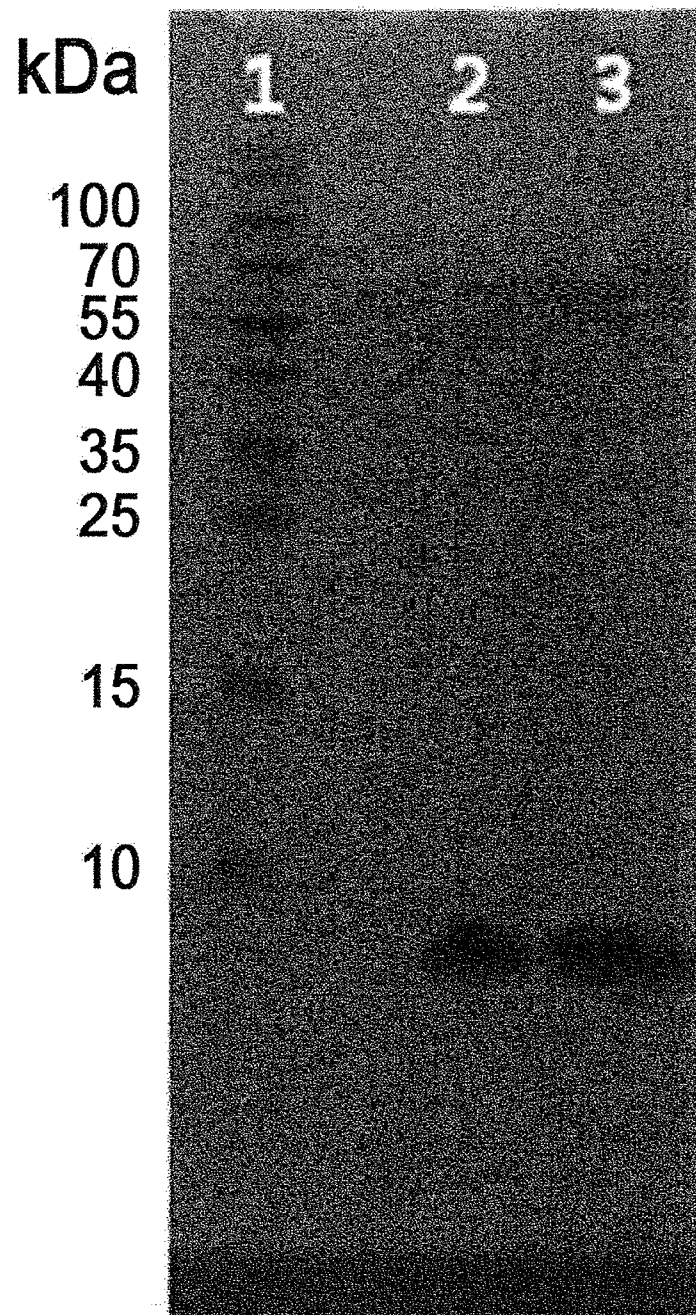
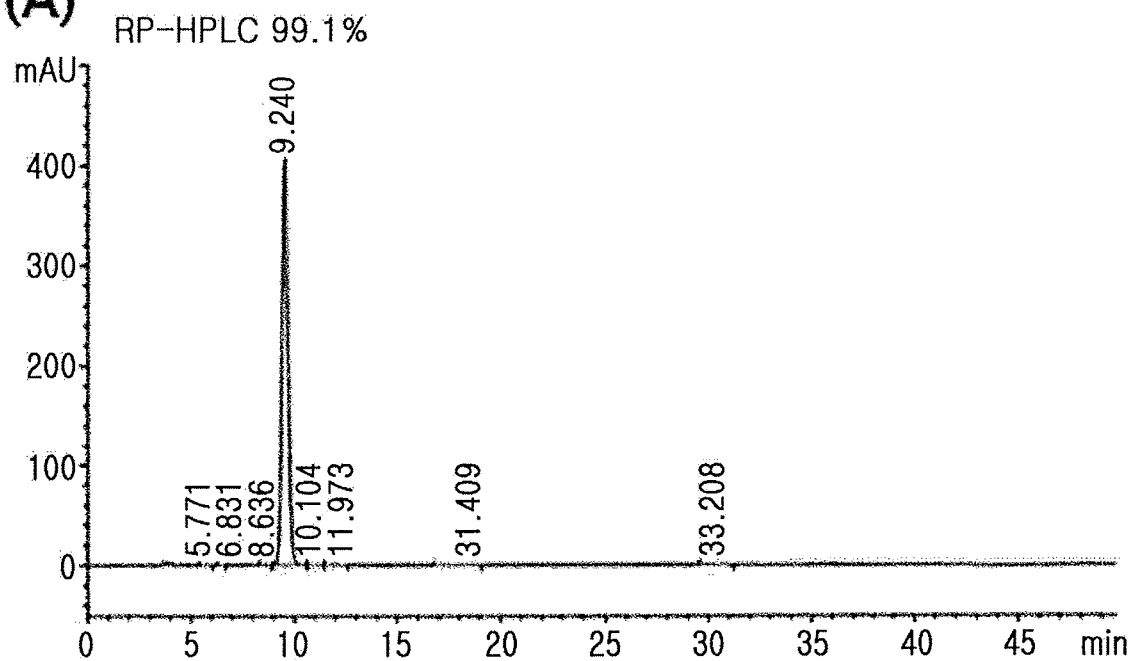


