

ALLO-280W01_sequence_listing
SEQUENCE LISTING

<110> MEDIMMUNE LIMITED

<120> Amino acid derivatives

<130> ALLO-280W01

<150> US61/862,497

<151> 2013-08-05

<160> 17

<170> BiSSAP 1.3

<210> 1

<211> 1365

<212> DNA

<213> Methanosarcina mazei

<220>

<223> PyIRS Methanosarcina mazei WT nucleotide sequence

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cctaccagaa cgaaaaaggc aatgccaaaa tccgttgcca gagccccgaa acctcttgag	360
aatacagaag cggcacaggc tcaaccttct ggatctaaat tttcacctgc gataccgggt	420
tccaccaag agtcagtttc tgtcccggca tctgtttcaa catcaatatc aagcatttct	480
acaggagcaa ctgcatccgc actggtaaaa ggaatacga accccattac atccatgtct	540
gcccctgttc aggcaagtgc ccccgcaact acgaagagcc agactgacag gcttgaagtc	600
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gataccgaac tttcaaaaca gatcttcagg gttgacaaga acttctgcct gagacccatg	900
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gtagtcggac ccataccgct tgaccgggaa tgggggtattg ataaaccctg gataggggca	1260
ggtttcgggc tcgaacgcct tctaaagggt aaacacgact ttaaaaatat caagagagct	1320

ALLO-280w01_sequence_listing

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1365

<210> 2

<211> 454

<212> PRT

<213> Methanosarcina mazei

<220>

<223> PyIRS, Methanosarcina mazei WT amino acid sequence

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Arg	Ser	Lys	Ile	Tyr	Ile	Glu	Met	Ala	Cys	Gly	Asp	His	Leu	Val	Val
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Asn	Asn	Ser	Arg	Ser	Ser	Arg	Thr	Ala	Arg	Ala	Leu	Arg	His	His	Lys
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Tyr	Arg	Lys	Thr	Cys	Lys	Arg	Cys	Arg	Val	Ser	Asp	Glu	Asp	Leu	Asn
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Lys	Phe	Leu	Thr	Lys	Ala	Asn	Glu	Asp	Gln	Thr	Ser	Val	Lys	Val	Lys
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Ser	Val	Ser	Val	Pro	Ala	Ser	Val	Ser	Thr	Ser	Ile	Ser	Ser	Ile	Ser
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Thr	Ser	Met	Ser	Ala	Pro	Val	Gln	Ala	Ser	Ala	Pro	Ala	Leu	Thr	Lys
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	210					215					220				
Ser	Arg	Arg	Lys	Lys	Asp	Leu	Gln	Gln	Ile	Tyr	Ala	Glu	Glu	Arg	Glu
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Arg	Gly	Phe	Leu	Glu	Ile	Lys	Ser	Pro	Ile	Leu	Ile	Pro	Leu	Glu	Tyr
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		275					280					285			
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305					310					315				320	
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Gly	Cys	Thr	Arg	Glu	Asn	Leu	Glu	Ser	Ile	Ile	Thr	Asp	Phe	Leu	Asn
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His	Leu	Gly	Ile	Asp	Phe	Lys	Ile	Val	Gly	Asp	Ser	Cys	Met	Val	Tyr
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Val	Val	Gly	Pro	Ile	Pro	Leu	Asp	Arg	Glu	Trp	Gly	Ile	Asp	Lys	Pro
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Asp	Phe	Lys	Asn	Ile	Lys	Arg	Ala	Ala	Arg	Ser	Glu	Ser	Tyr	Tyr	Asn
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ALLO-280W01_sequence_listing

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<210> 3
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> PyIRS Methanosarcina mazei Y384F mutant nucleotide sequence

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gcatgcgagg accaccttgt tgtaaacaac tccaggagca gcaggactgc aagagcgctc      180
aggcaccaca aatacaggaa gacctgcaaa cgctgcaggg ttctcgatga ggatctcaat      240
aagttcctca caaaggcaaa cgaagaccag acaagcgtaa aagtcaaggt cgtttctgcc      300
cctaccagaa cgaaaaaggc aatgccaaaa tccgttgcca gagccccgaa acctcttgag      360
aatacagaag cggcacaggc tcaaccttct ggatctaaat ttccacctgc gataccgggt      420
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ctgttaaacc caaagatga gatttccctg aattccggca agcctttcag ggagcttgag      660
tccgaattgc tctctcgag aaaaaaagac ctgcagcaga tctacgcgga agaaagggag      720
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gtagtcggac ccataccgct tgaccgggaa tgggggtatt ataaaccctg gataggggca     1260
ggtttcgggc tcgaacgcct tctaaagggt aaacacgact ttaaaaatat caagagagct     1320
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<210> 4
<211> 454
<212> PRT
<213> Artificial Sequence

