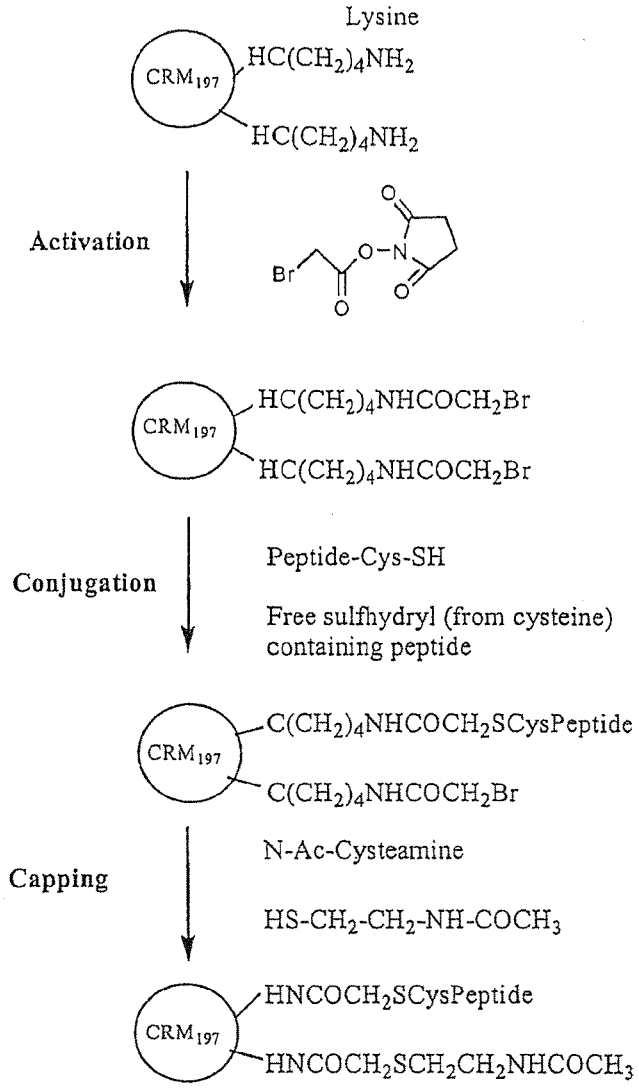


Capped CRM Conjugate

Figure 1

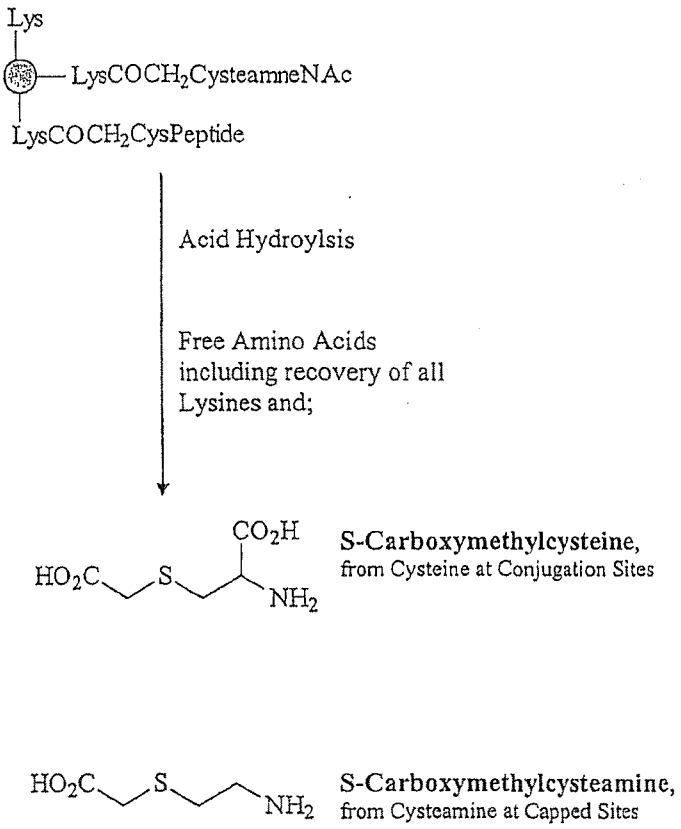

Lys
LysCOCH2CysteamneNAc
LysCOCH2CysPeptide
Acid Hydroylsis
Free Amino Acids
including recovery of all
Lysines and;
CO2H
HO2C
S
NH2
S-Carboxymethylcysteine,
from Cysteine at Conjugation Sites
HO2C
S
NH2
S-Carboxymethylcysteamine,
from Cysteamine at Capped Sites