[FIG. 1]

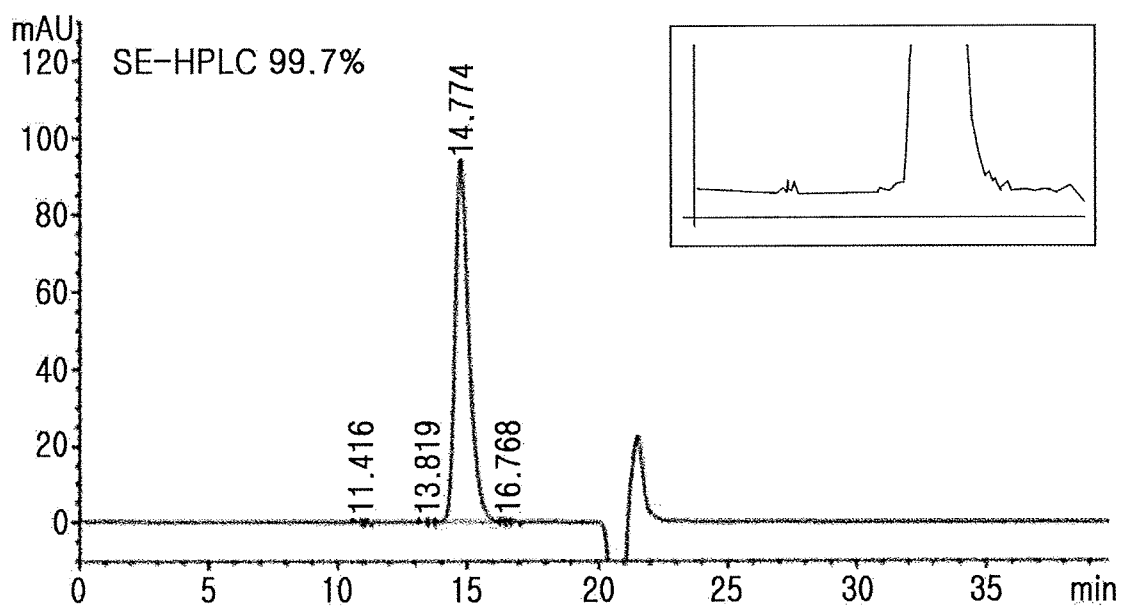


[FIG. 2]

(A)