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<223> PyIRS Methanosarcina mazei Y384F mutant amino acid sequence

<400> 4

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Arg Ser Lys Ile Tyr Ile Glu Met Ala Cys Gly Asp His Leu Val Val
      35      40      45
Asn Asn Ser Arg Ser Ser Arg Thr Ala Arg Ala Leu Arg His His Lys
      50      55      60
Tyr Arg Lys Thr Cys Lys Arg Cys Arg Val Ser Asp Glu Asp Leu Asn
65      70      75      80
Lys Phe Leu Thr Lys Ala Asn Glu Asp Gln Thr Ser Val Lys Val Lys
      85      90      95
Val Val Ser Ala Pro Thr Arg Thr Lys Lys Ala Met Pro Lys Ser Val
      100      105      110
Ala Arg Ala Pro Lys Pro Leu Glu Asn Thr Glu Ala Ala Gln Ala Gln
      115      120      125
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      130      135      140
Ser Val Ser Val Pro Ala Ser Val Ser Thr Ser Ile Ser Ser Ile Ser
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Thr Gly Ala Thr Ala Ser Ala Leu Val Lys Gly Asn Thr Asn Pro Ile
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Thr Ser Met Ser Ala Pro Val Gln Ala Ser Ala Pro Ala Leu Thr Lys
      180      185      190
Ser Gln Thr Asp Arg Leu Glu Val Leu Leu Asn Pro Lys Asp Glu Ile
      195      200      205
Ser Leu Asn Ser Gly Lys Pro Phe Arg Glu Leu Glu Ser Glu Leu Leu
      210      215      220
Ser Arg Arg Lys Lys Asp Leu Gln Gln Ile Tyr Ala Glu Glu Arg Glu
225      230      235      240
Asn Tyr Leu Gly Lys Leu Glu Arg Glu Ile Thr Arg Phe Phe Val Asp
      245      250      255
Arg Gly Phe Leu Glu Ile Lys Ser Pro Ile Leu Ile Pro Leu Glu Tyr
      260      265      270
Ile Glu Arg Met Gly Ile Asp Asn Asp Thr Glu Leu Ser Lys Gln Ile
      275      280      285
Phe Arg Val Asp Lys Asn Phe Cys Leu Arg Pro Met Leu Ala Pro Asn
      290      295      300
Leu Tyr Asn Tyr Leu Arg Lys Leu Asp Arg Ala Leu Pro Asp Pro Ile
305      310      315      320
Lys Ile Phe Glu Ile Gly Pro Cys Tyr Arg Lys Glu Ser Asp Gly Lys
      325      330      335
Glu His Leu Glu Glu Phe Thr Met Leu Asn Phe Cys Gln Met Gly Ser
      340      345      350
Gly Cys Thr Arg Glu Asn Leu Glu Ser Ile Ile Thr Asp Phe Leu Asn
      355      360      365
His Leu Gly Ile Asp Phe Lys Ile Val Gly Asp Ser Cys Met Val Phe
      370      375      380
Gly Asp Thr Leu Asp Val Met His Gly Asp Leu Glu Leu Ser Ser Ala
385      390      395      400
Val Val Gly Pro Ile Pro Leu Asp Arg Glu Trp Gly Ile Asp Lys Pro
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Trp Ile Gly Ala Gly Phe Gly Leu Glu Arg Leu Leu Lys Val Lys His
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<211> 72

<212> DNA

<213> Methanosarcina mazei

<220>

<223> tRNA^{Pyl} Methanosarcina mazei Go1

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aaagtaataa tttcttgggt agtttgcagt tttaaaatta tgttttaaaa tggactatca 180
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acgaaacacc 250

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<211> 372
<212> DNA
<213> Artificial Sequence

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aatacgtgac gtagaaagta ataatttctt gggtagtttg cagtttttaa aattatgttt 180
taaaatggac tatcatatgc ttaccgtaac ttgaaagtat ttcgatttct tggctttata 240
tatcttgttg aaaggacgaa acaccgaatt ctctagactc gagggaaacc tgatcatgta 300
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<211> 1104
<212> DNA
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ggaaagctta cccttaaatt tatttgcact actggaaaac tacctgttcc atggccaaca 180
cttgtcacta ctttctctta tgggtgttcaa tgcttttccc gttatccgga tcatatgaaa 240
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aaactcgagt acaactataa ctacacacat gtatacatca cggcagacaa acaaaagaat 480
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<210> 9
 <211> 367
 <212> PRT
 <213> Unknown

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35      40      45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50      55      60
Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65      70      75      80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85      90      95
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100      105      110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115      120      125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130      135      140
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145      150      155      160
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165      170      175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180      185      190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195      200      205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210      215      220
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ALLO-280w01_sequence_listing

