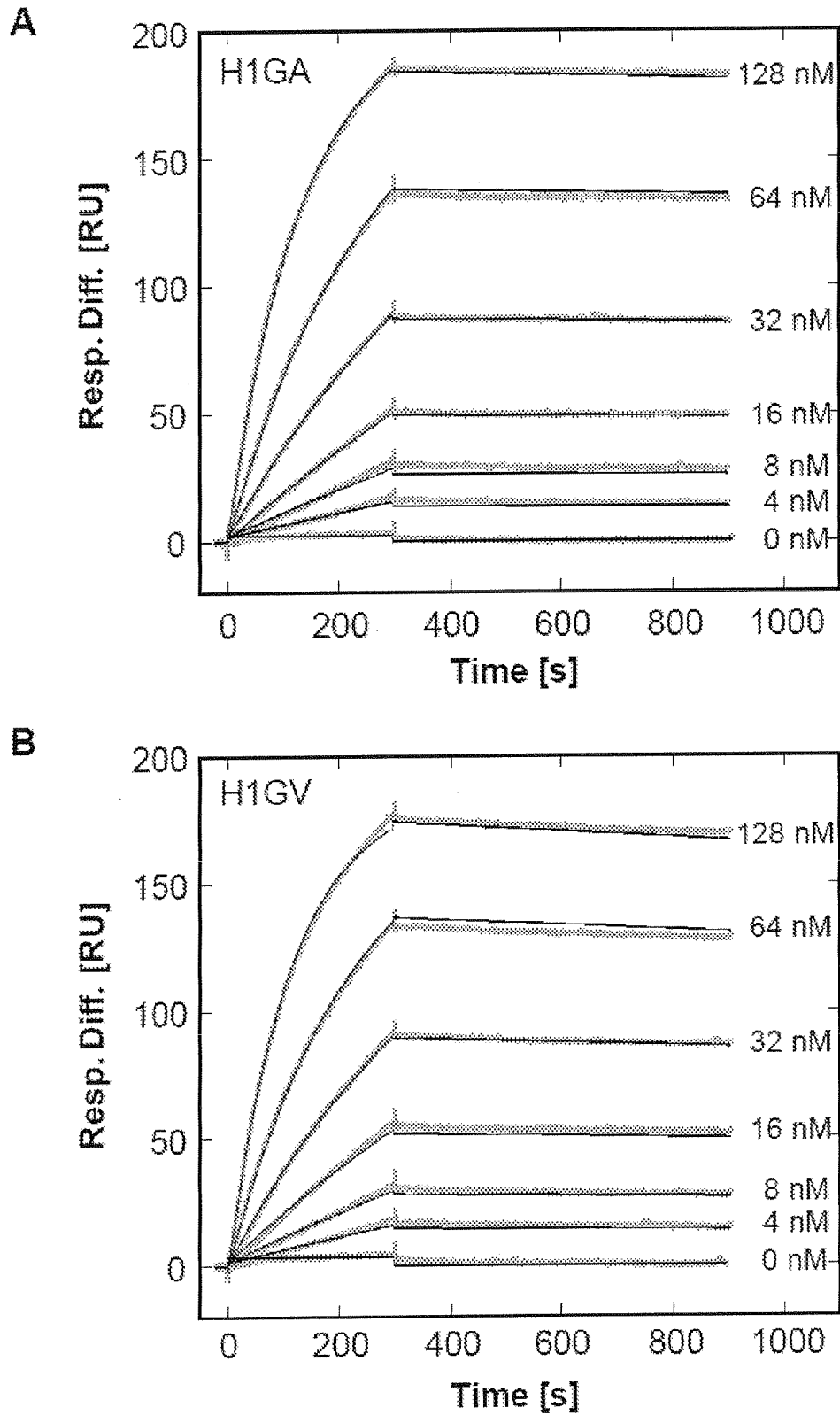


FIG. 21

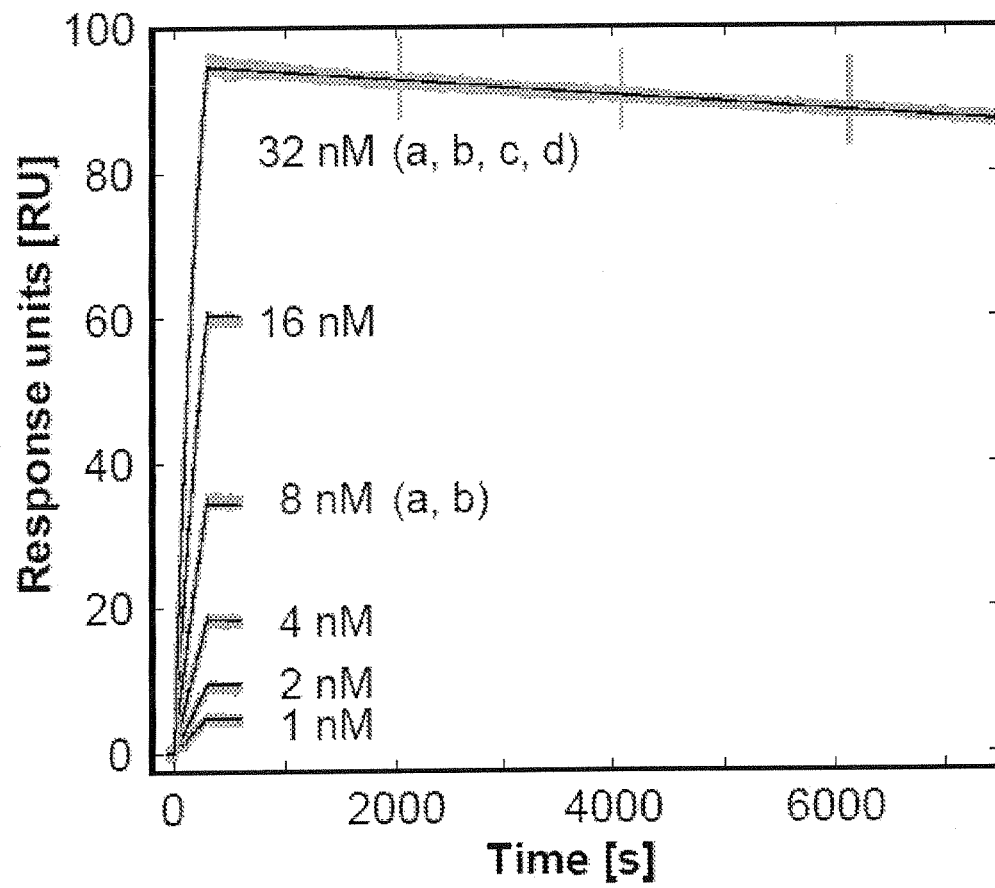


FIG. 22

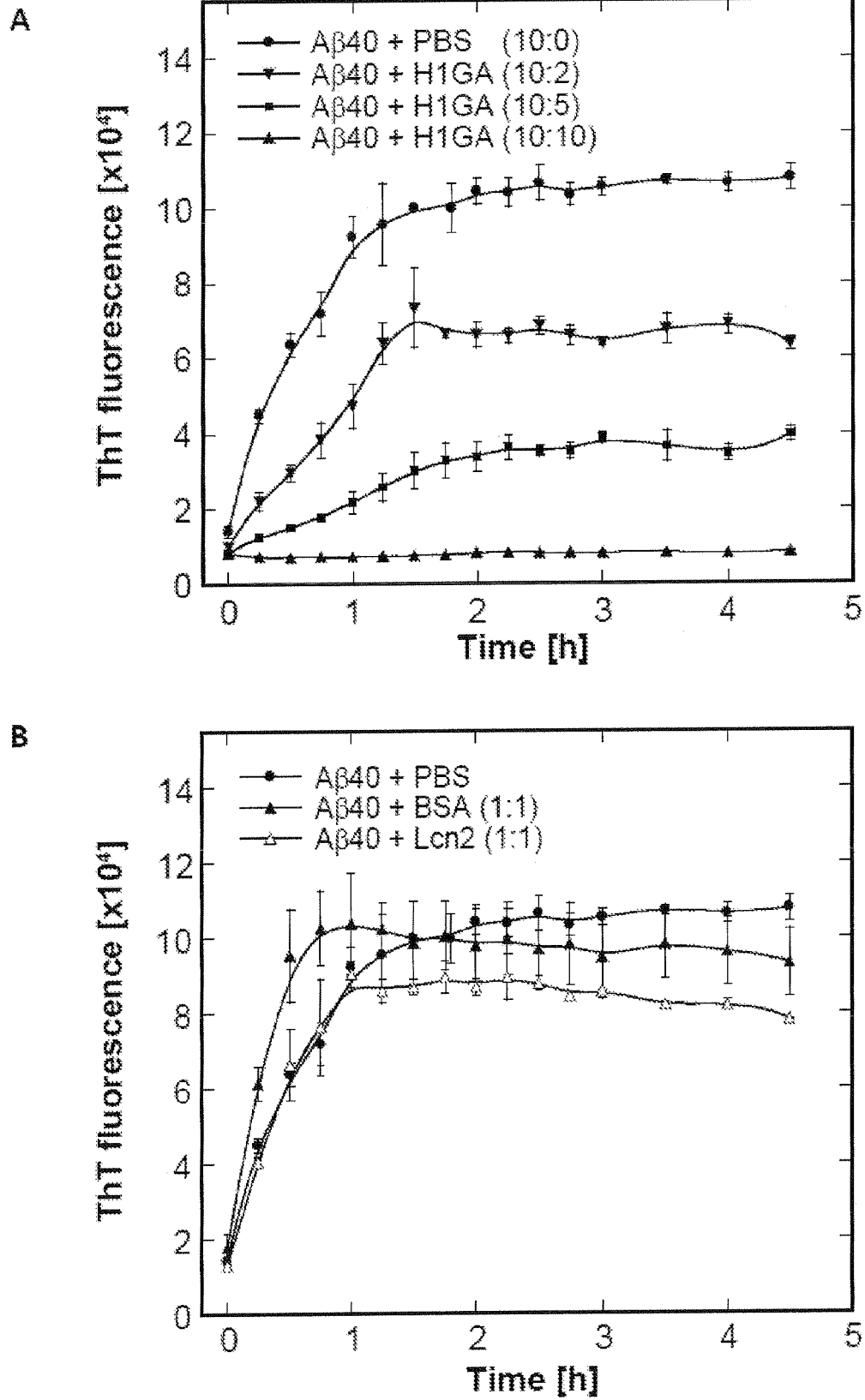


FIG. 23

	K_D [nM]	
	H1GA	H1GV
Aβ40 (Capture ELISA, Fig 19)	4.2 $\pm$ 0.3	4.9 $\pm$ 0.3
Trx-Aβ28 (Capture ELISA, Fig 19)	3.8 $\pm$ 0.4	4.2 $\pm$ 0.4
MBP-Aβ40 (SPR, Fig 20) *	0.48	1.1
Aβ40 (SPR, Fig 21) **	0.095	-
* dissociation time not sufficiently long		
** value more reliable since dissociation time long enough		

[illegible]