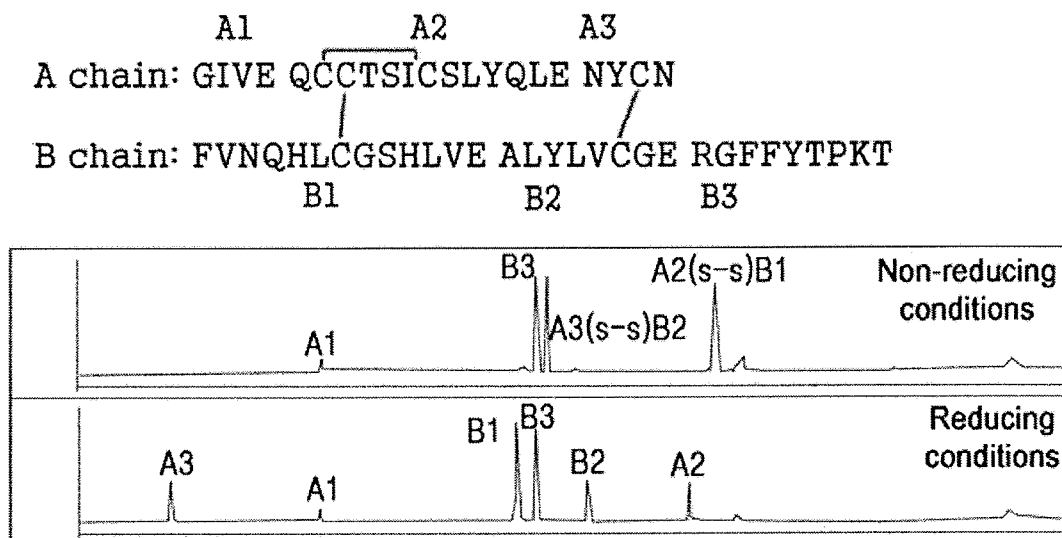


(B)

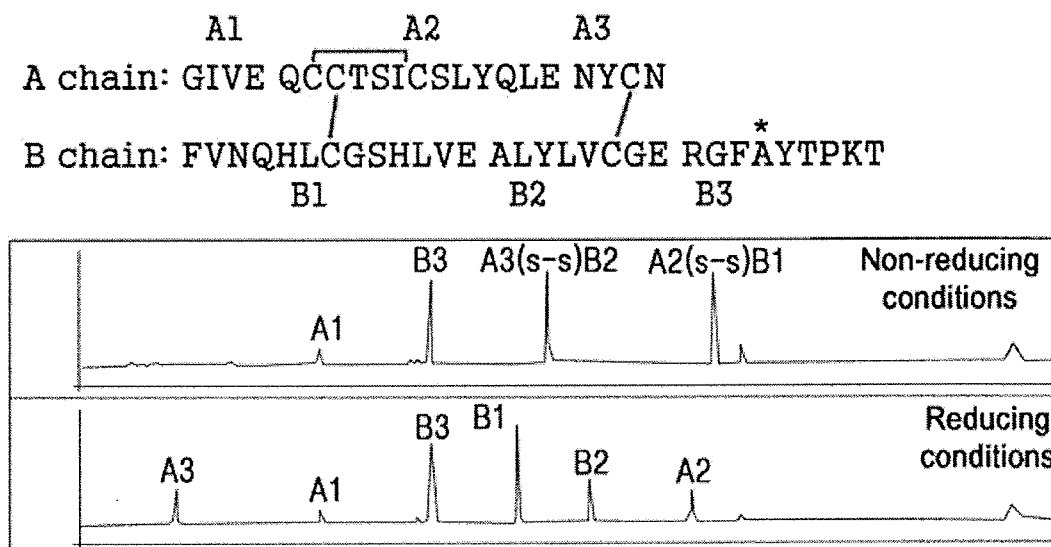


[FIG. 3]