Figure 2

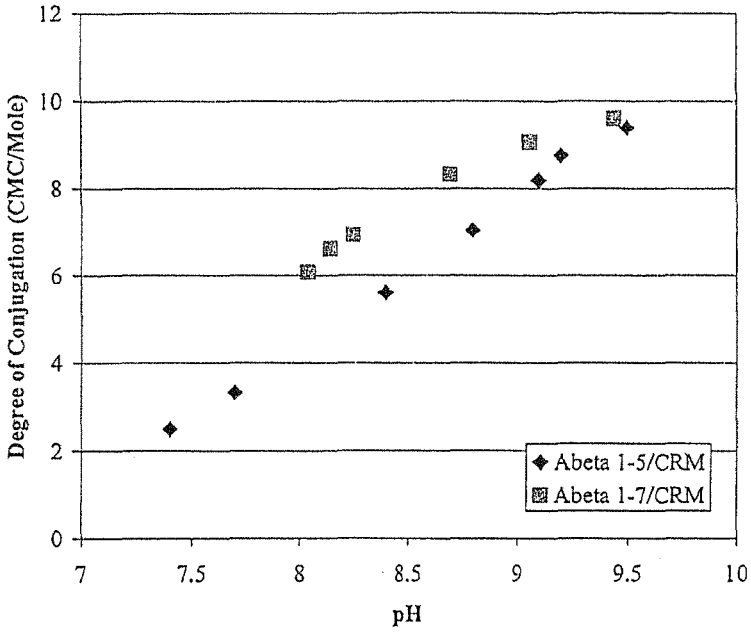

12
10
8
6
4
2
0
Degree of Conjugation (CMC/Mole)
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7.5
8
8.5
9
9.5
10
pH
Abeta 1-5/CRM
Abeta 1-7/CRM

Figure 3

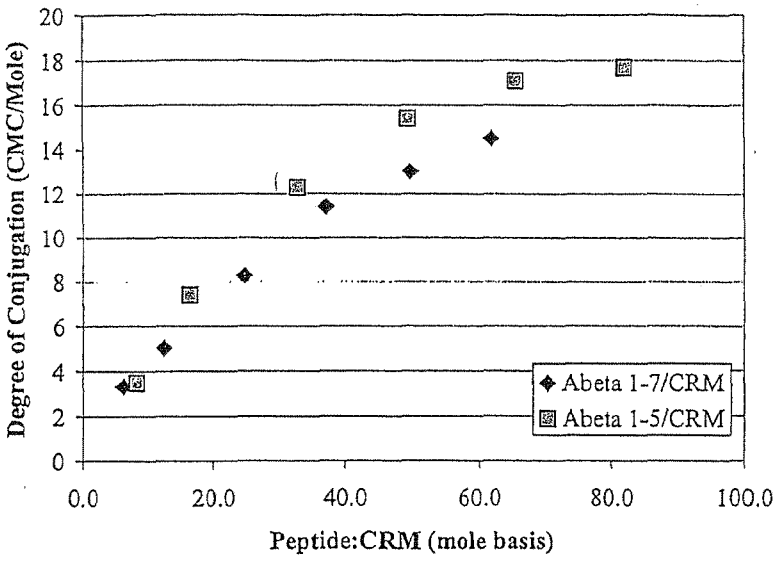

Degree of Conjugation (CMC/Mole)
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18
16
14
12
10
8
6
4
2
0
0.0
20.0
40.0
60.0
80.0
100.0
Peptide:CRM (mole basis)
Abeta 1-7/CRM
Abeta 1-5/CRM

