SEQUENCE LISTING

<110> Avipep Pty Ltd

<120> IMMUNO-CONJUGATES AND METHODS FOR PRODUCING THEM

<130> 509430

<160> 135

<170> PatentIn version 3.5

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

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1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr
20 25 30

<210> 3
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1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr
20 25 30

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser
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Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser
20 25 30

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<400> 7

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser
20 25 30

<210> 8
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<400> 8

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser
20 25 30

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

<210> 10
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<212> PRT
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

<210> 11
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<220>
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<400> 11

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

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<400> 12

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp
20 25 30

<210> 13
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<212> PRT
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<400> 13

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

<210> 14
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
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<210> 15
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1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 16
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Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
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Glu Arg Ala Thr Leu Ser Cys
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<210> 17
<211> 23
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<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 17

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys
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<210> 18
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<400> 18

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1 5 10 15

Glu Arg Ala Thr Leu Ser Cys
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<210> 19
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Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys
20

<210> 20
<211> 23
<212> PRT
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<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 20

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys
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<210> 21
<211> 23
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 21

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

Asp Arg Val Thr Ile Thr Cys
20

<210> 22
<211> 23
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 22

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys
20

<210> 23
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<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 23

Asp Ile Gln Met Thr Gln Ser Pro Asp Phe Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys
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<210> 24
<211> 23
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 24

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 25
<211> 23
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 25

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys
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<210> 26
<211> 23

<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 26

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys
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<210> 27
<211> 23
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<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 27

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

Glu Lys Val Thr Ile Thr Cys
20

<210> 28
<211> 23
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 28

Glu Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly
1 5 10 15

Asp Lys Val Asn Ile Ser Cys
20

<210> 29
<211> 23
<212> PRT
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<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 29

Ala Ile Arg Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

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<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 30

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

Asp Arg Val Thr Ile Thr Cys
20

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<220>
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<400> 31

Asn Ile Gln Met Thr Gln Ser Pro Ser Ala Met Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
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<210> 32
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<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

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Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys
20

<210> 33
<211> 23
<212> PRT
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<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 33

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys
20

<210> 34
<211> 23
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 34

Asp Val Val Met Thr Gln Ser Pro Ala Phe Leu Ser Val Thr Pro Gly
1 5 10 15

Glu Lys Val Thr Ile Thr Cys
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<210> 35
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<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 35

Val Ile Trp Met Thr Gln Ser Pro Ser Leu Leu Ser Ala Ser Thr Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys
20

<210> 36
<211> 23
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody kappa light chain

<400> 36

Ala Ile Arg Met Thr Gln Ser Pro Ser Ser Phe Ser Ala Ser Thr Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys

20

<210> 37
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody lambda light chain

<400> 37

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1 5 10 15

Lys Val Thr Ile Ser Cys
20

<210> 38
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody lambda light chain

<400> 38

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys
20

<210> 39
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody lambda light chain

<400> 39

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys
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<210> 40
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<220>
<223> amino acid sequence within FR1 of a human antibody lambda light chain

<400> 40

Gln Ser Ala Leu Thr Gln Pro Arg Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Val Thr Ile Ser Cys
20

<210> 41
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody lambda light chain

<400> 41

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Arg Ile Thr Cys
20

<210> 42
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody lambda light chain

<400> 42

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys
20

<210> 43
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence within FR1 of a human antibody lambda light chain

<400> 43

Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala
1 5 10 15

Ser Val Lys Leu Thr Cys
20

<210> 44
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence of FR1 of a camelid immunoglobulin

<400> 44

Gly Gly Ser Val Gln Thr Gly Gly Ser Leu Arg Leu Ser Cys Glu Ile
1 5 10 15

Ser Gly Leu Thr Phe Asp
20

<210> 45
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence of FR1 of a camelid immunoglobulin

<400> 45

Gly Gly Ser Val Gln Thr Gly Gly Ser Leu Arg Leu Ser Cys Ala Val
1 5 10 15

Ser Gly Phe Ser Phe Ser
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<210> 46
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence of FR1 of a camelid immunoglobulin

<400> 46

Gly Gly Ser Glu Gln Gly Gly Gly Ser Leu Arg Leu Ser Cys Ala Ile
1 5 10 15

Ser Gly Tyr Thr Tyr Gly
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<210> 47
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence of FR1 of a camelid immunoglobulin

<400> 47

Gly Gly Ser Val Gln Pro Gly Gly Ser Leu Thr Leu Ser Cys Thr Val
1 5 10 15

Ser Gly Ala Thr Tyr Ser
20

<210> 48
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence of FR1 of a camelid immunoglobulin

<400> 48

Gly Gly Ser Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Thr Gly
1 5 10 15

Ser Gly Phe Pro Tyr Ser
20

<210> 49
<211> 21
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence of FR1 of a camelid immunoglobulin

<400> 49

Gly Gly Ser Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Val Ala
1 5 10 15

Gly Phe Gly Thr Ser
20

<210> 50
<211> 21
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence of FR1 of a camelid immunoglobulin

<400> 50

Gly Gly Ser Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Val Ser
1 5 10 15

Phe Ser Pro Ser Ser
20

<210> 51
<211> 24
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence of FR1 of a spiny dogfish shark IgNAR

<400> 51

Ala Trp Val Glu Gln Thr Pro Arg Thr Ala Lys Glu Thr Gly Glu Ser
1 5 10 15

Leu Thr Ile Asn Cys Val Leu Thr
20

<210> 52
<211> 25
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence of FR1 of a nurse shark IgNAR

<400> 52

Ala Arg Val Asp Gln Thr Pro Lys Thr Ile Thr Lys Glu Thr Gly Glu
1 5 10 15

Ser Leu Thr Ile Asn Cys Val Leu Ser
20 25

<210> 53
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence of a linker

<400> 53

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 54
<211> 702
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding AVP04-07 anti-TAG72 diabody

<400> 54
caggtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcggtgg cggcggcagc 360

gatatcgtga tgacccagag cccgagcagc ctgccggtga gcgtgggcga aaaagtgacc 420

ctgagctgca aaagcagcca gagcctgctg tatagcggca atcagaaaaa ctatctggcg 480

tggtatcagc agaaaccggg tcagagcccg aaactgctga tttattgggc gagcacccgt 540

gaaagcggcg tgccggatcg ttttaccggc agcggtagcg gcaccgattt taccctgagc 600

attagcagcg tggaaaccga agatctggcg gtgtattatt gccagcagta ttatagctat 660

ccgctgacct ttggtgcggg caccaaactg gtgctgaaac gt 702

<210> 55
<211> 234
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of AVP04-07 anti-TAG72 diabody

<400> 55

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro
115 120 125

Ser Ser Leu Pro Val Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys
130 135 140

Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala
145 150 155 160

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
165 170 175

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
180 185 190

Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp
195 200 205

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe
210 215 220

Gly Ala Gly Thr Lys Leu Val Leu Lys Arg
225 230

<210> 56
<211> 702
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-07 anti-TAG72 diabody designated AVP04-50 comprising cysteine residues in FR1 and a N-terminal serine

<400> 56
agcgtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcggtgg cggcggcagc 360

gatatcgtga tgacccagag ctgcagcagc tgcccggtga gcgtgggcga aaaagtgacc 420

ctgagctgca aaagcagcca gagcctgctg tatagcggca atcagaaaaa ctatctggcg 480

tggtatcagc agaaaccggg tcagagcccg aaactgctga tttattgggc gagcacccgt 540

gaaagcggcg tgccggatcg ttttaccggc agcggtagcg gcaccgattt taccctgagc 600

attagcagcg tggaaaccga agatctggcg gtgtattatt gccagcagta ttatagctat 660

ccgctgacct ttggtgcggg caccaaactg gtgctgaaac gt 702

<210> 57
<211> 234
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-07 anti-TAG72 diabody designated AVP04-50 comprising cysteine residues in FR1 and a N-terminal serine

<400> 57

Ser Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

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Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
     50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
            100                 105                 110

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Cys
        115                 120                 125

Ser Ser Cys Pro Val Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys
    130                 135                 140

Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala
145                 150                 155                 160

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
                165                 170                 175

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
            180                 185                 190

Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp
        195                 200                 205

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe
    210                 215                 220

Gly Ala Gly Thr Lys Leu Val Leu Lys Arg
225                 230
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<210> 58
<211> 735
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding AVP07-17 anti-Her2 diabody

<400> 58

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tcctgtaagg gttctggata cagctttacc agctactgga tcgcctgggt gcgccagatg     120

cccgggaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac     180

agcccgtcct tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac     240

ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt atttttgtgc gagacatgac     300

gtgggatatt gcagtagttc caactgcgca aagtggcctg aatacttcca gcattggggc     360
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cagggcaccc tggtcaccgt ttcctcaggt ggaggcggtt cacagtctgt gttgacgcag 420

ccgccctcag tgtctgcggc cccaggacag aaggtcacca tctcctgctc tggaagcagc 480

tccaacattg ggaataatta tgtatcctgg taccagcagc tcccaggaac agtccccaaa 540

ctcctcatct atggtcacac caatcggccc gcaggggtcc ctgaccgatt ctctggctcc 600

aagtctggca cctcagcctc cctggccatc agtgggttcc ggtccgagga tgaggctgat 660

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ctgaccgtcc taggt 735

<210> 59
<211> 245
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of AVP07-17 anti-Her2 diabody