FIG. 26

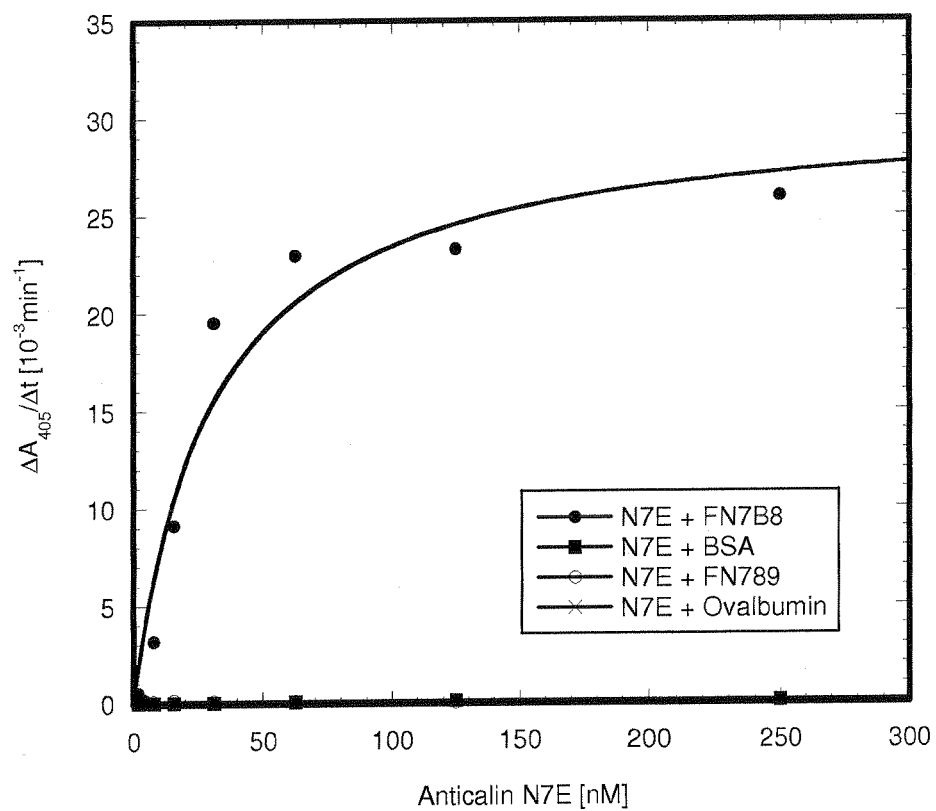


FIG. 27

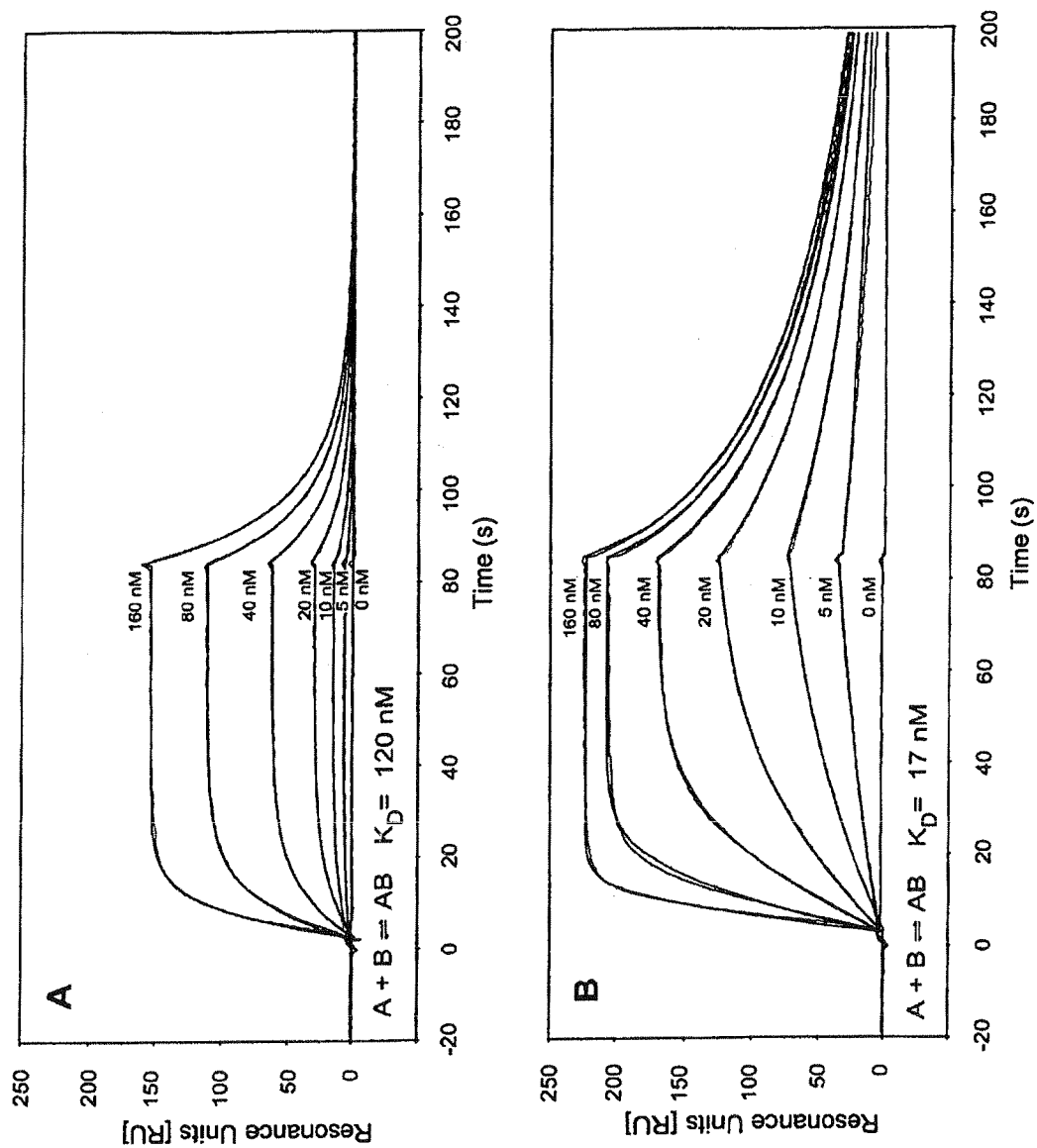