Figure 4

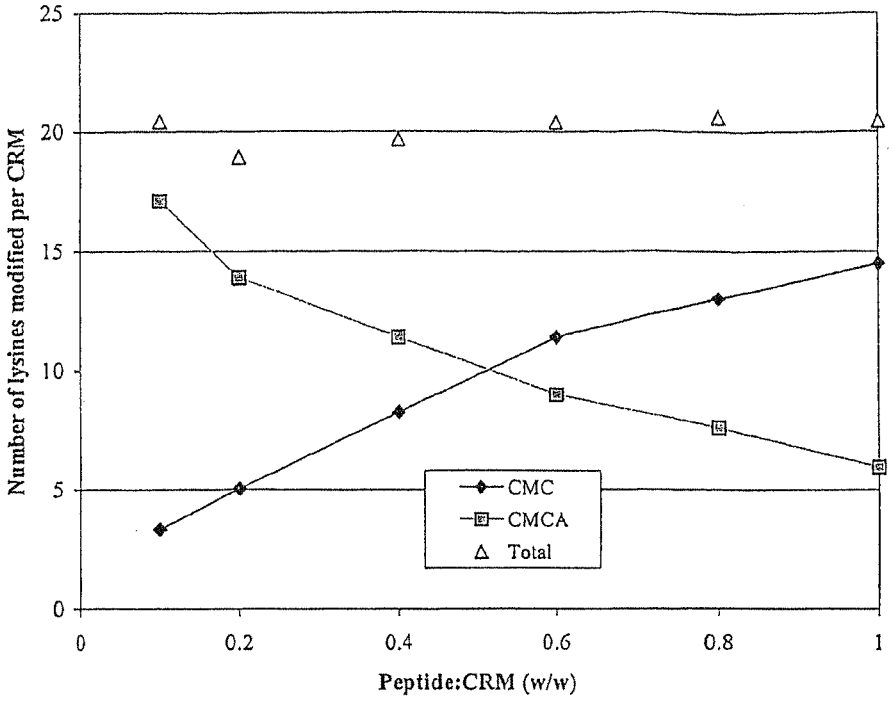

25
20
15
10
5
0
0
0.2
0.4
0.6
0.8
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Number of lysines modified per CRM
Peptide:CRM (w/w)
CMC
CMCA
Total

Figure 5

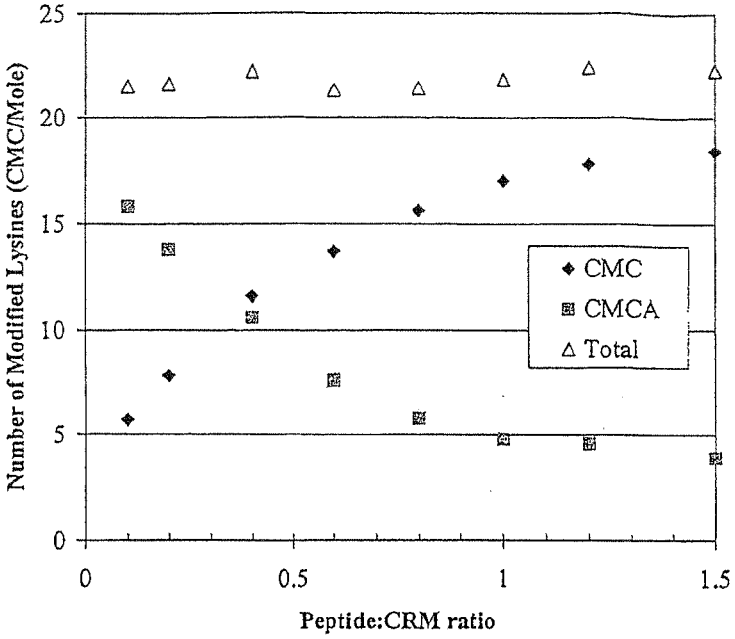

25
20
15
10
5
0
0
0.5
1
1.5
Number of Modified Lysines (CMC/Mole)
Peptide:CRM ratio
CMC
CMCA
Total