<400> 59

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp
100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
130 135 140

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

Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly
165 170 175

Thr Val Pro Lys Leu Leu Ile Tyr Gly His Thr Asn Arg Pro Ala Gly
180 185 190

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

Ala Ile Ser Gly Phe Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala
210 215 220

Ala Trp Asp Asp Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Thr Val Leu Gly
245

<210> 60
<211> 696
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding AVP02-60 anti-MUC1 diabody

<400> 60
gaagtgcagc tggttgaaag cggtggcgga gtggtgcagc caggtggaag cctgcgtctg 60

agctgcgcag caagcggttt acctttagc agctatggca tgagctgggt gcgtcaggcg 120

ccggataaag gcctggaact ggtggcgacc attaacagca acggtggaag cacctattat 180

ccggatagcg tgaaaggccg ttttaccatt agccgtgata acagcaaaaa caccctgtat 240

ctgcagatga acagcctgcg taccgaagat accgcggtgt attattgcgc gcgtgatcgt 300

gatggctatg atgaaggctt tgattattgg ggccagggca ccctggtgac cgtgagcagc 360

ggtgggggcg gaagccagat tcagctgacc cagagcccga gcagcctgag cgcaagcgtg 420

ggtgatcgtg tgaccattac ctgcagcgcg agcagcagcg tgagctatat gcattggtat 480

cagcagaaac cgggcaaagc gccgaaacgt tggatttatg ataccagcaa actggcgagc 540

ggcgtgccga gccgttttag cggcagcggc agcggcaccg attatacctt taccattagc 600

agcctgcagc cggaagatat tgcgacctat tattgccagc agtggagcag caacccgccg 660

acctttggcc agggcaccaa actgcagatt aaacgt 696

<210> 61
<211> 232
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of AVP02-60 anti-MUC1 diabody

<400> 61

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met Ser Trp Val Arg Gln Ala Pro Asp Lys Gly Leu Glu Leu Val
        35                  40                  45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

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

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Ile Gln
        115                 120                 125

Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
    130                 135                 140

Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr
145                 150                 155                 160

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
                165                 170                 175

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
            180                 185                 190

Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
        195                 200                 205

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr Phe Gly Gln
    210                 215                 220

Gly Thr Lys Leu Gln Ile Lys Arg
225                 230
```

<210> 62
<211> 702
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-07 anti-TAG72 diabody designated AVP04-84 comprising cysteine residues in FR1 and a N-terminal serine

<400> 62
agcgtgcagc tgcagcagtg cgatgcgtgc ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat ttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcggtgg cggcggcagc 360

gatatcgtga tgacccagag cccgagcagc ctgccggtga gcgtgggcga aaaagtgacc 420

ctgagctgca aaagcagcca gagcctgctg tatagcggca atcagaaaaa ctatctggcg 480

tggtatcagc agaaaccggg tcagagcccg aaactgctga tttattgggc gagcacccgt 540

gaaagcggcg tgccggatcg ttttaccggc agcggtagcg gcaccgattt taccctgagc 600

attagcagcg tggaaaccga agatctggcg gtgtattatt gccagcagta ttatagctat 660

ccgctgacct ttggtgcggg caccaaactg gtgctgaaac gt 702

<210> 63
<211> 234
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-07 anti-TAG72 diabody designated AVP04-84 comprising cysteine residues in FR1 and a N-terminal serine

<400> 63

Ser Val Gln Leu Gln Gln Cys Asp Ala Cys Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro
115 120 125

Ser Ser Leu Pro Val Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys
130 135 140

Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala
145 150 155 160

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
165 170 175

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
180 185 190

Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp
195 200 205

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe
210 215 220

Gly Ala Gly Thr Lys Leu Val Leu Lys Arg
225 230

<210> 64
<211> 735
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP07-17 anti-Her2 diabody designated AVP07-63 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 64
agcgtgcagc tggtgcagtc tggggcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcgcctgggt gcgccagatg 120

cccgggaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac 240

ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt atttttgtgc gagacatgac 300

gtgggatatg cgagtagttc caacgcggca aagtggcctg aatacttcca gcattggggc 360

cagggcaccc tggtcaccgt ttcctcaggt ggaggcggtt cacagtctgt gttgacgcag 420

ccgtgcagca gctgcgcggc cccaggacag aaggtcacca tctcctgctc tggaagcagc 480

tccaacattg ggaataatta tgtatcctgg taccagcagc tcccaggaac agtccccaaa 540

ctcctcatct atggtcacac caatcggccc gcaggggtcc ctgaccgatt ctctggctcc 600

aagtctggca cctcagcctc cctggccatc agtgggttcc ggtccgagga tgaggctgat 660

tattactgtg cagcatggga tgacagcctg agtggttggg tgttcggcgg agggaccaag 720

ctgaccgtcc taggt 735

<210> 65
<211> 245
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP07-17 anti-Her2 diabody designated AVP07-63 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 65

Ser Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Val Gly Tyr Ala Ser Ser Ser Asn Ala Ala Lys Trp
100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Cys Ser Ser
130 135 140

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

Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly
165 170 175

Thr Val Pro Lys Leu Leu Ile Tyr Gly His Thr Asn Arg Pro Ala Gly
180 185 190

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

Ala Ile Ser Gly Phe Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala
210 215 220

Ala Trp Asp Asp Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Thr Val Leu Gly
245

<210> 66
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence of mutagenic primer for substituting the N-terminal Gln residue with a Ser residue in AVP04-07

<400> 66
cccagccggc catggcgagc gtgcagctgc agcagagcg 39

<210> 67
<211> 38
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence of mutagenic primer for substituting the N-terminal Gln residue with a Ser residue in AVP04-07

<400> 67
cgctctgctg cagctgcacg ctcgccatgg ccggctgg 38

<210> 68
<211> 57
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence of mutagenic primer for replacing cysteine for alanines residues into AVP07-17

<400> 68
gcgagacatg acgtgggata tgcgagtagt tccaacgcgg caaagtggcc tgaatac 57

<210> 69
<211> 57
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence of mutagenic primer for replacing cysteine for alanines residues into AVP07-17

<400> 69
gtattcaggc cactttgccg cgttggaact actcgcatat cccacgtcat gtctcgc 57

<210> 70
<211> 1255
<212> PRT
<213> Homo sapiens

<400> 70

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu

```
1               5                  10                  15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
            20                  25                  30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
        35                  40                  45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
    50                  55                  60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65                  70                  75                  80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
                85                  90                  95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
            100                 105                 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
        115                 120                 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
    130                 135                 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145                 150                 155                 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
                165                 170                 175

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

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
        195                 200                 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
    210                 215                 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225                 230                 235                 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
                245                 250                 255

His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
            260                 265                 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
```

275 280 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
290 295 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305 310 315 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
325 330 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
340 345 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
355 360 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
370 375 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385 390 395 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
405 410 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
420 425 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
435 440 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
450 455 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465 470 475 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
485 490 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
500 505 510

Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
515 520 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
530 535 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys

545 550 555 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
565 570 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
580 585 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
595 600 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
610 615 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
625 630 635 640

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

Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
660 665 670

Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
675 680 685

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

Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
705 710 715 720

Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
725 730 735

Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
740 745 750

Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
755 760 765

Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
770 775 780

Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
785 790 795 800

Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
805 810 815

Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly

820 825 830

Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
835 840 845

Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
850 855 860

Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
865 870 875 880

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
885 890 895

Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
900 905 910

Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
915 920 925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
930 935 940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
945 950 955 960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
965 970 975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
980 985 990

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
995 1000 1005

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr
1010 1015 1020

Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly
1025 1030 1035

Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg
1040 1045 1050

Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu
1055 1060 1065

Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
1070 1075 1080

Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu

1085 1090 1095

Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser
1100 1105 1110

Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val
1115 1120 1125

Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
1130 1135 1140

Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro
1145 1150 1155

Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Ala Lys Thr Leu
1160 1165 1170

Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly
1175 1180 1185

Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala
1190 1195 1200

Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp
1205 1210 1215

Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro
1220 1225 1230

Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
1235 1240 1245

Leu Gly Leu Asp Val Pro Val
1250 1255

<210> 71
<211> 750
<212> PRT
<213> Homo sapiens

<400> 71

Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
1 5 10 15

Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
20 25 30

Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
35 40 45

Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
50 55 60

```
Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His Asn Phe Thr Gln Ile
65                  70                  75                  80

Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
                85                  90                  95

Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
            100                 105                 110

Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
        115                 120                 125

Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
    130                 135                 140

Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
145                 150                 155                 160

Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
                165                 170                 175

Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
            180                 185                 190

Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
        195                 200                 205

Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
    210                 215                 220

Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
225                 230                 235                 240

Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
                245                 250                 255

Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
            260                 265                 270

Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
        275                 280                 285

Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
    290                 295                 300

Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
305                 310                 315                 320

Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
                325                 330                 335
```

Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
340 345 350

Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
355 360 365

Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
370 375 380

Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
385 390 395 400

Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
405 410 415

Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
420 425 430

Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
435 440 445

Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
450 455 460

Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
465 470 475 480

Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
485 490 495

Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
500 505 510

Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
515 520 525

Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
530 535 540

Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
545 550 555 560

Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
565 570 575

Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
580 585 590

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
595 600 605

```
Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
    610                 615                 620

Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
625                 630                 635                 640

Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
                645                 650                 655

Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
            660                 665                 670

Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
        675                 680                 685

His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
    690                 695                 700

Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
705                 710                 715                 720

Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
                725                 730                 735

Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
            740                 745                 750
```

<210> 72
<211> 475
<212> PRT
<213> Homo sapiens

<400> 72

```
Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
1               5                   10                  15

Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
            20                  25                  30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
        35                  40                  45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
    50                  55                  60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65                  70                  75                  80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
                85                  90                  95
```

```
Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
            100                 105                 110

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
        115                 120                 125

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    130                 135                 140

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
145                 150                 155                 160

Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val His
                165                 170                 175

Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu
            180                 185                 190

Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys
        195                 200                 205

Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr Thr
    210                 215                 220

Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser Thr His His Ser
225                 230                 235                 240

Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln Leu
                245                 250                 255

Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn Leu
            260                 265                 270

Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu
        275                 280                 285

Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly
    290                 295                 300

Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val
305                 310                 315                 320

Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp
                325                 330                 335

Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr
            340                 345                 350

Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe
        355                 360                 365
```

```
Ser Ala Gln Ser Gly Ala Gly Val Pro Gly Trp Gly Ile Ala Leu Leu
    370                 375                 380

Val Leu Val Cys Val Leu Val Ala Leu Ala Ile Val Tyr Leu Ile Ala
385                 390                 395                 400

Leu Ala Val Cys Gln Cys Arg Arg Lys Asn Tyr Gly Gln Leu Asp Ile
                405                 410                 415

Phe Pro Ala Arg Asp Thr Tyr His Pro Met Ser Glu Tyr Pro Thr Tyr
            420                 425                 430

His Thr His Gly Arg Tyr Val Pro Pro Ser Ser Thr Asp Arg Ser Pro
        435                 440                 445

Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly Ser Ser Leu Ser Tyr Thr
    450                 455                 460

Asn Pro Ala Val Ala Ala Thr Ser Ala Asn Leu
465                 470                 475
```

<210> 73
<211> 307
<212> PRT
<213> Homo sapiens

<400> 73

```
Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
1               5                   10                  15

Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
            20                  25                  30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
        35                  40                  45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
    50                  55                  60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65                  70                  75                  80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
                85                  90                  95

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
            100                 105                 110

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
        115                 120                 125
```

```
Gly Ser Thr Ala Pro Pro Ala Gln Gly Val Thr Ser Ala Pro Glu Thr
     130                 135                 140

Arg Pro Pro Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
145                 150                 155                 160

Ala Pro Asp Asn Arg Pro Ala Leu Ala Ser Thr Ala Pro Pro Val His
                165                 170                 175

Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu
            180                 185                 190

Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys
        195                 200                 205

Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr Thr
    210                 215                 220

Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser Thr His His Ser
225                 230                 235                 240

Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln Leu
                245                 250                 255

Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn Leu
            260                 265                 270

Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu
        275                 280                 285

Leu Gln Arg Asp Ile Ser Glu Met Val Ser Ile Gly Leu Ser Phe Pro
    290                 295                 300

Met Leu Pro
305
```

<210> 74
<211> 702
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-07 anti-TAG72 diabody designated AVP04-85 comprising cysteine residues in FR1 and a N-terminal serine

<400> 74

```
agcgtgcagc tgcagcagag cgatgcggaa ctggtgtgcc cgggctgcag cgtgaaaatt       60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat      120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat      180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat      240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg      300
```

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcggtgg cggcggcagc 360

gatatcgtga tgacccagag cccgagcagc ctgccggtga gcgtgggcga aaaagtgacc 420

ctgagctgca aaagcagcca gagcctgctg tatagcggca atcagaaaaa ctatctggcg 480

tggtatcagc agaaaccggg tcagagcccg aaactgctga tttattgggc gagcacccgt 540

gaaagcggcg tgccggatcg ttttaccggc agcggtagcg gcaccgattt taccctgagc 600

attagcagcg tggaaaccga agatctggcg gtgtattatt gccagcagta ttatagctat 660

ccgctgacct ttggtgcggg caccaaactg gtgctgaaac gt 702

<210> 75
<211> 234
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-07 anti-TAG72 diabody designated AVP04-85 comprising cysteine residues in FR1 and a N-terminal serine

<400> 75

Ser Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Cys Pro Gly Cys
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro
115 120 125

Ser Ser Leu Pro Val Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys
130 135 140

Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala
145 150 155 160

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
165 170 175

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
180 185 190

Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp
195 200 205

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe
210 215 220

Gly Ala Gly Thr Lys Leu Val Leu Lys Arg
225 230

<210> 76
<211> 702
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-07 anti-TAG72 diabody designated AVP04-78 comprising cysteine residues in FR1 and a N-terminal serine

<400> 76
agcgtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcggtgg cggcggcagc 360

gatatcgtga tgacccagag cccgagcagc ctgccggtgt gcgtgggctg caaagtgacc 420

ctgagctgca aaagcagcca gagcctgctg tatagcggca atcagaaaaa ctatctggcg 480

tggtatcagc agaaaccggg tcagagcccg aaactgctga tttattgggc gagcacccgt 540

gaaagcggcg tgccggatcg ttttaccggc agcggtagcg gcaccgattt taccctgagc 600

attagcagcg tggaaaccga agatctggcg gtgtattatt gccagcagta ttatagctat 660

ccgctgacct ttggtgcggg caccaaactg gtgctgaaac gt 702

<210> 77
<211> 234
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-07 anti-TAG72 diabody designated AVP04-78 comprising cysteine residues in FR1 and a N-terminal serine

<400> 77

Ser Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro
115 120 125

Ser Ser Leu Pro Val Cys Val Gly Cys Lys Val Thr Leu Ser Cys Lys
130 135 140

Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala
145 150 155 160

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
165 170 175

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
180 185 190

Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp
195 200 205

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe
210 215 220

Gly Ala Gly Thr Lys Leu Val Leu Lys Arg
225 230

<210> 78
<211> 696
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP02-60 anti-MUC1 diabody designated AVP02-101 comprising cysteine residues in FR1 and a

N-terminal serine

<400> 78
agcgtgcagc tggttgaaag cggtggcgga gtggtgcagc caggtggaag cctgcgtctg 60

agctgcgcag caagcggttt acctttagc agctatggca tgagctgggt gcgtcaggcg 120

ccggataaag gcctggaact ggtggcgacc attaacagca acggtggaag cacctattat 180

ccggatagcg tgaaaggccg ttttaccatt agccgtgata acagcaaaaa caccctgtat 240

ctgcagatga acagcctgcg taccgaagat accgcggtgt attattgcgc gcgtgatcgt 300

gatggctatg atgaaggctt tgattattgg ggccagggca ccctggtgac cgtgagcagc 360

ggtgggggcg gaagccagat tcagctgacc cagagctgca gcagctgcag cgcaagcgtg 420

ggtgatcgtg tgaccattac ctgcagcgcg agcagcagcg tgagctatat gcattggtat 480

cagcagaaac cgggcaaagc gccgaaacgt tggatttatg ataccagcaa actggcgagc 540

ggcgtgccga gccgttttag cggcagcggc agcggcaccg attatacctt taccattagc 600

agcctgcagc cggaagatat tgcgacctat tattgccagc agtggagcag caacccgccg 660

acctttggcc agggcaccaa actgcagatt aaacgt 696

<210> 79
<211> 232
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP02-60 anti-MUC1 diabody designated AVP02-101 comprising cysteine residues in FR1 and a N-terminal serine

<400> 79

Ser Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Asp Lys Gly Leu Glu Leu Val
35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Ile Gln
115 120 125

Leu Thr Gln Ser Cys Ser Ser Cys Ser Ala Ser Val Gly Asp Arg Val
130 135 140

Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr
145 150 155 160

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
165 170 175

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
180 185 190

Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
195 200 205

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr Phe Gly Gln
210 215 220

Gly Thr Lys Leu Gln Ile Lys Arg
225 230

<210> 80
<211> 696
<212> PRT
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP02-60 anti-MUC1 diabody designated AVP02-104 comprising cysteine residues in FR1 and a N-terminal serine

<400> 80

Ala Gly Cys Gly Thr Gly Cys Ala Gly Cys Thr Gly Gly Thr Thr Gly
1 5 10 15

Ala Ala Thr Gly Cys Gly Gly Thr Gly Gly Cys Thr Gly Cys Gly Thr
20 25 30

Gly Gly Thr Gly Cys Ala Gly Cys Cys Ala Gly Gly Thr Gly Gly Ala
35 40 45

Ala Gly Cys Cys Thr Gly Cys Gly Thr Cys Thr Gly Ala Gly Cys Thr
50 55 60

Gly Cys Gly Cys Ala Gly Cys Ala Ala Gly Cys Gly Gly Thr Thr Thr
65 70 75 80

Thr Ala Cys Cys Thr Thr Thr Ala Gly Cys Ala Gly Cys Thr Ala Thr
85 90 95