FIG. 27

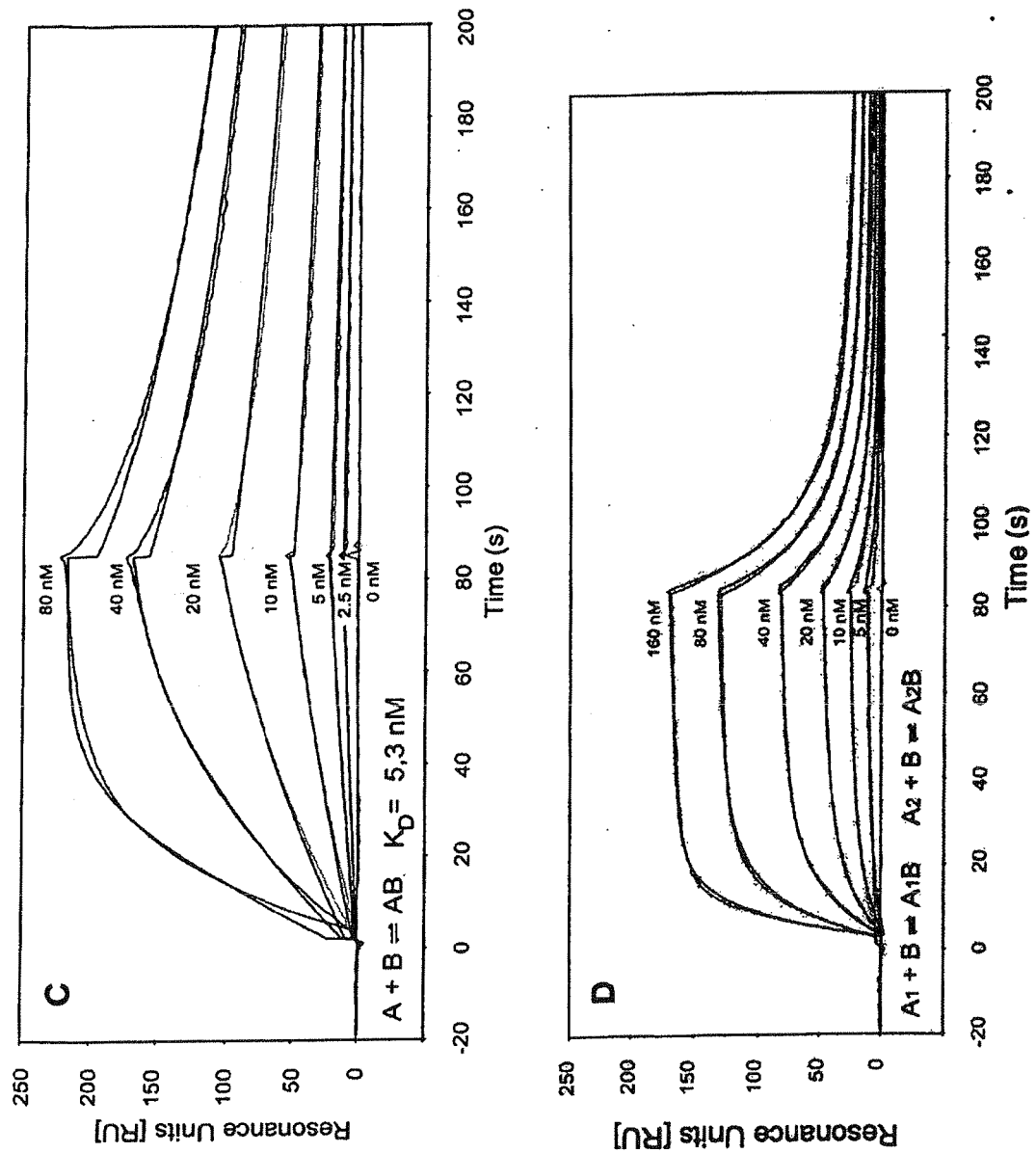


FIG. 28