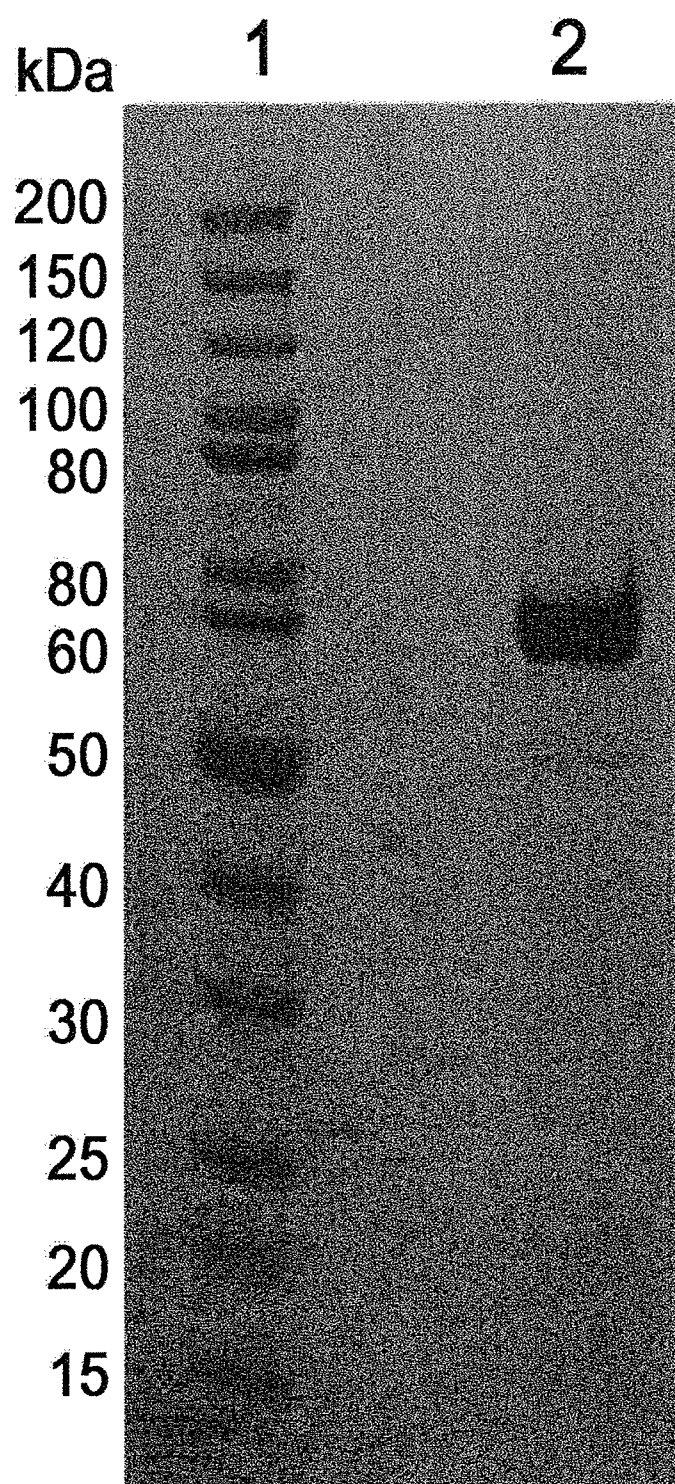
(A) Glu-C cleavage fragment of native insulin sequence