Figure 6

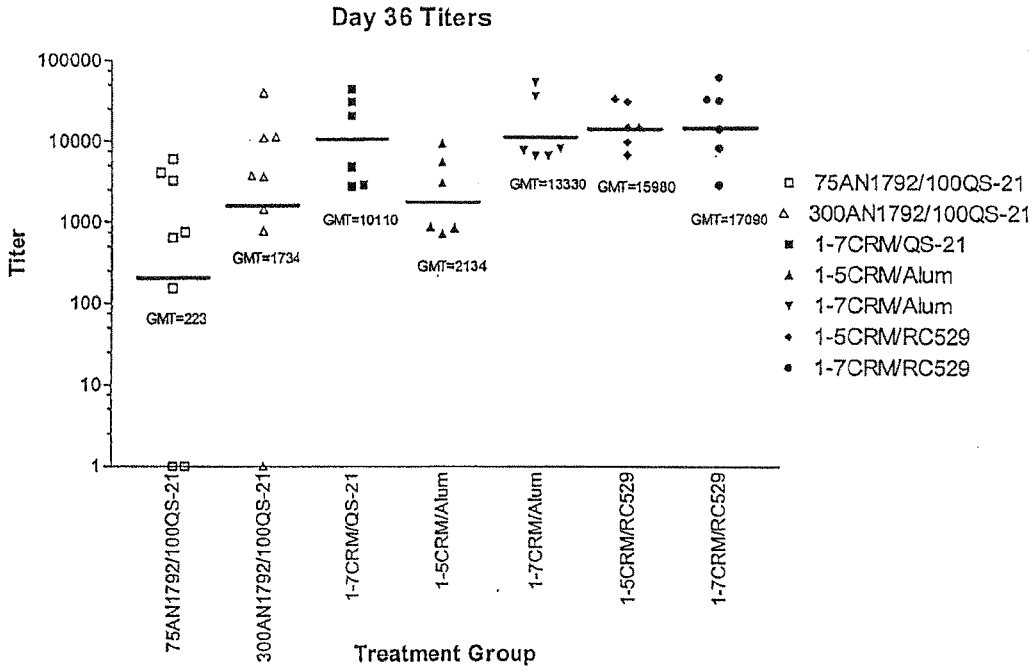

Day 36 Titers
Titer
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10000
1000
100
10
1
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GMT=1734
GMT=10110
GMT=2134
GMT=13330
GMT=15980
GMT=17090
75AN1792/100QS-21
300AN1792/100QS-21
1-7CRM/QS-21
1-5CRM/Alum
1-7CRM/Alum
1-5CRM/RC529
1-7CRM/RC529
Treatment Group

Figure 7

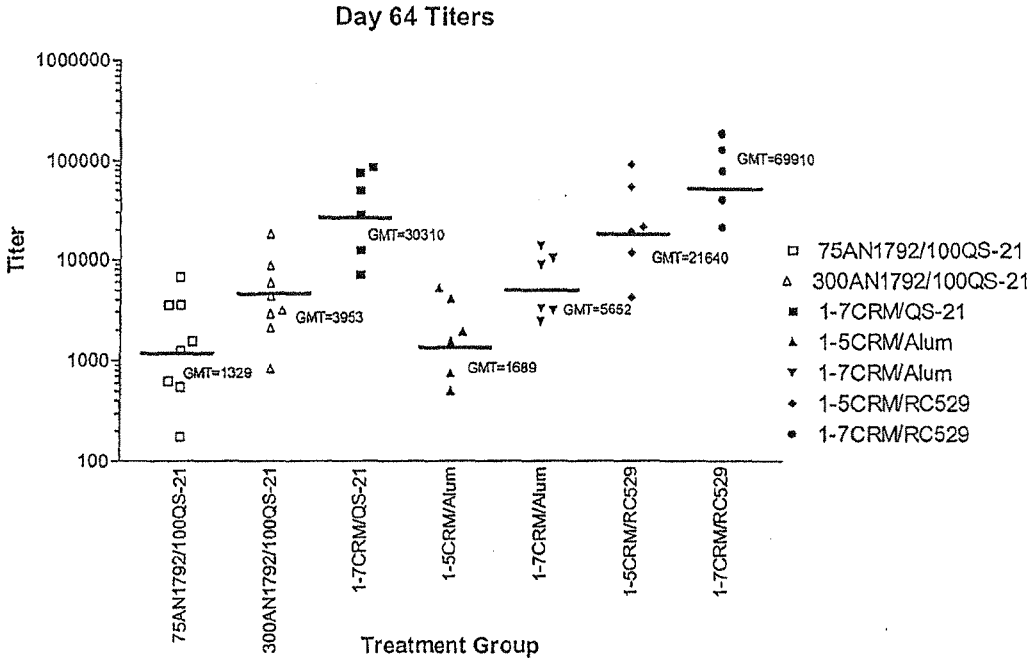

Day 64 Titers
Titer
1000000
100000
10000
1000
100
GMT=1329
GMT=3953
GMT=30310
GMT=1689
GMT=5652
GMT=21640
GMT=69910
75AN1792/100QS-21
300AN1792/100QS-21
1-7CRM/QS-21
1-5CRM/Alum
1-7CRM/Alum
1-5CRM/RC529
1-7CRM/RC529
Treatment Group