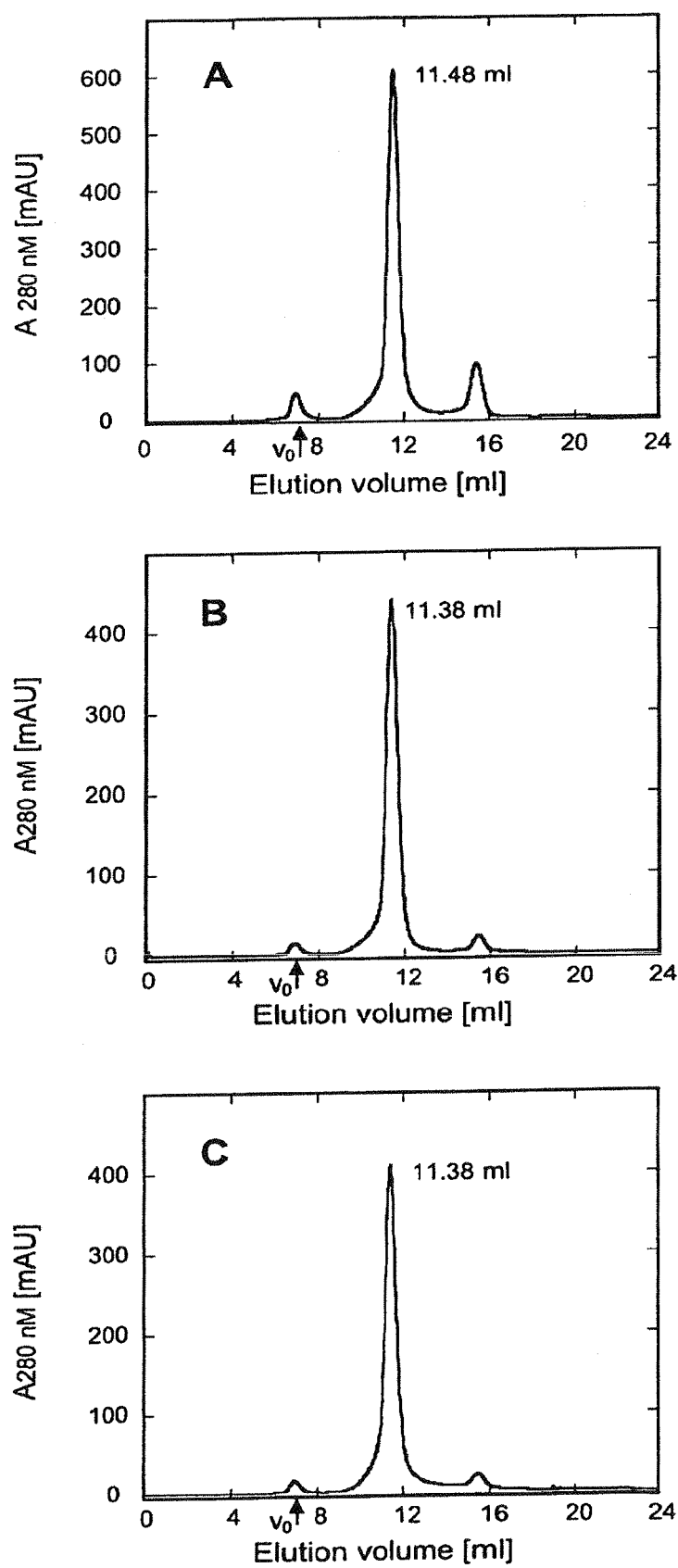
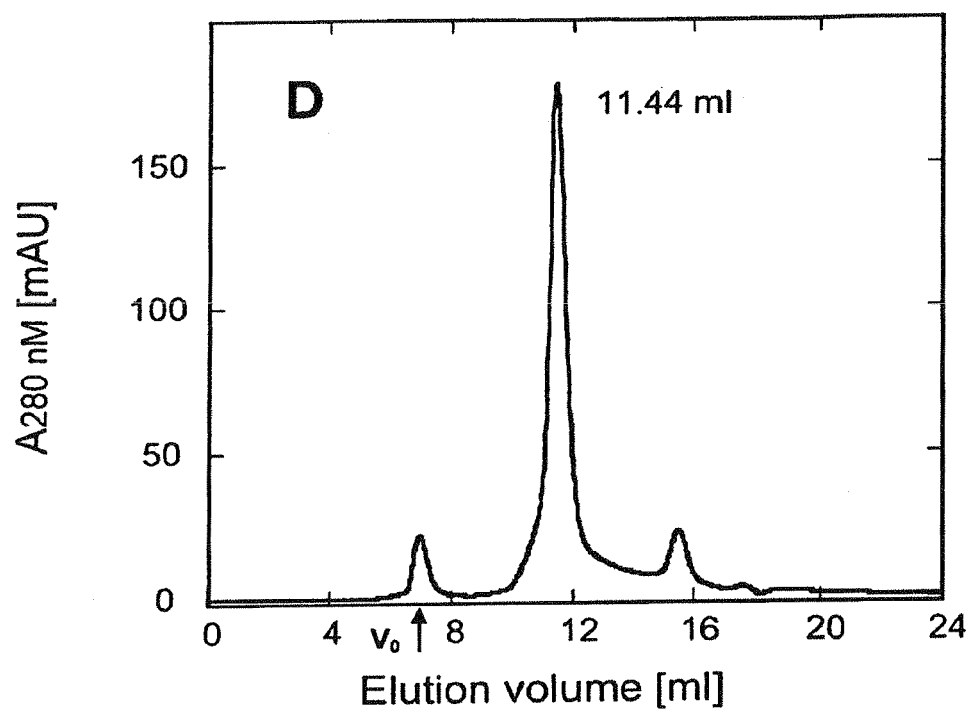


