

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> Bispecific Anti-MUC16 X Anti-CD28 Antibodies and Uses Thereof

<130> 10493-W001/118003-49320

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<150> 62/815,861

<151> 2019-03-19

<150> 62/782,142

<151> 2018-12-19

<160> 54

<170> FastSEQ for Windows Version 4.0

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tcctgtacag cttctggatt cgcctttggt gatcatacta tgagctgggt ccgccaggct 120
ccaggaagg ggctggagtg ggtaggtttc attagaagta gagcttatgg tgggacaaca 180
gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caaaagcatc 240
gcctatctgc aaatggacag cctgaaaacc gaggacacag ccgtgtatta ttgtactagc 300
gggggatatg atagtagtct tcattactac tattactacc acggtatgga cgtctggggc 360
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 1             5             10            15
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ala Phe Gly Asp His
          20          25          30
Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
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		35					40					45				
Gly	Phe	Ile	Arg	Ser	Arg	Ala	Tyr	Gly	Gly	Thr	Thr	Glu	Tyr	Ala	Ala	
	50					55					60					
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Ile	
65					70					75					80	
Ala	Tyr	Leu	Gln	Met	Asp	Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr	
				85					90					95		
Tyr	Cys	Thr	Ser	Gly	Gly	Tyr	Asp	Ser	Ser	Leu	His	Tyr	Tyr	Tyr	Tyr	
			100				105						110			
Tyr	His	Gly	Met	Asp	Val	Trp	Gly	Arg	Gly	Thr	Thr	Val	Thr	Val	Ser	
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Ser																

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<210> 6
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Ile Arg Ser Arg Ala Tyr Gly Gly Thr Thr
1 5 10

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actagcgggg gatatgatag tagtcttcat tactactatt actaccacgg tatggacgtc 60

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<400> 8

Thr Ser Gly Gly Tyr Asp Ser Ser Leu His Tyr Tyr Tyr Tyr Tyr His
1 5 10 15
Gly Met Asp Val
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<210> 9

<211> 324

<212> DNA

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<220>

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<400> 9

gaaatttgtg tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccttg gacgttcggc 300
caagggacca aggtggaaat caaa 324

<210> 10

<211> 108

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<400> 10

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

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cagagtgtta gcagcagcta c

21

<210> 12

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Gln	Ser	Val	Ser	Ser	Ser	Tyr
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9

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Gly Ala Ser
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<400> 15
cagcagtatg gtagctcacc ttggacg 27

<210> 16
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<400> 16
Gln Gln Tyr Gly Ser Ser Pro Trp Thr
1 5

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acctgcactg tctctggtgg ctccatcagt agttactact ggagctggat ccggcagccc 120
ccagggaagg gactggagtg gattgggtat atctattaca gtgggatcac ccactacaac 180
ccctccctca agagtcgagt caccatatca gtagacacgt ccaagatcca gttctccctg 240
aagctgagtt ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag atgggggggtt 300
cggaggggact actactacta cggtatggac gtctggggcc aagggaccac ggtcaccgtc 360
tcctca 366

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 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Tyr Ser Gly Ile Thr His Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Ile Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Trp Gly Val Arg Arg Asp Tyr Tyr Tyr Tyr Gly Met Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 19
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 <212> DNA
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<400> 19
 ggtggctcca tcagtagtta ctac

24

<210> 20
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<400> 20
 Gly Gly Ser Ile Ser Ser Tyr Tyr
 1 5

<210> 21
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<400> 21

atctattaca gtgggatcac c

21

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<212> PRT

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<400> 22

Ile Tyr Tyr Ser Gly Ile Thr
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<210> 23

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<212> DNA

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<400> 23

gcgagatggg gggttcggag ggactactac tactacggta tggacgtc

48

<210> 24

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<212> PRT

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<400> 24

Ala Arg Trp Gly Val Arg Arg Asp Tyr Tyr Tyr Tyr Gly Met Asp Val
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ccaggggaagg ggctggagtg ggtttcatac gttacttttt ttaatagtgc catatactac 180
gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctcactgtat 240
ctgcaaatac acagcctgag agccgaggac acggccgtat attactgtgc gagagaaaga 300
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<400> 26
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 Arg Asp Tyr
20 25 30
Ser Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Tyr Val Thr Phe Phe Asn Ser Ala Ile Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Arg Glu Pro Ile Val Gly Gly Phe Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

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<400> 27
ggattcacct tccgtgacta ctcc 24