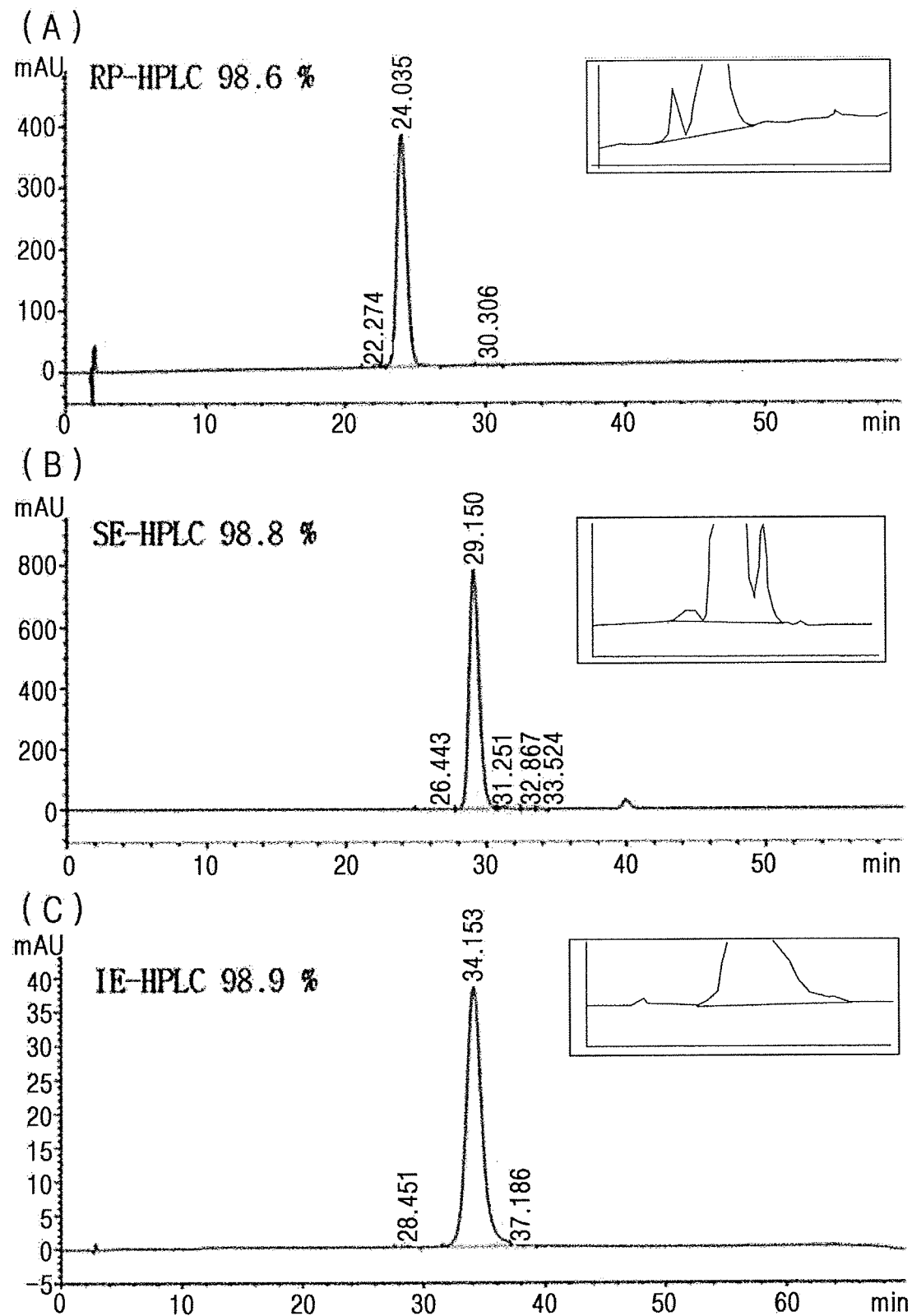
(B) Glu-C cleavage fragment of insulin analog (No. 7) sequence



[FIG. 4]