FIG. 28



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

<210> 1

<211> 88

<212> DNA

<213> Artificial

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kaagatgnnk gccaccatct atgagctg 88

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kacttttggt ccaggttcc 79

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gtggtgag 68

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<221> misc_feature

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 gggagaac 68

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 <210> 6
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 <212> DNA
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 <210> 7
 <211> 54
 <212> DNA
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ggtg 64

<210> 9
<211> 40
<212> DNA
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<220>
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<400> 10
ttcagggagg ccagagatt tggagaagcg gatgaagttc 40

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<220>
<223> Phage display vector phNGAL102 with CamR used as backbone for
NNK-Library

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tgaaatgaat agttcgacaa aaatctagat aacgagggca aaaaatgaaa aagacagcta 180
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<210> 12
<211> 4963
<212> DNA
<213> Artificial

<220>
<223> Phage display vector phNGAL108 with AmpR used for Sloning Library

<400> 12

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<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

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acaaacttgc	atctggaggc	aaaccctgac actggagtgc tcacagtctc ctgggagagg 120

```

agcaccaccc cagacattac tggttataga attaccacaa cccctacaaa cgccagcag 180
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agtcccggcc tggagtacaa tgtcagtgtt tacactgtca aggatgacaa ggaaagtgtc 300
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atcaccgaca gctccatcgg tctgcgttgg accccgctga attcctccac catcatcgg 420
tatcgtatca ccgttggtgc tgctggtgaa gggatcccgga tctttgaaga cttcgttgac 480
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aatctctgc ctggtacaga atatgtagtg agtgtctcca gtgtctacga acaacatgag 840
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taagctt 907

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

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<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

```

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<400> 14

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```

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

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 accccgctga attcctccac catcatcggt tatcgatatca ccgttggtgc tgctggtgaa 180
 gggatcccga tctttgaaga cttcggtgac tcctccggtg gttactacac cgttaccggt 240
 ctggaacccg ggatcgacta cgacatctcc gttatcacc tgatcaacgg tggatgaatcc 300
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 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

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agcaccaccc cagacattac tggttataga attaccacaa cccctacaaa cggccagcag      180
ggaaattcct tggaagaagt ggtccatgct gatcagagct cctgcacttt tgataacctg      240
agtcccggcc tggagtacaa tgtcagtgtt tacactgtca aggatgacaa ggaaagtgtc      300
cctatctctg ataccatcat cccagctgtt cctcctccca ctgacctgcg attaccaac      360
attggtccag acaccatgcg tgtcacctgg gctccacccc catccattga tttaaccaac      420
ttcctggtgc gttactcacc tgtgaaaaat gaggaagatg ttgcagagtt gtcaatttct      480
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cttgattccc caactggcat tgacttttct gatattactg ccaactcttt tactgtgcac      660
tggattgctc ctcgagccac catcactggc tacaggatcc gccatcatcc cgagcacttc      720
agtgggagac ctcgagaaga tcgggtgccc cactctcgga attccatcac ctcaccaac      780
ctcactccag gcacagagta tgtggtcagc atcgttgctc ttaatggcag agaggaaagt      840
cccttattga ttggccaaca atcaacagtt agcgctcacc atcaccatca ccattaataa      900
gctt                                     904
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<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