<210> 28
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<400> 28
Gly Phe Thr Phe Arg Asp Tyr Ser
1 5

<210> 29
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<400> 29
gttactttttt ttaatagtc cata

24

<210> 30
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<400> 30
Val Thr Phe Phe Asn Ser Ala Ile
1 5

<210> 31
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<400> 31
gcgagagaaa gagagcctat tgtgggggggc ttgactac

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<210> 32
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<400> 32
Ala Arg Glu Arg Glu Pro Ile Val Gly Gly Phe Asp Tyr
1 5 10

<210> 33
<211> 324
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<400> 33

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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaa                                     324
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<400> 34

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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 Arg Ala Ser Gln Ser Ile Ser Ser Tyr
          20          25          30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35          40          45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65          70          75          80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
          85          90          95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
          100          105
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<210> 36

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<400> 36
Gln Ser Ile Ser Ser Tyr
1 5

<210> 37
<211> 9
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<220>
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<400> 37
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9

<210> 38
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<400> 38
Ala Ala Ser
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<210> 39
<211> 30
<212> DNA
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<400> 39
caacagagtt acagtacccc tccgatcacc

30

<210> 40
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<400> 40
Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
1 5 10

<210> 41
<211> 354

<212> DNA
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tcctgtgcag cctccggatt caccttcagt aggaataata tgcactgggt ccgccaggct 120
ccagggaagg gactggaata tgtttcaggt attagtagta atgggggtcg cacatattat 180
gcagactctg tgaagggcag attcaccatc tccagagaca attccaagaa cacgctgtat 240
cttcaaattgg gcggcctgag agctgcggac atggctgtgt atttctgtac gagagatgac 300
gagctgcttt cctttgacta ctggggccag ggaaccctgg tcactgtctc ctca 354

<210> 42
<211> 118
<212> PRT
<213> Artificial Sequence

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<400> 42
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val
35 40 45
Ser Gly Ile Ser Ser Asn Gly Gly Arg Thr Tyr Tyr Ala 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 Gly Gly Leu Arg Ala Ala Asp Met Ala Val Tyr Phe Cys
85 90 95
Thr Arg Asp Asp Glu Leu Leu Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser
115

<210> 43
<211> 24
<212> DNA
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<400> 43
ggattcacct tcagtaggaa taat

24

<210> 44
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<213> Artificial Sequence

<220>

<223> synthetic

<400> 44

Gly Phe Thr Phe Ser Arg Asn Asn
1 5

<210> 45

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 45

attagtagta atgggggtcg caca

24

<210> 46

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 46

Ile Ser Ser Asn Gly Gly Arg Thr
1 5

<210> 47

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 47

acgagagatg acgagctgct ttcctttgac tac

33

<210> 48

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> synthetic

<400> 48

Thr Arg Asp Asp Glu Leu Leu Ser Phe Asp Tyr

1

5

10

<210> 49

<211> 875

<212> PRT

<213> Artificial Sequence

<220>

<223> hMUC16 membrane-proximal domain
(P13810-P14451).mFc ; Accession# NP_078966

<400> 49

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Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
 20      25      30
Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly
 35      40      45
Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Thr Gly Pro Gly Leu
 50      55      60
Asp Arg Glu Gln Leu Tyr Leu Glu Leu Ser Gln Leu Thr His Ser Ile
 65      70      75      80
Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
 85      90      95
Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly Val Val
100     105     110
Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn Leu Arg Tyr
115     120     125
Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn Ile Thr Asp
130     135     140
Asn Val Met Gln His Leu Leu Ser Pro Leu Phe Gln Arg Ser Ser Leu
145     150     155     160
Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg Ser Val Lys
165     170     175
Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr Leu Gln Pro
180     185     190
Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His Glu Leu Ser
195     200     205
Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser Leu Asp Lys
210     215     220
Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Pro Asp Glu Pro
225     230     235     240
Pro Thr Thr Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro Leu Ser Glu
245     250     255
Ala Thr Thr Ala Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe
260     265     270
Thr Ile Ser Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala
275     280     285
Thr Phe Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg Pro Leu
290     295     300
Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile
305     310     315     320
Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr
325     330     335