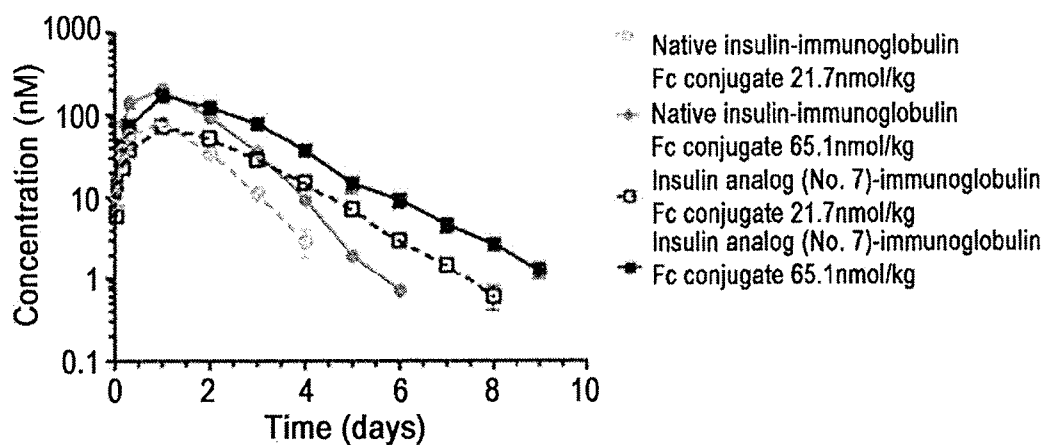


[FIG. 5]

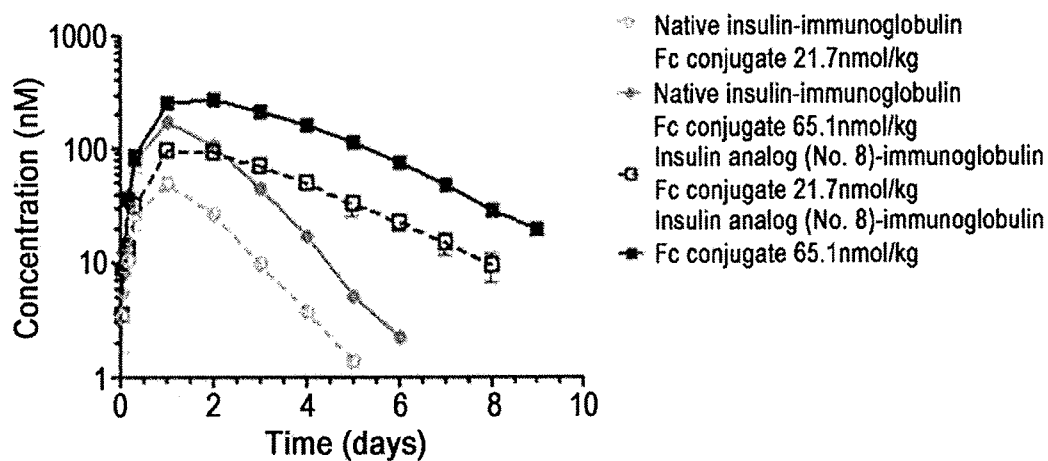


[FIG. 6]

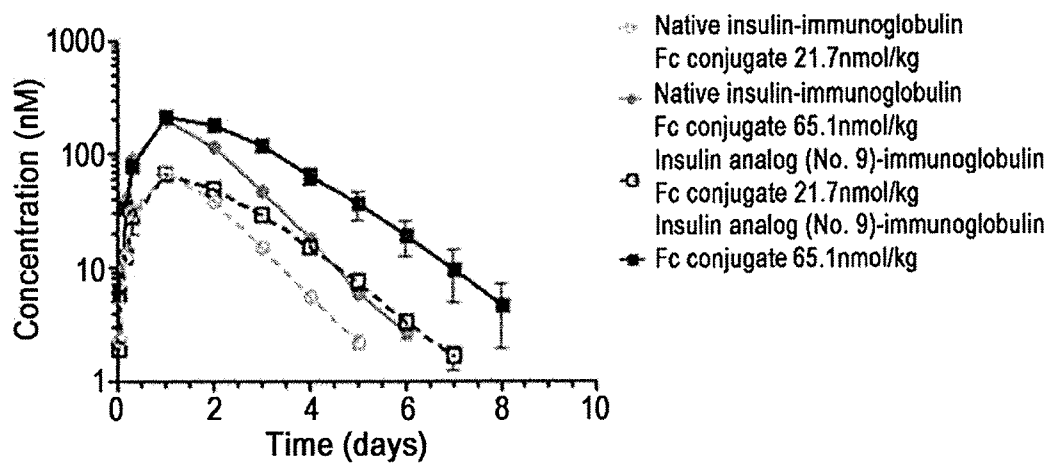
(A)