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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

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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 gtacggg'gcgc  420
acgaaagaac tgacaaacga gctgaaggaa aattttatcc gcttttccaa atctctgggc    480
ctccctgaaa accacatcgt cttccctgtc ccaatcgacc agtgtatcga cggc          534
  
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<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

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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 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
  
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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
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ctgctgcgtg aggataagga tccgcgtaaa atgtacgcga ccatttacga gttgaaagaa 180
gataaatcat ataacgtcac cagcgtgcgt tttcgtagca agaaatgcca ctacctgatt 240
cgtacctttg tgccggggag ccagccgggc gagtttactt taggcctgat taaaagtaaa 300
ccggggccaca catcattctt ggtccgcgtt gtgagcacca actacaacca gcatgccattg 360
gtgtttcttca agaccgtggc acagaaccgc gagtactttt tcatcacact gtacgggdcgc 420
acgaaagaac tgacaagcga gctgaaggaa aattttatcc gcttttccaa 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
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 cgtctgctg aggataagga tccggcaaaa atgggttcga ccatttacga gttgaaagaa 180
 gataaatcat ataacgtcac caaagtgatg tttcaacgta agaaatgcaa atacatgatt 240
 aatacctttg tgccggggag ccagccgggc gagtttactt taggcgcaat taaaagtcct 300
 ccggggcccta catcaacctt ggtccgcgtc gtgagcacca actacaacca gcatgccatg 360

gtgtttcttca agcacgtgtt ccagaaccgc gactactttc acatcacact gtacgggcgc 420
 acgaaagaac tgacaagcga gctgaaggaa aattttatcc gcttttccaa atctctgggc 480
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<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

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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
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<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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agataacgag ggcaaaaaat gaaaaagaca gctatcgca ttgcagtggc tctggctggc 180
ttcgtaccg tagcgaggc ccaggactcc acctcagacc tgatcccagc cccacctctg 240
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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 ctcaaacag ggagtacttc 600
aagatcacc tctacgggag aaccaaggag ctgacttcgg aactaaagga gaacttcac 660

cgcttctcca aatctctggg cctccctgaa aaccacatcg tcttccctgt cccaatcgac	720
cagtgtatcg acggcagcgc ttggtctcac ccgcagttcg aaaaataata agcttgacct	780
gtgaagtgaa aaatggcgca cattgtgcga cttttttttt gtctgccgtt taccgctact	840
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tgctgttagc aatggcaaca acgttgcgca aactattaac tggcgaacta cttactctag	2040
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gctcggccct tccggctggc tggtttattg ctgataaatc tggagccggt gagcgtggct	2160
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cctcactgat taagcattgg taggaattaa tgatgtctcg tttagataaa agtaaagtga	2340
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<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
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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
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<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
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 ccggaattaa agtcaccgtt gagcatccgg ataaactgga agagaaattc ccacagggttg 180
 cggcaactgg cgatggccct gacattatct tctgggcaca cgaccgcttt ggtggctacg 240
 ctcaatctgg cctgttggtt gaaatcacc cggacaaagc gttccaggac aagctgtatc 300
 cgtttacctg ggatgccgta cgttacaacg gcaagctgat tgcttaccg atcgctgttg 360
 aagcgttatc gctgatttat acaaagatc tgctgccgaa cccgccaaaa acctgggaag 420
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 tgcaagaacc gtacttcacc tggccgctga ttgctgctga cgggggttat gcgttcaagt 540
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 gtctgacctt cctggttgac ctgattaaaa acaaacacat gaatgcagac accgattact 660
 ccatcgcaga agctgccttt aataaaggcg aaacagcgat gaccatcaac ggcccgtggg 720
 catggtccaa catcgacacc agcaaagtga attatggtgt aacgggtactg ccgaccttca 780
 aggggtcaacc atccaaaccg ttcgttggcg tgctgagcgc aggtattaac gccgccagtc 840
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 aagcggttaa taaagacaaa ccgctgggtg ccgtagcgct gaagtcttac gaggaagagt 960
 tggcgaaaga tccacgtatt gccgccacca tggaaaacgc ccagaaagggt gaaatcatgc 1020
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<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