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Cys	Thr	Tyr	His	Pro	Asp	Pro	Val	Gly	Pro	Gly	Leu	Asp	Ile	Gln	Gln		
			340					345					350				
Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	His	Gly	Val	Thr	Gln	Leu	Gly		
		355					360					365					
Phe	Tyr	Val	Leu	Asp	Arg	Asp	Ser	Leu	Phe	Ile	Asn	Gly	Tyr	Ala	Pro		
		370				375					380						
Gln	Asn	Leu	Ser	Ile	Arg	Gly	Glu	Tyr	Gln	Ile	Asn	Phe	His	Ile	Val		
385					390					395					400		
Asn	Trp	Asn	Leu	Ser	Asn	Pro	Asp	Pro	Thr	Ser	Ser	Glu	Tyr	Ile	Thr		
			405						410					415			
Leu	Leu	Arg	Asp	Ile	Gln	Asp	Lys	Val	Thr	Thr	Leu	Tyr	Lys	Gly	Ser		
		420						425					430				
Gln	Leu	His	Asp	Thr	Phe	Arg	Phe	Cys	Leu	Val	Thr	Asn	Leu	Thr	Met		
		435					440					445					
Asp	Ser	Val	Leu	Val	Thr	Val	Lys	Ala	Leu	Phe	Ser	Ser	Asn	Leu	Asp		
		450				455					460						
Pro	Ser	Leu	Val	Glu	Gln	Val	Phe	Leu	Asp	Lys	Thr	Leu	Asn	Ala	Ser		
465					470					475					480		
Phe	His	Trp	Leu	Gly	Ser	Thr	Tyr	Gln	Leu	Val	Asp	Ile	His	Val	Thr		
			485					490						495			
Glu	Met	Glu	Ser	Ser	Val	Tyr	Gln	Pro	Thr	Ser	Ser	Ser	Ser	Thr	Gln		
			500					505						510			
His	Phe	Tyr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Pro	Tyr	Ser	Gln	Asp		
		515					520					525					
Lys	Ala	Gln	Pro	Gly	Thr	Thr	Asn	Tyr	Gln	Arg	Asn	Lys	Arg	Asn	Ile		
		530				535					540						
Glu	Asp	Ala	Leu	Asn	Gln	Leu	Phe	Arg	Asn	Ser	Ser	Ile	Lys	Ser	Tyr		
545					550					555					560		
Phe	Ser	Asp	Cys	Gln	Val	Ser	Thr	Phe	Arg	Ser	Val	Pro	Asn	Arg	His		
			565					570						575			
His	Thr	Gly	Val	Asp	Ser	Leu	Cys	Asn	Phe	Ser	Pro	Leu	Ala	Arg	Arg		
			580					585					590				
Val	Asp	Arg	Val	Ala	Ile	Tyr	Glu	Glu	Phe	Leu	Arg	Met	Thr	Arg	Asn		
		595					600					605					
Gly	Thr	Gln	Leu	Gln	Asn	Phe	Thr	Leu	Asp	Arg	Ser	Ser	Val	Leu	Val		
		610				615					620						
Asp	Gly	Tyr	Ser	Pro	Asn	Arg	Asn	Glu	Pro	Leu	Thr	Gly	Asn	Ser	Asp		
625					630					635					640		
Leu	Pro	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	Pro	Pro	Cys	Lys		
			645					650						655			
Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro		
			660				665					670					
Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr		
		675					680					685					
Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser		
		690				695				700							
Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Thr	His		
705					710					715					720		
Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser	Ala	Leu	Pro	Ile		
			725					730						735			
Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn		
			740				745					750					
Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys		
		755					760					765					
Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu		

770		775		780
Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe				
785		790		800
Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu				
	805		810	815
Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr				
	820		825	830
Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg				
	835		840	845
Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His				
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Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys				
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<210> 50

<211> 367

<212> PRT

<213> Artificial Sequence

<220>

<223> hCD28 ecto (N19-P152).mFc ; Accession# NP_006130

<400> 50

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn				
1		5		10
Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu				
	20		25	30
Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys				
	35		40	45
Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser Lys Thr				
	50		55	60
Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr Phe Tyr				
65		70		75
Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile				
	85		90	95
Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly				
	100		105	110
Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe				
	115		120	125
Pro Gly Pro Ser Lys Pro Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys				
	130		135	140
Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val				
	145		150	155
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser				
	165		170	175
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp				
	180		185	190
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln				
	195		200	205
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser				
	210		215	220
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys				
	225		230	235
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile				

				245				250					255				
Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro		
			260					265					270				
Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met		
		275					280					285					
Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn		
	290					295					300						
Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser		
305					310					315					320		
Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn		
				325					330					335			
Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu		
		340						345					350				
His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys			
		355					360					365					