```
Gly Gly Cys Ala Thr Gly Ala Gly Cys Thr Gly Gly Gly Thr Gly Cys
            100                 105                 110

Gly Thr Cys Ala Gly Gly Cys Gly Cys Cys Gly Gly Ala Thr Ala Ala
        115                 120                 125

Ala Gly Gly Cys Cys Thr Gly Gly Ala Ala Cys Thr Gly Gly Thr Gly
    130                 135                 140

Gly Cys Gly Ala Cys Cys Ala Thr Thr Ala Ala Cys Ala Gly Cys Ala
145                 150                 155                 160

Ala Cys Gly Gly Thr Gly Gly Ala Ala Gly Cys Ala Cys Cys Thr Ala
                165                 170                 175

Thr Thr Ala Thr Cys Cys Gly Gly Ala Thr Ala Gly Cys Gly Thr Gly
            180                 185                 190

Ala Ala Ala Gly Gly Cys Cys Gly Thr Thr Thr Thr Ala Cys Cys Ala
        195                 200                 205

Thr Thr Ala Gly Cys Cys Gly Thr Gly Ala Thr Ala Ala Cys Ala Gly
    210                 215                 220

Cys Ala Ala Ala Ala Ala Cys Ala Cys Cys Cys Thr Gly Thr Ala Thr
225                 230                 235                 240

Cys Thr Gly Cys Ala Gly Ala Thr Gly Ala Ala Cys Ala Gly Cys Cys
                245                 250                 255

Thr Gly Cys Gly Thr Ala Cys Cys Gly Ala Ala Gly Ala Thr Ala Cys
            260                 265                 270

Cys Gly Cys Gly Gly Thr Gly Thr Ala Thr Thr Ala Thr Thr Gly Cys
        275                 280                 285

Gly Cys Gly Cys Gly Thr Gly Ala Thr Cys Gly Thr Gly Ala Thr Gly
    290                 295                 300

Gly Cys Thr Ala Thr Gly Ala Thr Gly Ala Ala Gly Gly Cys Thr Thr
305                 310                 315                 320

Thr Gly Ala Thr Thr Ala Thr Thr Gly Gly Gly Gly Cys Cys Ala Gly
                325                 330                 335

Gly Gly Cys Ala Cys Cys Cys Thr Gly Gly Thr Gly Ala Cys Cys Gly
            340                 345                 350

Thr Gly Ala Gly Cys Ala Gly Cys Gly Gly Thr Gly Gly Gly Gly Gly
        355                 360                 365
```

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Cys Gly Gly Ala Ala Gly Cys Cys Ala Gly Ala Thr Thr Cys Ala Gly
370                 375                 380

Cys Thr Gly Ala Cys Cys Cys Ala Gly Ala Gly Cys Cys Cys Gly Ala
385                 390                 395                 400

Gly Cys Ala Gly Cys Cys Thr Gly Ala Gly Cys Gly Cys Ala Ala Gly
                405                 410                 415

Cys Gly Thr Gly Gly Gly Thr Gly Ala Thr Cys Gly Thr Gly Thr Gly
            420                 425                 430

Ala Cys Cys Ala Thr Thr Ala Cys Cys Thr Gly Cys Ala Gly Cys Gly
        435                 440                 445

Cys Gly Ala Gly Cys Ala Gly Cys Ala Gly Cys Gly Thr Gly Ala Gly
    450                 455                 460

Cys Thr Ala Thr Ala Thr Gly Cys Ala Thr Thr Gly Gly Thr Ala Thr
465                 470                 475                 480

Cys Ala Gly Cys Ala Gly Ala Ala Ala Cys Cys Gly Gly Gly Cys Ala
                485                 490                 495

Ala Ala Gly Cys Gly Cys Cys Gly Ala Ala Ala Cys Gly Thr Thr Gly
            500                 505                 510

Gly Ala Thr Thr Thr Ala Thr Gly Ala Thr Ala Cys Cys Ala Gly Cys
        515                 520                 525

Ala Ala Ala Cys Thr Gly Gly Cys Gly Ala Gly Cys Gly Gly Cys Gly
    530                 535                 540

Thr Gly Cys Cys Gly Ala Gly Cys Cys Gly Thr Thr Thr Thr Ala Gly
545                 550                 555                 560

Cys Gly Gly Cys Ala Gly Cys Gly Gly Cys Ala Gly Cys Gly Gly Cys
                565                 570                 575

Ala Cys Cys Gly Ala Thr Thr Ala Thr Ala Cys Cys Thr Thr Thr Ala
            580                 585                 590

Cys Cys Ala Thr Thr Ala Gly Cys Ala Gly Cys Cys Thr Gly Cys Ala
        595                 600                 605

Gly Cys Cys Gly Gly Ala Ala Gly Ala Thr Ala Thr Thr Gly Cys Gly
    610                 615                 620

Ala Cys Cys Thr Ala Thr Thr Ala Thr Thr Gly Cys Cys Ala Gly Cys
625                 630                 635                 640
```

Ala Gly Thr Gly Gly Ala Gly Cys Ala Gly Cys Ala Ala Cys Cys Cys
645 650 655

Gly Cys Cys Gly Ala Cys Cys Thr Thr Thr Gly Gly Cys Cys Ala Gly
660 665 670

Gly Gly Cys Ala Cys Cys Ala Ala Ala Cys Thr Gly Cys Ala Gly Ala
675 680 685

Thr Thr Ala Ala Ala Cys Gly Thr
690 695

<210> 81
<211> 232
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP02-60 anti-MUC1 diabody designated AVP02-104 comprising cysteine residues in FR1 and a N-terminal serine

<400> 81

Ser Val Gln Leu Val Glu Cys Gly Gly Cys Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Asp Lys Gly Leu Glu Leu Val
35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Ile Gln
115 120 125

Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
130 135 140

Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr
145 150 155 160

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
165 170 175

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
180 185 190

Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
195 200 205

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr Phe Gly Gln
210 215 220

Gly Thr Lys Leu Gln Ile Lys Arg
225 230

<210> 82
<211> 696
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP02-60 anti-MUC1 diabody designated AVP02-102 comprising cysteine residues in FR1 and a N-terminal serine

<400> 82
agcgtgcagc tggttgaaag cggtggcgga gtggtgcagc caggtggaag cctgcgtctg 60

agctgcgcag caagcggttt acctttagc agctatggca tgagctgggt gcgtcaggcg 120

ccggataaag gcctggaact ggtggcgacc attaacagca acggtggaag cacctattat 180

ccggatagcg tgaaaggccg ttttaccatt agccgtgata acagcaaaaa caccctgtat 240

ctgcagatga acagcctgcg taccgaagat accgcggtgt attattgcgc gcgtgatcgt 300

gatggctatg atgaaggctt tgattattgg ggccagggca ccctggtgac cgtgagcagc 360

ggtgggggcg gaagccagat tcagctgacc cagagcccga gcagcctgag cgcatgcgtg 420

ggttgccgtg tgaccattac ctgcagcgcg agcagcagcg tgagctatat gcattggtat 480

cagcagaaac cgggcaaagc gccgaaacgt tggatttatg ataccagcaa actggcgagc 540

ggcgtgccga gccgttttag cggcagcggc agcggcaccg attatacctt taccattagc 600

agcctgcagc cggaagatat tgcgacctat tattgccagc agtggagcag caacccgccg 660

acctttggcc agggcaccaa actgcagatt aaacgt 696

<210> 83
<211> 232
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP02-60 anti-MUC1 diabody designated AVP02-102 comprising cysteine residues in FR1 and a N-terminal serine

<400> 83

```
Ser Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met Ser Trp Val Arg Gln Ala Pro Asp Lys Gly Leu Glu Leu Val
        35                  40                  45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

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

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Ile Gln
        115                 120                 125

Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Cys Val Gly Cys Arg Val
    130                 135                 140

Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr
145                 150                 155                 160

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
                165                 170                 175

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
            180                 185                 190

Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
        195                 200                 205

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr Phe Gly Gln
    210                 215                 220

Gly Thr Lys Leu Gln Ile Lys Arg
225                 230
```

<210> 84
<211> 696
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP02-60 anti-MUC1 diabody designated AVP02-105 comprising cysteine residues in FR1 and a