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 275 280 285
 Gly Pro Cys Ala Glu Leu Val Val Leu Gly Thr Ala Ala Ala Ala Ala
 290 295 300
 Ala Gly Asn Leu Thr Cys Ile Val Ala Ile Gly Asn Glu Asn Arg Gly
 305 310 315 320
 Ile Leu Ser Pro Cys Gly Arg Cys Arg Gln Val Leu Leu Asp Leu His
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<210> 10

<211> 1104

<212> DNA

<213> Artificial Sequence

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<223> GFPY40 nucleotide sequence

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cttgtcacta ctttctctta tgggtgttcaa tgcttttccc gttatccgga tcatatgaaa	240
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ttcaaagatg acgggaacta caagacgcgt gctgaagtca agtttgaagg tgataccctt	360
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<210> 11

<211> 367

<212> PRT

ALLO-280W01_sequence_listing

<213> Artificial Sequence

<220>

<223> GFPY40 amino acid sequence

<220>

<221> MUTAGEN

<222> 40

<223> Xaa = unspecified nnAA

<400> 11

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35      40      45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50      55      60
Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65      70      75      80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85      90      95
Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100     105     110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115     120     125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130     135     140
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145     150     155     160
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165     170     175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180     185     190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195     200     205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210     215     220
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Gln Ala Lys Pro Leu
225     230     235     240
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245     250     255
Ser Ile Pro Ile Ser Glu Asp Tyr Ser Val Ala Ser Ala Ala Leu Ser
260     265     270
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275     280     285
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290     295     300
Ala Gly Asn Leu Thr Cys Ile Val Ala Ile Gly Asn Glu Asn Arg Gly
305     310     315     320
Ile Leu Ser Pro Cys Gly Arg Cys Arg Gln Val Leu Leu Asp Leu His
325     330     335
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<210> 12

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-Her2 (4D5) gamma nucleotide sequence

<400> 12

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ggtgatggct ttacgcgat ggactactgg ggccagggca ccctgggtcac cgtctcgagt      420
gctagacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      480
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tggaactcag gcgccctgac cagcggcggtg cacaccttcc cggctgtcct acagtcctca      600
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      720
aaatcttgtg acaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga      780
ccgtcagtct tcctcttccc cccaaaaccc aaggacacc tcctgatctc ccggaccct      840
gaggtcacat gcgtgggtggg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgaggagg gcagtacaac      960
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactgggt gaatggcaag     1020
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag     1140
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc     1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     1260
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg     1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1380
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<210> 13
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-Her2 (4D5) gamma amino acid sequence

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<400> 13
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
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Asp Thr Thr Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
20      25      30
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn
35      40      45
Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly
50      55      60
Leu Glu Trp Val Ser Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr
65      70      75      80
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys

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ALLO-280WO1_sequence_listing

Asn	Thr	Leu	Tyr	85	Gln	Met	Asn	Ser	90	Leu	Arg	Ala	Glu	Asp	95	Thr	Ala
Val	Tyr	Tyr	Cys	100	Ser	Arg	Trp	Gly	105	Gly	Asp	Gly	Phe	Tyr	110	Ala	Met
Tyr	Trp	Gly	Gln	115	Gly	Thr	Leu	Val	120	Thr	Val	Ser	Ser	Ala	125	Ser	Thr
Gly	Pro	Ser	Val	130	Phe	Pro	Leu	Ala	135	Pro	Ser	Ser	Lys	Ser	140	Thr	Ser
Gly	Thr	Ala	Ala	145	Leu	Gly	Cys	Leu	150	Val	Lys	Asp	Tyr	Phe	155	Pro	Glu
Val	Thr	Val	Ser	160	Trp	Asn	Ser	Gly	165	Ala	Leu	Thr	Ser	Gly	170	Val	His
Phe	Pro	Ala	Val	175	Leu	Gln	Ser	Ser	180	Gly	Leu	Tyr	Ser	Leu	185	Ser	Ser
Val	Thr	Val	Pro	190	Ser	Ser	Ser	Leu	195	Gly	Thr	Gln	Thr	Tyr	200	Ile	Cys
Val	Asn	His	Lys	205	Pro	Ser	Asn	Thr	210	Lys	Val	Asp	Lys	Lys	215	Val	Glu
Lys	Ser	Cys	Asp	220	Lys	Thr	His	Thr	225	Cys	Pro	Pro	Cys	Pro	230	Ala	Pro
Leu	Leu	Gly	Gly	235	Pro	Ser	Val	Phe	240	Leu	Phe	Pro	Pro	Lys	245	Pro	Lys
Thr	Leu	Met	Ile	250	Ser	Arg	Thr	Pro	255	Glu	Val	Thr	Cys	Val	260	Val	Val
Val	Ser	His	Glu	265	Asp	Pro	Glu	Val	270	Lys	Phe	Asn	Trp	Tyr	275	Val	Asp
Val	Glu	Val	His	280	Asn	Ala	Lys	Thr	285	Lys	Pro	Arg	Glu	Glu	290	Gln	Tyr
Ser	Thr	Tyr	Arg	295	Val	Val	Ser	Val	300	Leu	Thr	Val	Leu	His	305	Gln	Asp
Leu	Asn	Gly	Lys	310	Glu	Tyr	Lys	Cys	315	Val	Ser	Asn	Lys	Ala	320	Leu	Pro
Ala	Pro	Ile	Glu	325	Lys	Thr	Ile	Ser	330	Lys	Ala	Lys	Gly	Gln	335	Pro	Arg
Pro	Gln	Val	Tyr	340	Pro	Leu	Pro	Pro	345	Ser	Arg	Glu	Glu	Met	350	Thr	Lys
Gln	Val	Ser	Leu	355	Cys	Leu	Val	Lys	360	Gly	Phe	Tyr	Pro	Ser	365	Asp	Ile
Ala	Val	Glu	Trp	370	Glu	Ser	Asn	Gly	375	Gln	Pro	Glu	Asn	Asn	380	Tyr	Lys
Thr	Pro	Pro	Val	385	Asp	Ser	Asp	Gly	390	Ser	Phe	Phe	Leu	Tyr	395	Ser	Lys
Leu	Thr	Val	Asp	400	Lys	Ser	Arg	Trp	405	Gln	Gly	Asn	Val	Phe	410	Ser	Cys
Ser	Val	Met	His	415	Glu	Ala	Leu	His	420	Asn	His	Tyr	Thr	Gln	425	Lys	Ser
Ser	Leu	Ser	Pro	430	Gly	Lys			435						440		
				445					450						455		
				460					465						470		