Figure 8

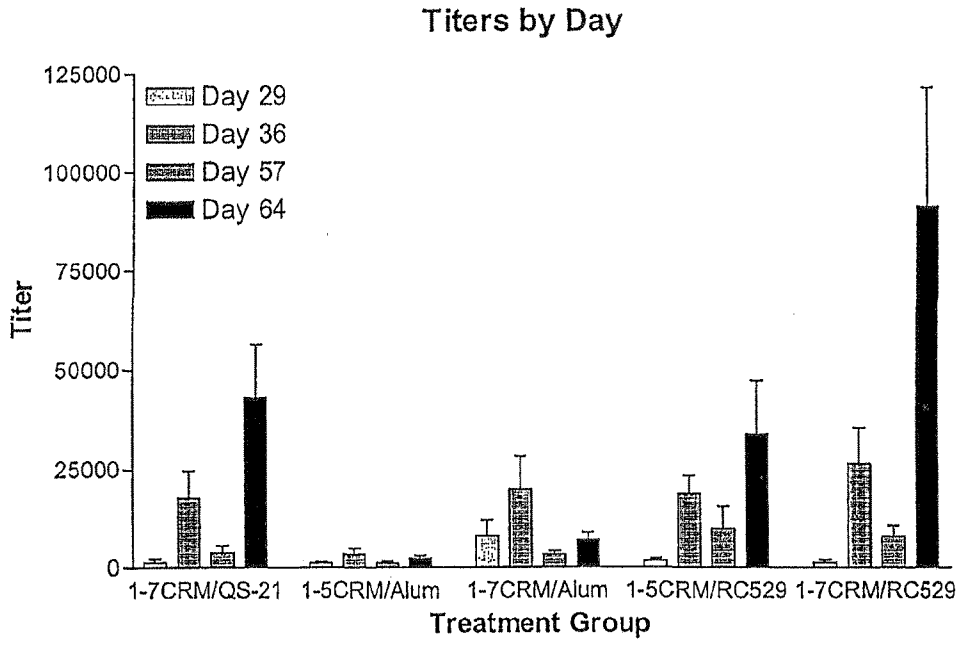

Titers by Day
125000
100000
75000
50000
25000
0
Titer
Day 29
Day 36
Day 57
Day 64
1-7CRM/QS-21
1-5CRM/Alum
1-7CRM/Alum
1-5CRM/RC529
1-7CRM/RC529
Treatment Group

Figure 9

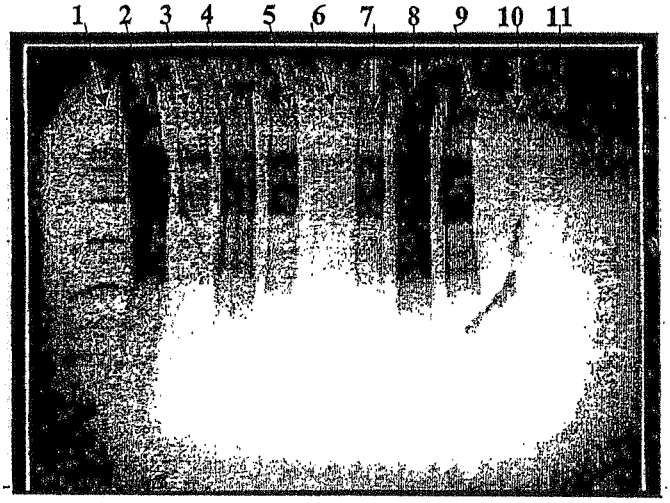


Figure 10

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<150> US 60/530,480

<151> 2003-12-17

<160> 54

<170> PatentIn version 3.3

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His Asp

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35 40 45

Asp Trp Lys Glu Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala Gly
50 55 60

Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
65 70 75 80

Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val
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Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
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Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val
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Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu
    290                 295                 300

Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala
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Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
                325                 330                 335

Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp
            340                 345                 350

Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe
        355                 360                 365

Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly His
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Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp Asn Thr
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Val Glu Asp Ser Ile Ile Arg Thr Gly Phe Gln Gly Glu Ser Gly His
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Asp Ile Lys Ile Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val
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420 425 430

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His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg Ala Ile
450 455 460

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465 470 475 480

Asn Gly Val His Ala Asn Leu His Val Ala Phe His Arg Ser Ser Ser
485 490 495

Glu Lys Ile His Ser Asn Glu Ile Ser Ser Asp Ser Ile Gly Val Leu
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