N-terminal serine

<400> 84
agcgtgcagc tggttgaaag cggtggcgga gtggtgtgcc caggttgcag cctgcgtctg 60

agctgcgcag caagcggttt acctttagc agctatggca tgagctgggt gcgtcaggcg 120

ccggataaag gcctggaact ggtggcgacc attaacagca acggtggaag cacctattat 180

ccggatagcg tgaaaggccg ttttaccatt agccgtgata acagcaaaaa caccctgtat 240

ctgcagatga acagcctgcg taccgaagat accgcggtgt attattgcgc gcgtgatcgt 300

gatggctatg atgaaggctt tgattattgg ggccagggca ccctggtgac cgtgagcagc 360

ggtgggggcg gaagccagat tcagctgacc cagagcccga gcagcctgag cgcaagcgtg 420

ggtgatcgtg tgaccattac ctgcagcgcg agcagcagcg tgagctatat gcattggtat 480

cagcagaaac cgggcaaagc gccgaaacgt tggatttatg ataccagcaa actggcgagc 540

ggcgtgccga gccgttttag cggcagcggc agcggcaccg attatacctt taccattagc 600

agcctgcagc cggaagatat tgcgacctat tattgccagc agtggagcag caacccgccg 660

acctttggcc agggcaccaa actgcagatt aaacgt 696

<210> 85
<211> 232
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP02-60 anti-MUC1 diabody designated AVP02-105 comprising cysteine residues in FR1 and a N-terminal serine

<400> 85

Ser Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Cys Pro Gly Cys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Asp Lys Gly Leu Glu Leu Val
35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Gln
100 105 110

```
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Ile Gln
        115                 120                 125

Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
    130                 135                 140

Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr
145                 150                 155                 160

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
                165                 170                 175

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
            180                 185                 190

Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
        195                 200                 205

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr Phe Gly Gln
    210                 215                 220

Gly Thr Lys Leu Gln Ile Lys Arg
225                 230
```

<210> 86
<211> 735
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP07-17 anti-HER2 diabody designated AVP07-88 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 86

```
agcgtgcagc tggtgcagtg tggggcatgt gtgaaaaagc ccggggagtc tctgaagatc       60

tcctgtaagg gttctggata cagctttacc agctactgga tcgcctgggt gcgccagatg      120

cccgggaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac      180

agcccgtcct tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac      240

ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt atttttgtgc gagacatgac      300

gtgggatatg cgagtagttc caacgcggca aagtggcctg aatacttcca gcattggggc      360

cagggcaccc tggtcaccgt ttcctcaggt ggaggcggtt cacagtctgt gttgacgcag      420

ccgccctcag tgtctgcggc cccaggacag aaggtcacca tctcctgctc tggaagcagc      480

tccaacattg ggaataatta tgtatcctgg taccagcagc tcccaggaac agtccccaaa      540

ctcctcatct atggtcacac caatcggccc gcaggggtcc ctgaccgatt ctctggctcc      600

aagtctggca cctcagcctc cctggccatc agtgggttcc ggtccgagga tgaggctgat      660

tattactgtg cagcatggga tgacagcctg agtggttggg tgttcggcgg agggaccaag      720

ctgaccgtcc taggt                                                       735
```

<210> 87
<211> 245
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP07-17 anti-HER2 diabody designated AVP07-88 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 87

```
Ser Val Gln Leu Val Gln Cys Gly Ala Cys Val Lys Lys Pro Gly Glu
1               5                  10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
        35                  40                  45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg His Asp Val Gly Tyr Ala Ser Ser Ser Asn Ala Ala Lys Trp
            100                 105                 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
    130                 135                 140

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

Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly
                165                 170                 175

Thr Val Pro Lys Leu Leu Ile Tyr Gly His Thr Asn Arg Pro Ala Gly
            180                 185                 190

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

Ala Ile Ser Gly Phe Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala
    210                 215                 220
```

Ala Trp Asp Asp Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Thr Val Leu Gly
245

<210> 88
<211> 735
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP07-17 anti-HER2 diabody designated AVP07-90 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 88
agcgtgcagc tggtgcagtg tggggcatgt gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcgcctgggt gcgccagatg 120

cccgggaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac 240

ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt atttttgtgc gagacatgac 300

gtgggatatg cgagtagttc caacgcggca aagtggcctg aatacttcca gcattggggc 360

cagggcaccc tggtcaccgt ttcctcaggt ggaggcggtt cacagtctgt gttgacgcag 420

ccgccctcag tgtctgcggc cccaggacag aaggtcacca tctcctgctc tggaagcagc 480

tccaacattg ggaataatta tgtatcctgg taccagcagc tcccaggaac agtccccaaa 540

ctcctcatct atggtcacac caatcggccc gcaggggtcc ctgaccgatt ctctggctcc 600

aagtctggca cctcagcctc cctggccatc agtgggttcc ggtccgagga tgaggctgat 660

tattactgtg cagcatggga tgacagcctg agtggttggg tgttcggcgg agggaccaag 720

ctgaccgtcc taggt 735

<210> 89
<211> 245
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP07-17 anti-HER2 diabody designated AVP07-90 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 89

Ser Val Gln Leu Val Gln Cys Gly Ala Cys Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Val Gly Tyr Ala Ser Ser Ser Asn Ala Ala Lys Trp
100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
130 135 140

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

Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly
165 170 175

Thr Val Pro Lys Leu Leu Ile Tyr Gly His Thr Asn Arg Pro Ala Gly
180 185 190

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

Ala Ile Ser Gly Phe Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala
210 215 220

Ala Trp Asp Asp Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Thr Val Leu Gly
245

<210> 90
<211> 735
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP07-17 anti-HER2 diabody designated AVP07-89 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 90
tctgtgcagc tggtgcagtc tggggcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcgcctgggt gcgccagatg 120

cccgggaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac 240

ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt atttttgtgc gagacatgac 300

gtgggatatg cgagtagttc caacgcggca aagtggcctg aatacttcca gcattggggc 360

cagggcaccc tggtcaccgt ttcctcaggt ggaggcggtt cacagtctgt gttgacgcag 420

ccgccctcag tgtctgcgtg tccaggatgt aaggtcacca tctcctgctc tggaagcagc 480

tccaacattg ggaataatta tgtatcctgg taccagcagc tcccaggaac agtccccaaa 540

ctcctcatct atggtcacac caatcggccc gcaggggtcc ctgaccgatt ctctggctcc 600

aagtctggca cctcagcctc cctggccatc agtgggttcc ggtccgagga tgaggctgat 660

tattactgtg cagcatggga tgacagcctg agtggttggg tgttcggcgg agggaccaag 720

ctgaccgtcc taggt 735

<210> 91
<211> 245
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP07-17 anti-HER2 diabody designated AVP07-89 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 91

Ser Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Val Gly Tyr Ala Ser Ser Ser Asn Ala Ala Lys Trp
100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
130 135 140

Ser Ala Cys Pro Gly Cys Lys Val Thr Ile Ser Cys Ser Gly Ser Ser
145 150 155 160

Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly
165 170 175

Thr Val Pro Lys Leu Leu Ile Tyr Gly His Thr Asn Arg Pro Ala Gly
180 185 190

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

Ala Ile Ser Gly Phe Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala
210 215 220

Ala Trp Asp Asp Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Thr Val Leu Gly
245

<210> 92
<211> 735
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP07-17 anti-HER2 diabody designated AVP07-91 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 92
agcgtgcagc tggtgcagtc tggggcagag gtgaaatgtc ccgggtgttc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcgcctgggt gcgccagatg 120

cccgggaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac 240

ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt atttttgtgc gagacatgac 300

gtgggatatg cgagtagttc caacgcggca aagtggcctg aatacttcca gcattggggc 360

cagggcaccc tggtcaccgt ttcctcaggt ggaggcggtt cacagtctgt gttgacgcag 420

ccgccctcag tgtctgcggc cccaggacag aaggtcacca tctcctgctc tggaagcagc 480

tccaacattg ggaataatta tgtatcctgg taccagcagc tcccaggaac agtccccaaa 540

ctcctcatct atggtcacac caatcggccc gcaggggtcc ctgaccgatt ctctggctcc 600

aagtctggca cctcagcctc cctggccatc agtgggttcc ggtccgagga tgaggctgat 660

tattactgtg cagcatggga tgacagcctg agtggttggg tgttcggcgg agggaccaag 720

ctgaccgtcc taggt 735

<210> 93
<211> 245
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP07-17 anti-HER2 diabody designated AVP07-91 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 93

Ser Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Cys Pro Gly Cys
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Val Gly Tyr Ala Ser Ser Ser Asn Ala Ala Lys Trp
100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
130 135 140

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

Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly
165 170 175

Thr Val Pro Lys Leu Leu Ile Tyr Gly His Thr Asn Arg Pro Ala Gly
180 185 190

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

Ala Ile Ser Gly Phe Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala
210 215 220

Ala Trp Asp Asp Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Thr Val Leu Gly
245

<210> 94
<211> 696
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP02-60 anti-MUC1 diabody designated AVP02-103 comprising cysteine residues in FR1 and a N-terminal serine