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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
agatccggc gctggataaa gaactgaaag cgaaaggtaa gagcgcgctg atgttcaacc	480
tgcaagaacc gtacttcacc tggccgctga ttgctgctga cgggggttat gcgttcaagt	540
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ccatcgcaga agctgccttt aataaaggcg aaacagcgat gaccatcaac ggcccgtggg	720
catggtccaa catcgacacc agcaaagtga attatggtgt aacggtactg ccgaccttca	780
agggtcaacc atccaaaccg ttcgttggcg tgctgagcgc aggtattaac gccgccagtc	840
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aagcggttaa taaagacaaa ccgctgggtg ccgtagcgct gaagtcttac gaggaagagt	960
tggcgaaaga tccacgtatt gccgccacca tggaaaacgc ccagaaagg t gaaatcatgc	1020
cgaacatccc gcagatgtcc gctttctggt atgccgtgcg tactgcggtg atcaacgccg	1080
ccagcggtcg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt atcaccagc	1140
gatcccatca ccaccatcat caccagaact tgtacttcca ggacgctgaa ttccgtcacg	1200
actccggtta cgaagttcac caccagaagc tggttttctt cgctgaagac gttggttcca	1260
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<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
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 cgggtccgggt ggtggtgacg ctgaattccg tcacgactcc ggttacgaag ttcaccacca 180
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 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 gcaaaactga acatcgatca aaaccctggc actgcgccga aatatggcat 240
 ccgtgggtatc ccgactctgc tgctgttcaa aaacggtgaa gtggcggcaa ccaaagtggg 300
 tgcactgtct aaaggtcagt 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 agggaatgca	120
attctcagag aagacaaaga cccgcaaaag atgtatgcca ccatctatga gctgaaagaa	180
gacaagagct acaatgtcac ctccgtcctg tttaggaaaa agaagtgtga ctactggatc	240
aggacttttg ttccagggttc ccagccaggc gagttcacgc tgggcaacat taagagttac	300
cctggattaa cgagttacct cgtccgagtgt gtgagcacca actacaacca gcatgctatg	360
gtgttcttca agaaagtttc tcaaaacagg gagtacttca agatcacctt 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

caggactcca cctcagacct gatcccagcc ccacctctga gcaagggtccc tctgcagcag	60
aacttccagg acaaccaatt ccatgggaag tggatatgtg taggttgtgc agggaatgtg	120
ttgctcagag aagacaaaga cccgcttaag atgtatgcca ccatctatga gctgaaagaa	180
gacaagagct acaatgtcac cagtgtcggg tttgatgata agaagtgttt gtacaagatc	240
cggacttttg ttccagggttc ccagccaggc gagttcacgc tgggcaggat taagagtgtg	300
cctggaggta cgagttggct cgtccgagtgt gtgagcacca actacaacca gcatgctatg	360
gtgttcttca aggaggttgc gcaaaacagg gagacgttca atatcacctt 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

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

acgctcagag aagacaaaga cccgctgaag atgtatgcc aatctatga gctgaaagaa 180
gacaagagct acaatgtcac cagtgtcggg tttaggttga agaagtgtaa ttacaagatc 240
cggacttttg ttccagggtc ccagccaggc gagttcacgc tgggcattat taagagtcag 300
cctggaatga cgagttatct cgtccgagtg gtgagcacca actacaacca gcatgctatg 360
gtgtttcttca agacggttgg gcaaaacagg gagatgttca atatcaccct 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
caggactcca cctcagacct gatcccagcc ccacctctga gcaagggtccc tctgcagcag 60
aacttccagg acaaccaatt ccatgggaag tggatatgtg taggtgttgc aggaataag 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
gtgttcttca 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

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 gaagtggat	180
gtggtaggtc tcgcagggaa tgcaattctc agagaagaca aagacccgca aaagatgtat	240
gccaccatct atgagctgaa agaagacaag agctacaatg tcacctccgt cctgttttagg	300
aaaaagaagt gtgactactg gatcaggact tttgttcag gttcccagcc aggcgagttc	360
acgctgggca acattaagag ttaccctgga ttaacgagtt acctcgccg agtggtgagc	420
accaactaca accagcatgc tatggtgttc ttcaagaaag tttctcaaaa caggagtagc	480
ttcaagatca ccctctacgg gagaaccaag gagctgactt cggaactaaa ggagaacttc	540
atccgcttct ccaaattctt gggcctccct gaaaaccaca tcgtcttccc tgtcccaatc	600
gaccagtgtg tcgacggcag cgcttggtcc caccgcagtc 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

actgcgggtg 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 is c or 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 gcaaggtccc tctgcagcag 60
aacttcagg acaaccaatt ccatgggaag tggatatgtg taggtgctgc agggaaatgtg 120
ttgctcagag aagacaaaga cccgcttaag atgtatgccca ccattctatga gctgaaagaa 180
gacaagagct acaatgtcac cagtgtcggg tttgatgata agaagtgttt gtacaagatc 240
cggacttttg ttccaggttc ccagccaggc gagttcacgc tgggcaggat taagagttag 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> 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 tttgatgata agaagtgttt gtacaagatc 240
 cggacttttg ttccaggttc ccagccaggc gagttcacgc tgggcaggat taagagtgag 300
 cctggaggta cgagttggct cgtccgagtg gtgagcacca actacaacca gcatgctatg 360
 gtgtttcttca aggaggttgc gcaaaacagg gagacgttca atatcacctt 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