<210> 14

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-Her2 (4D5) gamma_K274amber nucleotide sequence

<400> 14

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gagggtgcagc tggtggagtc tggcggtggc ttggtacagc cgggcggggtc cctgcgcctc 120

tcctgtgccg cttccggatt caacatcaaa gacacgtata ttactgggt ccgctcaggca 180

cctggcaagg gtctggagtg ggtgagccgc atttatccta ccaatggtta cactcgctac 240

gccgactctg tgaagggccg cttcaccatc agcgccgaca cgtccaagaa caccctgtat 300

ALLO-280W01_sequence_listing

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ctgcaaatga acagcctgcg tgccgaggac accgcggtgt attactgcag ccgctggggc 360
ggtgatggct tttagcgat ggactactgg ggccagggca ccctgggtcac cgtctcgagt 420
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc 660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
aatcttgtg aaaaaactca cacatgcccc ccggtgccag cacctgaact cctgggggga 780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 840
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcta gttcaactgg 900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 960
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1140
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccggtg 1260
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cagaagagcc tctccctgtc tccgggtaaa tga 1413

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<210> 15

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-Her2 (4D5) gamma_K274amber amino acid sequence

<220>

<221> MUTAGEN

<222> 297

<223> Xaa = pyrrolysine analogue of formula III.1 or 1A.1

<400> 15

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

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ALLO-280w01_sequence_listing

Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp
115 120 125
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225 230 235 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
245 250 255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
260 265 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
275 280 285
Val Ser His Glu Asp Pro Glu Val Xaa Phe Asn Trp Tyr Val Asp Gly
290 295 300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305 310 315 320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
325 330 335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
340 345 350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
355 360 365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
370 375 380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385 390 395 400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
420 425 430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
435 440 445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
450 455 460
Ser Leu Ser Pro Gly Lys
465 470

<210> 16

<211> 705

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-Her2 (4D5) Kappa nucleotide sequence

<400> 16

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atcacttgcc gtgctagcca ggatgtgaat acagcggtag cctggtatca gcagaaacct	180
ggcaaagccc ctaagctcct gatctattct gcatcctttt tgtacagcgg cgtgccgagc	240
cgcttcagcg gcagccgttc tggtagcgat ttactctca ccatcagctc tctgcaaccg	300
gaagattttg caacttacta ctgtcaacag cactacacca ctcctccgac gttcggccaa	360

ALLO-280w01_sequence_listing

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gggaccaagg tggaaatcga acgtacggtg gctgcacccat ctgtcttcat cttcccgcca      420
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      480
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      540
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg      600
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      660
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<210> 17
 <211> 234
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-Her2 (4D5) Kappa amino acid sequence

<400> 17
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 20 25 30
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
 35 40 45
 Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 50 55 60
 Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser
 65 70 75 80
 Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr
 100 105 110
 Thr Thr Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Glu Arg
 115 120 125
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 130 135 140
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 145 150 155 160
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 165 170 175
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 180 185 190
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 195 200 205
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 210 215 220
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230