<400> 94
agcgtgcagc tggtttgcag cggttgcgga gtggtgcagc caggtggaag cctgcgtctg 60

agctgcgcag caagcggttt acctttagc agctatggca tgagctgggt gcgtcaggcg 120

ccggataaag gcctggaact ggtggcgacc attaacagca acggtggaag cacctattat 180

ccggatagcg tgaaaggccg ttttaccatt agccgtgata acagcaaaaa caccctgtat 240

ctgcagatga acagcctgcg taccgaagat accgcggtgt attattgcgc gcgtgatcgt 300

gatggctatg atgaaggctt tgattattgg ggccagggca ccctggtgac cgtgagcagc 360

ggtgggggcg gaagccagat tcagctgacc cagagcccga gcagcctgag cgcaagcgtg 420

ggtgatcgtg tgaccattac ctgcagcgcg agcagcagcg tgagctatat gcattggtat 480

cagcagaaac cgggcaaagc gccgaaacgt tggatttatg ataccagcaa actggcgagc 540

ggcgtgccga gccgttttag cggcagcggc agcggcaccg attatacctt taccattagc 600

agcctgcagc cggaagatat tgcgacctat tattgccagc agtggagcag caacccgccg 660

acctttggcc agggcaccaa actgcagatt aaacgt 696

<210> 95
<211> 232
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP02-60 anti-MUC1 diabody designated AVP02-103 comprising cysteine residues in FR1 and a N-terminal serine

<400> 95

Ser Val Gln Leu Val Cys Ser Gly Cys Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Asp Lys Gly Leu Glu Leu Val
35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Ile Gln
115 120 125

Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
130 135 140

Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr
145 150 155 160

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser
165 170 175

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
180 185 190

Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
195 200 205

Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr Phe Gly Gln
210 215 220

Gly Thr Lys Leu Gln Ile Lys Arg
225 230

<210> 96
<211> 735
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP07-17 anti-HER2 diabody designated AVP07-68 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 96
agcgtgcagc tggtgcagtc tggggcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcgcctgggt gcgccagatg 120

cccgggaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac 240

ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt atttttgtgc gagacatgac 300

gtgggatatg cgagtagttc caacgcggca aagtggcctg aatacttcca gcattggggc 360

cagggcaccc tggtcaccgt ttcctcaggt ggaggcggtt cacagtctgt gttgacgcag 420

ccgtgcagca gctgcgcggc cccaggacag aaggtcacca tctcctgctc tggaagcagc 480

tccaacattg ggaataatta tgtatcctgg taccagcagc tcccaggaac agtccccaaa 540

ctcctcatct atggtcacac caatcggccc gcaggggtcc ctgaccgatt ctctggctcc 600

aagtctggca cctcagcctc cctggccatc agtgggttcc ggtccgagga tgaggctgat 660

tattactgtg cagcatggga tgacagcctg agtggttggg tgttcggcgg agggaccaag 720

ctgaccgtcc taggt 735

<210> 97
<211> 245
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP07-17 anti-HER2 diabody designated AVP07-68 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 97

Ser Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Val Gly Tyr Ala Ser Ser Ser Asn Ala Ala Lys Trp
100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Cys Ser Ser
130 135 140

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

Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly
165 170 175

Thr Val Pro Lys Leu Leu Ile Tyr Gly His Thr Asn Arg Pro Ala Gly
180 185 190

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

Ala Ile Ser Gly Phe Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala
210 215 220

Ala Trp Asp Asp Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Thr Val Leu Gly
245

<210> 98
<211> 702
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-07 anti-TAG72 diabody designated AVP04-51 comprising cysteine residues in FR1 and a N-terminal serine

<400> 98
agcgtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcggtgg cggcggcagc 360

gatatcgtga tgacccagag cccgagcagc ctgccgtgca gcgtgggcga aaaatgcacc 420

ctgagctgca aaagcagcca gagcctgctg tatagcggca atcagaaaaa ctatctggcg 480

tggtatcagc agaaaccggg tcagagcccg aaactgctga tttattgggc gagcacccgt 540

gaaagcggcg tgccggatcg ttttaccggc agcggtagcg gcaccgattt taccctgagc 600

attagcagcg tggaaaccga agatctggcg gtgtattatt gccagcagta ttatagctat 660

ccgctgacct ttggtgcggg caccaaactg gtgctgaaac gt 702

<210> 99
<211> 234

<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-07 anti-TAG72 diabody designated AVP04-51 comprising cysteine residues in FR1 and a N-terminal serine

<400> 99

```
Ser Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1               5                  10                  15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
            100                 105                 110

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro
        115                 120                 125

Ser Ser Leu Pro Cys Ser Val Gly Glu Lys Cys Thr Leu Ser Cys Lys
    130                 135                 140

Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala
145                 150                 155                 160

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
                165                 170                 175

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
            180                 185                 190

Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp
        195                 200                 205

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe
    210                 215                 220

Gly Ala Gly Thr Lys Leu Val Leu Lys Arg
225                 230
```

<210> 100
<211> 732
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-07 anti-TAG72 scFv designated AVP04-70 comprising cysteine residues in FR1 and a N-terminal serine

<400> 100
agcgtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcggtgg cggcggcagc 360

ggtggcggcg gcagcggtgg cggcggcagc gatatcgtga tgacccagag ctgcagcagc 420

tgcccggtga gcgtgggcga aaaagtgacc ctgagctgca aaagcagcca gagcctgctg 480

tatagcggca atcagaaaaa ctatctggcg tggtatcagc agaaaccggg tcagagcccg 540

aaactgctga tttattgggc gagcacccgt gaaagcggcg tgccggatcg ttttaccggc 600

agcggtagcg gcaccgattt taccctgagc attagcagcg tggaaaccga agatctggcg 660

gtgtattatt gccagcagta ttatagctat ccgctgacct ttggtgcggg caccaaactg 720

gtgctgaaac gt 732

<210> 101
<211> 244
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-07 anti-TAG72 scFv designated AVP04-70 comprising cysteine residues in FR1 and a N-terminal serine

<400> 101

Ser Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Ile Val Met Thr Gln Ser Cys Ser Ser Cys Pro Val Ser
130 135 140

Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu
145 150 155 160

Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser
180 185 190

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Ser Ile Ser Ser Val Glu Thr Glu Asp Leu Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
225 230 235 240

Val Leu Lys Arg

<210> 102
<211> 687
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-07 anti-TAG72 triabody designated AVP04-74 comprising cysteine residues in FR1 and a N-terminal serine

<400> 102
agcgtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcgatat cgtgatgacc 360

cagagctgca gcagctgccc ggtgagcgtg ggcgaaaaag tgaccctgag ctgcaaaagc 420

agccagagcc tgctgtatag cggcaatcag aaaaactatc tggcgtggta tcagcagaaa 480

ccgggtcaga gcccgaaact gctgatttat tgggcgagca cccgtgaaag cggcgtgccg 540

gatcgtttta ccggcagcgg tagcggcacc gattttaccc tgagcattag cagcgtggaa 600

accgaagatc tggcggtgta ttattgccag cagtattata gctatccgct gacctttggt 660

gcgggcacca aactggtgct gaaacgt 687

<210> 103
<211> 229
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-07 anti-TAG72 triabody designated AVP04-74 comprising cysteine residues in FR1 and a N-terminal serine

<400> 103

Ser Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Asp Ile Val Met Thr Gln Ser Cys Ser Ser Cys Pro Val
115 120 125

Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu
130 135 140

Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
145 150 155 160

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
165 170 175

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
180 185 190

Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp Leu Ala Val Tyr Tyr
195 200 205

Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
210 215 220

Leu Val Leu Lys Arg
225

<210> 104
<211> 765
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP07-17 anti-HER2 scFv designated AVP07-71 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 104
agcgtgcagc tggtgcagtc tggggcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcgcctgggt gcgccagatg 120

cccgggaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac 240

ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt atttttgtgc gagacatgac 300

gtgggatatg cgagtagttc caacgcggca aagtggcctg aatacttcca gcattggggc 360

cagggcaccc tggtcaccgt ttcctcaggt ggaggcggtt caggtggagg cggttcaggt 420

ggaggcggtt cacagtctgt gttgacgcag ccgtgcagca gctgcgcggc cccaggacag 480

aaggtcacca tctcctgctc tggaagcagc tccaacattg ggaataatta tgtatcctgg 540

taccagcagc tcccaggaac agtccccaaa ctcctcatct atggtcacac caatcggccc 600

gcaggggtcc ctgaccgatt ctctggctcc aagtctggca cctcagcctc cctggccatc 660

agtgggttcc ggtccgagga tgaggctgat tattactgtg cagcatggga tgacagcctg 720

agtggttggg tgttcggcgg agggaccaag ctgaccgtcc taggt 765

<210> 105
<211> 255
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP07-17 anti-HER2 scFv designated AVP07-71 comprising cysteine residues in FR1, removal of cysteine residues in CDR3H and a N-terminal serine

<400> 105

Ser Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Val Gly Tyr Ala Ser Ser Ser Asn Ala Ala Lys Trp
100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Gln Ser Val Leu Thr Gln Pro Cys Ser Ser Cys Ala Ala Pro Gly Gln
145 150 155 160

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
165 170 175

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Val Pro Lys Leu Leu
180 185 190

Ile Tyr Gly His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser
195 200 205

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg
210 215 220

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
225 230 235 240

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
245 250 255

<210> 106
<211> 55

<212> DNA
<213> artificial

<220>
<223> nucleotide sequence of mutagenic primer for introducing cysteine residues at Kabat positions L8 and L11 of the FR1 region of the VL chain in AVP04-07