(B)



(C)



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<220>
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 ctggagaact actgcaac 258

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<223> Analog 1

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Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
35 40 45
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys
50 55 60
Arg Ala Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln
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Leu Glu Asn Tyr Cys Asn
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<223> Analog 2

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cagggtggagc tgggcggggg ccctgggtgca ggcagcctgc agcccttggc cctggagggg 180
tccctgcaga agcgtggcgc ggtggaacaa tgctgtacca gcatctgctc cctctaccag 240
ctggagaact actgcaac 258

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<213> Artificial Sequence

<220>

<223> Analog 2

<400>

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Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg Arg
20 25 30
Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
35 40 45
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys
50 55 60

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Arg Gly Ala Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln
65 70 75 80

Leu Glu Asn Tyr Cys Asn
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cagggtggagc tgggcggggg cccgtgtgca ggcagcctgc agcccttggc cctggagggg 180
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Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg Arg
20 25 30
Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Pro
35 40 45
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys
50 55 60
Arg Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln
65 70 75 80
Leu Glu Asn Ala Cys Asn
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OPA14248-PCT.txt

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ctggagaact actgcaac 258

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

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gaacgagcgt tcttctacac acccaagacc cgccgggagg cagaggacct gcagggtgggg 120
cagggtggagc tgggcggggg ccttggtgca ggcagcctgc agcccttggc cctggagggg 180
tccctgcaga agcgtggcat tgtggaacaa tgctgtacca gcatctgctc cctctaccag 240
ctggagaact actgcaac 258

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<220>
<223> Analog 5

OPA14248-PCT.txt

<400> 28
Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
1 5 10 15
Leu Val Cys Gly Glu Arg Ala Phe Phe Tyr Thr Pro Lys Thr Arg Arg
20 25 30
Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
35 40 45
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys
50 55 60
Arg Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln
65 70 75 80
Leu Glu Asn Tyr Cys Asn
85

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gaacgaggcg cgtttcacac acccaagacc cgccgggagg cagaggacct gcagggtggg 120
cagggtggagc tgggcggggg ccttggtgca ggcagcctgc agcccttggc cctggagggg 180
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ctggagaact actgcaac 258

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Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
1 5 10 15
Leu Val Cys Gly Glu Arg Gly Ala Phe Tyr Thr Pro Lys Thr Arg Arg
20 25 30
Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
35 40 45
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys
50 55 60
Arg Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln
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Leu Glu Asn Tyr Cys Asn

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 cagggtggagc tgggcggggg ccctggtgca ggcagcctgc agcccttggc cctggagggg 180
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 ctggagaact actgcaac 258

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

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<220>
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 cagggtggagc tgggcggggg ccctggtgca ggcagcctgc agcccttggc cctggagggg 180
 9

OPA14248-PCT.txt

tccctgcaga agcgtggcat tgtggaacaa tgctgtacca gcatctgctc cctcgaacag 240
ctggagaact actgcaactg a 261

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Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg Arg
20 25 30
Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
35 40 45
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys
50 55 60
Arg Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Glu Gln
65 70 75 80
Leu Glu Asn Tyr Cys Asn
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cagggtggagc tgggcggggg ccctggtgca ggcagcctgc agcccttggc cctggagggg 180
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ctggagaact actgcaactg a 261

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<220>
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<400> 36
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1 5 10 15
10

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Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg Arg
20 25 30
Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
35 40 45
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys
50 55 60
Arg Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Asn Gln
65 70 75 80
Leu Glu Asn Tyr Cys Asn
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<221> VARIANT
<222> (2)
<223> Xaa is Ile or Ala

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<221> VARIANT
<222> (14)
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Glu Asn Xaa Cys Asn
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 <223> Xaa is Phe or Ala

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 Leu Val Cys Gly Glu Arg Xaa Xaa Xaa Tyr Thr Pro Lys Thr
 20 25 30

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 20 25 30