<400> 106
gatatcgtga tgacccagag ctgcagcagc tgcccggtga gcgtgggcga aaaag 55

<210> 107
<211> 55
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence of mutagenic primer for introducing cysteine residues at Kabat positions L8 and L11 of the FR1 region of the VL chain in AVP04-07

<400> 107
ctttttcgcc cacgctcacc gggcagctgc tgcagctctg ggtcatcacg atatc 55

<210> 108
<211> 735
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP07-17 anti-HER2 diabody designated AVP07-86 replacing CDR3H Cysteine residues Cys104 (Kabat numbering H100) and Cys109 (H100E) with Alanines and comprising a N-terminal serine

<400> 108
agcgtgcagc tggtgcagtc tggggcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcgcctgggt gcgccagatg 120

cccgggaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac 240

ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt atttttgtgc gagacatgac 300

gtgggatatg cgagtagttc caacgcggca aagtggcctg aatacttcca gcattggggc 360

cagggcaccc tggtcaccgt ttcctcaggt ggaggcggtt cacagtctgt gttgacgcag 420

ccgccctcag tgtctgcggc cccaggacag aaggtcacca tctcctgctc tggaagcagc 480

tccaacattg ggaataatta tgtatcctgg taccagcagc tcccaggaac agtccccaaa 540

ctcctcatct atggtcacac caatcggccc gcaggggtcc ctgaccgatt ctctggctcc 600

aagtctggca cctcagcctc cctggccatc agtgggttcc ggtccgagga tgaggctgat 660

tattactgtg cagcatggga tgacagcctg agtggttggg tgttcggcgg agggaccaag 720

ctgaccgtcc taggt 735

<210> 109
<211> 245
<212> PRT

<213> artificial

<220>
<223> amino acid sequence of modified AVP07-17 anti-HER2 diabody designated AVP07-86 replacing CDR3H Cysteine residues Cys104 (Kabat numbering H100) and Cys109 (H100E) with Alanines and comprising a N-terminal serine

<400> 109

Ser Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Val Gly Tyr Ala Ser Ser Ser Asn Ala Ala Lys Trp
100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
130 135 140

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

Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly
165 170 175

Thr Val Pro Lys Leu Leu Ile Tyr Gly His Thr Asn Arg Pro Ala Gly
180 185 190

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

Ala Ile Ser Gly Phe Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala
210 215 220

Ala Trp Asp Asp Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Thr Val Leu Gly
245

<210> 110
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence encoding VH of AVP04-07 anti-TAG-72

<400> 110
caggtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagc 345

<210> 111
<211> 115
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence encoding VH of AVP04-07 anti-TAG-72

<400> 111

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser
115

<210> 112
<211> 342
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding VL of AVP04-07 anti-TAG72

<400> 112
gatatcgtga tgacccagag cccgagcagc ctgccggtga gcgtgggcga aaaagtgacc 60

ctgagctgca aaagcagcca gagcctgctg tatagcggca atcagaaaaa ctatctggcg 120

tggtatcagc agaaaccggg tcagagcccg aaactgctga tttattgggc gagcacccgt 180

gaaagcggcg tgccggatcg ttttaccggc agcggtagcg gcaccgattt taccctgagc 240

attagcagcg tggaaaccga agatctggcg gtgtattatt gccagcagta ttatagctat 300

ccgctgacct ttggtgcggg caccaaactg gtgctgaaac gt 342

<210> 113
<211> 114
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of VL of AVP04-07 anti-TAG72

<400> 113

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Pro Val Ser Val Gly
1 5 10 15

Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser
65 70 75 80

Ile Ser Ser Val Glu Thr Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Val Leu
100 105 110

Lys Arg

<210> 114
<211> 714

<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding AVP04-07 anti-TAG72 diabody lacking a linker sequence

<400> 114
caggtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcgatat cgtgatgacc 360

cagagcccga gcagcctgcc ggtgagcgtg ggcgaaaaag tgaccctgag ctgcaaaagc 420

agccagagcc tgctgtatag cggcaatcag aaaaactatc tggcgtggta tcagcagaaa 480

ccgggtcaga gcccgaaact gctgatttat tgggcgagca cccgtgaaag cggcgtgccg 540

gatcgtttta ccggcagcgg tagcggcacc gattttaccc tgagcattag cagcgtggaa 600

accgaagatc tggcggtgta ttattgccag cagtattata gctatccgct gacctttggt 660

gcgggcacca aactggtgct gaaacgtgcg ggcaccaaac tggtgctgaa acgt 714

<210> 115
<211> 229
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of AVP04-07 anti-TAG72 diabody lacking a linker sequence

<400> 115

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Pro Val
115 120 125

Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu
130 135 140

Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
145 150 155 160

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
165 170 175

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
180 185 190

Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp Leu Ala Val Tyr Tyr
195 200 205

Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
210 215 220

Leu Val Leu Lys Arg
225

<210> 116
<211> 684
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding anti-TAG72 diabody lacking a linker sequence and amino acid N-terminal to linker (designated AVP04-09)

<400> 116
caggtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcgatatcgt gatgacccag 360

agcccgagca gcctgccggt gagcgtgggc gaaaaagtga ccctgagctg caaaagcagc 420

cagagcctgc tgtatagcgg caatcagaaa aactatctgg cgtggtatca gcagaaaccg 480

ggtcagagcc cgaaactgct gatttattgg gcgagcaccc gtgaaagcgg cgtgccggat 540

cgttttaccg gcagcggtag cggcaccgat tttaccctga gcattagcag cgtggaaacc 600

gaagatctgg cggtgtatta ttgccagcag tattatagct atccgctgac ctttggtgcg 660

ggcaccaaac tggtgctgaa acgt 684

<210> 117
<211> 228
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of AVP04-07 anti-TAG72 diabody lacking a linker sequence (designated AVP04-69)

<400> 117

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Pro Val Ser
115 120 125

Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu
130 135 140

Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
145 150 155 160

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser
165 170 175

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
180 185 190

Leu Ser Ile Ser Ser Val Glu Thr Glu Asp Leu Ala Val Tyr Tyr Cys
195 200 205

Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu

210 215 220

Val Leu Lys Arg
225

<210> 118
<211> 702
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-07 anti-TAG72 diabody designated AVP04-50 comprising cysteine residues in FR1

<400> 118
caggtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcggtgg cggcggcagc 360

gatatcgtga tgacccagag ctgcagcagc tgcccggtga gcgtgggcga aaaagtgacc 420

ctgagctgca aaagcagcca gagcctgctg tatagcggca atcagaaaaa ctatctggcg 480

tggtatcagc agaaaccggg tcagagcccg aaactgctga tttattgggc gagcacccgt 540

gaaagcggcg tgccggatcg ttttaccggc agcggtagcg gcaccgattt taccctgagc 600

attagcagcg tggaaaccga agatctggcg gtgtattatt gccagcagta ttatagctat 660

ccgctgacct ttggtgcggg caccaaactg gtgctgaaac gt 702

<210> 119
<211> 234
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-07 anti-TAG72 diabody designated AVP04-50 comprising cysteine residues in FR1

<400> 119

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Cys
115 120 125

Ser Ser Cys Pro Val Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys
130 135 140

Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala
145 150 155 160

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
165 170 175

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
180 185 190

Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp
195 200 205

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe
210 215 220

Gly Ala Gly Thr Lys Leu Val Leu Lys Arg
225 230

<210> 120
<211> 687
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-69 anti-TAG72 diabody designated AVP04-50 comprising cysteine residues in FR1 and lacking a linker sequence

<400> 120
caggtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcgatat cgtgatgacc 360

cagagctgca gcagctgccc ggtgagcgtg ggcgaaaaag tgaccctgag ctgcaaaagc 420

agccagagcc tgctgtatag cggcaatcag aaaaactatc tggcgtggta tcagcagaaa 480

ccgggtcaga gcccgaaact gctgatttat tgggcgagca cccgtgaaag cggcgtgccg 540

gatcgtttta ccggcagcgg tagcggcacc gattttaccc tgagcattag cagcgtggaa 600

accgaagatc tggcggtgta ttattgccag cagtattata gctatccgct gacctttggt 660

gcgggcacca aactggtgct gaaacgt 687

<210> 121
<211> 229
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified modified AVP04-69 anti-TAG72 diabody designated AVP04-50 comprising cysteine residues in FR1 and lacking a linker sequence

<400> 121

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Asp Ile Val Met Thr Gln Ser Cys Ser Ser Cys Pro Val
115 120 125

Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu
130 135 140

Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
145 150 155 160

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
165 170 175

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
180 185 190

Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp Leu Ala Val Tyr Tyr
195 200 205

Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
210 215 220

Leu Val Leu Lys Arg
225

<210> 122
<211> 684
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-09 anti-TAG72 diabody designated AVP04-50 comprising cysteine residues in FR1 and lacking a linker sequence and amino acid N-terminal to linker

<400> 122
caggtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcgatatcgt gatgacccag 360

agctgcagca gctgcccggt gagcgtgggc gaaaaagtga ccctgagctg caaaagcagc 420

cagagcctgc tgtatagcgg caatcagaaa aactatctgg cgtggtatca gcagaaaccg 480

ggtcagagcc cgaaactgct gatttattgg gcgagcaccc gtgaaagcgg cgtgccggat 540

cgttttaccg gcagcggtag cggcaccgat tttaccctga gcattagcag cgtggaaacc 600

gaagatctgg cggtgtatta ttgccagcag tattatagct atccgctgac ctttggtgcg 660

ggcaccaaac tggtgctgaa acgt 684

<210> 123
<211> 228
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified modified AVP04-09 anti-TAG72 diabody designated AVP04-50 comprising cysteine residues in FR1 and lacking a linker sequence and amino acid N-terminal to linker

<400> 123

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Asp Ile Val Met Thr Gln Ser Cys Ser Ser Cys Pro Val Ser
115 120 125

Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu
130 135 140

Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
145 150 155 160

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser
165 170 175

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
180 185 190

Leu Ser Ile Ser Ser Val Glu Thr Glu Asp Leu Ala Val Tyr Tyr Cys
195 200 205

Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
210 215 220

Val Leu Lys Arg
225

<210> 124
<211> 702
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-07 anti-TAG72 diabody with a N-terminal serine residue

<400> 124
agcgtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcggtgg cggcggcagc 360

gatatcgtga tgacccagag cccgagcagc ctgccggtga gcgtgggcga aaaagtgacc 420

ctgagctgca aaagcagcca gagcctgctg tatagcggca atcagaaaaa ctatctggcg 480

tggtatcagc agaaaccggg tcagagcccg aaactgctga tttattgggc gagcacccgt 540

gaaagcggcg tgccggatcg ttttaccggc agcggtagcg gcaccgattt taccctgagc 600

attagcagcg tggaaaccga agatctggcg gtgtattatt gccagcagta ttatagctat 660

ccgctgacct ttggtgcggg caccaaactg gtgctgaaac gt 702

<210> 125
<211> 234
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-07 anti-TAG72 diabody with a N-terminal serine residue

<400> 125

Ser Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro
115 120 125

Ser Ser Leu Pro Val Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys

130 135 140

Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala
145 150 155 160

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
165 170 175

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
180 185 190

Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp
195 200 205

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe
210 215 220

Gly Ala Gly Thr Lys Leu Val Leu Lys Arg
225 230

<210> 126
<211> 687
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-69 anti-TAG72 diabody lacking a linker sequence and comprising a N-terminal serine residue

<400> 126
agcgtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcgatat cgtgatgacc 360

cagagcccga gcagcctgcc ggtgagcgtg ggcgaaaaag tgaccctgag ctgcaaaagc 420

agccagagcc tgctgtatag cggcaatcag aaaaactatc tggcgtggta tcagcagaaa 480

ccgggtcaga gcccgaaact gctgatttat tgggcgagca cccgtgaaag cggcgtgccg 540

gatcgtttta ccggcagcgg tagcggcacc gattttaccc tgagcattag cagcgtggaa 600

accgaagatc tggcggtgta ttattgccag cagtattata gctatccgct gacctttggt 660

gcgggcacca aactggtgct gaaacgt 687

<210> 127
<211> 229
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-69 anti-TAG72 diabody lacking a linker sequence and comprising a N-terminal serine residue

<400> 127

Ser Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Pro Val
115 120 125

Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu
130 135 140

Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
145 150 155 160

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
165 170 175

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
180 185 190

Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp Leu Ala Val Tyr Tyr
195 200 205

Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
210 215 220

Leu Val Leu Lys Arg
225

<210> 128

<211> 684
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-09 anti-TAG72 diabody lacking a linker sequence and amino acid N-terminal to linker and comprising a N terminal serine residue

<400> 128
agcgtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat ttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcgatatcgt gatgacccag 360

agcccgagca gcctgccggt gagcgtgggc gaaaaagtga ccctgagctg caaaagcagc 420

cagagcctgc tgtatagcgg caatcagaaa aactatctgg cgtggtatca gcagaaaccg 480

ggtcagagcc cgaaactgct gatttattgg gcgagcaccc gtgaaagcgg cgtgccggat 540

cgttttaccg gcagcggtag cggcaccgat tttaccctga gcattagcag cgtggaaacc 600

gaagatctgg cggtgtatta ttgccagcag tattatagct atccgctgac ctttggtgcg 660

ggcaccaaac tggtgctgaa acgt 684

<210> 129
<211> 228
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-09 anti-TAG72 diabody lacking a linker sequence and amino acid N-terminal to linker and comprising a N terminal serine residue

<400> 129

Ser Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Pro Val Ser
115 120 125

Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu
130 135 140

Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
145 150 155 160

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser
165 170 175

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
180 185 190

Leu Ser Ile Ser Ser Val Glu Thr Glu Asp Leu Ala Val Tyr Tyr Cys
195 200 205

Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
210 215 220

Val Leu Lys Arg
225

<210> 130
<211> 687
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-50 anti-TAG72 diabody comprising cysteine residues in FR1 and a N-terminal serine residue and lacking a linker sequence

<400> 130
agcgtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcagcgatat cgtgatgacc 360

cagagctgca gcagctgccc ggtgagcgtg ggcgaaaaag tgaccctgag ctgcaaaagc 420

agccagagcc tgctgtatag cggcaatcag aaaaactatc tggcgtggta tcagcagaaa 480

ccgggtcaga gcccgaaact gctgatttat tgggcgagca cccgtgaaag cggcgtgccg 540

gatcgtttta ccggcagcgg tagcggcacc gattttaccc tgagcattag cagcgtggaa 600

accgaagatc tggcggtgta ttattgccag cagtattata gctatccgct gacctttggt 660

gcgggcacca aactggtgct gaaacgt 687

<210> 131
<211> 229
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-50 anti-TAG72 diabody comprising cysteine residues in FR1 and a N-terminal serine residue and lacking a linker sequence

<400> 131

Ser Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser Asp Ile Val Met Thr Gln Ser Cys Ser Ser Cys Pro Val
115 120 125

Ser Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu
130 135 140

Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
145 150 155 160

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
165 170 175

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
180 185 190

Thr Leu Ser Ile Ser Ser Val Glu Thr Glu Asp Leu Ala Val Tyr Tyr

195 200 205

Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys
210 215 220

Leu Val Leu Lys Arg
225

<210> 132
<211> 684
<212> DNA
<213> artificial

<220>
<223> nucleotide sequence encoding modified AVP04-50 anti-TAG72 diabody comprising cysteine residues in FR1 and a N-terminal serine residue and lacking a linker sequence and amino acid N-terminal to linker

<400> 132
agcgtgcagc tgcagcagag cgatgcggaa ctggtgaaac cgggcgcgag cgtgaaaatt 60

agctgcaaag cgagcggcta tacctttacc gatcatgcga ttcattgggt gaaacagaat 120

ccggaacagg gcctggaatg gattggctat tttagcccgg gcaacgatga ttttaaatat 180

aacgaacgtt ttaaaggcaa agcgaccctg accgcggata aaagcagcag caccgcgtat 240

ctgcagctga acagcctgac cagcgaagat agcgcggtgt atttttgcac ccgtagcctg 300

aatatggcgt attggggtca gggcacctcg gtcaccgtga gcgatatcgt gatgacccag 360

agctgcagca gctgcccggt gagcgtgggc gaaaaagtga ccctgagctg caaaagcagc 420

cagagcctgc tgtatagcgg caatcagaaa aactatctgg cgtggtatca gcagaaaccg 480

ggtcagagcc cgaaactgct gatttattgg gcgagcaccc gtgaaagcgg cgtgccggat 540

cgttttaccg gcagcggtag cggcaccgat tttaccctga gcattagcag cgtggaaacc 600

gaagatctgg cggtgtatta ttgccagcag tattatagct atccgctgac ctttggtgcg 660

ggcaccaaac tggtgctgaa acgt 684

<210> 133
<211> 228
<212> PRT
<213> artificial

<220>
<223> amino acid sequence of modified AVP04-50 anti-TAG72 diabody comprising cysteine residues in FR1 and a N-terminal serine residue and lacking a linker sequence and amino acid N-terminal to linker

<400> 133

Ser Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

```
Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
            100                 105                 110

Val Ser Asp Ile Val Met Thr Gln Ser Cys Ser Ser Cys Pro Val Ser
        115                 120                 125

Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu
    130                 135                 140

Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
145                 150                 155                 160

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser
                165                 170                 175

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
            180                 185                 190

Leu Ser Ile Ser Ser Val Glu Thr Glu Asp Leu Ala Val Tyr Tyr Cys
        195                 200                 205

Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
    210                 215                 220

Val Leu Lys Arg
225
```

<210> 134
<211> 5
<212> PRT
<213> artificial

<220>
<223> Linker

<400> 134

```
Gly Gly Gly Gly Ser
1               5
```

<210> 135

<211> 4
<212> PRT
<213> artificial

<220>
<223> Linker

<400> 135

Gly Gly Gly Gly
1