<210> 51

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> hMUC16 membrane-proximal domain
(P13810-P14451).mmH

<400> 51

Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu		
1				5				10					15				
Arg	Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys		
		20						25				30					
Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Glu	Ala	Thr	Gly	Val		
		35					40					45					
Asp	Ala	Ile	Cys	Thr	His	Arg	Pro	Asp	Pro	Thr	Gly	Pro	Gly	Leu	Asp		
	50					55					60						
Arg	Glu	Gln	Leu	Tyr	Leu	Glu	Leu	Ser	Gln	Leu	Thr	His	Ser	Ile	Thr		
65				70						75					80		
Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly		
			85					90						95			
Phe	Thr	His	Arg	Ser	Ser	Val	Pro	Thr	Ser	Thr	Gly	Val	Val	Ser			
		100					105					110					
Glu	Glu	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Asn	Asn	Leu	Arg	Tyr	Met		
		115					120					125					
Ala	Asp	Met	Gly	Gln	Pro	Gly	Ser	Leu	Lys	Phe	Asn	Ile	Thr	Asp	Asn		
	130					135					140						
Val	Met	Gln	His	Leu	Leu	Ser	Pro	Leu	Phe	Gln	Arg	Ser	Ser	Leu	Gly		
145				150						155					160		
Ala	Arg	Tyr	Thr	Gly	Cys	Arg	Val	Ile	Ala	Leu	Arg	Ser	Val	Lys	Asn		
			165						170					175			
Gly	Ala	Glu	Thr	Arg	Val	Asp	Leu	Leu	Cys	Thr	Tyr	Leu	Gln	Pro	Leu		
		180					185							190			
Ser	Gly	Pro	Gly	Leu	Pro	Ile	Lys	Gln	Val	Phe	His	Glu	Leu	Ser	Gln		
	195					200						205					
Gln	Thr	His	Gly	Ile	Thr	Arg	Leu	Gly	Pro	Tyr	Ser	Leu	Asp	Lys	Asp		
	210					215						220					

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<210> 52
 <211> 367
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCD28 ecto (N19-P152).mFc

<400> 52
 Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
 1 5 10 15
 Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
 20 25 30
 Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
 35 40 45
 Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser Lys Thr
 50 55 60
 Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr Phe Tyr
 65 70 75 80
 Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
 85 90 95
 Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
 100 105 110
 Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
 115 120 125
 Pro Gly Pro Ser Lys Pro Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
 130 135 140
 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
 145 150 155 160
 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
 165 170 175
 Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
 180 185 190
 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
 195 200 205
 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
 210 215 220
 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
 225 230 235 240
 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
 245 250 255
 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
 260 265 270
 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
 275 280 285
 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
 290 295 300
 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
 305 310 315 320
 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
 325 330 335
 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu

			340					345				350			
His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys	
		355					360					365			

<210> 53
 <211> 162
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCD28 ecto (N19-P152).mmH

<400> 53
 Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
 1 5 10 15
 Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
 20 25 30
 Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
 35 40 45
 Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser Lys Thr
 50 55 60
 Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr Phe Tyr
 65 70 75 80
 Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
 85 90 95
 Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
 100 105 110
 Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
 115 120 125
 Pro Gly Pro Ser Lys Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 130 135 140
 Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu His His His His
 145 150 155 160
 His His

<210> 54
 <211> 159
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse CD28 (Accession# NP_031668.3) mCD28 ecto
 (N20-L150).mmH

<400> 54
 Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val Asp Ser Asn
 1 5 10 15
 Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu Ala Lys Glu
 20 25 30
 Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val Glu Val Cys
 35 40 45
 Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg Ser Asn Ala

50						55					60					
Glu	Phe	Asn	Cys	Asp	Gly	Asp	Phe	Asp	Asn	Glu	Thr	Val	Thr	Phe	Arg	
65					70					75					80	
Leu	Trp	Asn	Leu	His	Val	Asn	His	Thr	Asp	Ile	Tyr	Phe	Cys	Lys	Ile	
				85					90					95		
Glu	Phe	Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Arg	Ser	Asn	Gly	
			100					105					110			
Thr	Ile	Ile	His	Ile	Lys	Glu	Lys	His	Leu	Cys	His	Thr	Gln	Ser	Ser	
		115					120					125				
Pro	Lys	Leu	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Gly	Gly	Glu	
	130					135					140					
Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	His	His	His	His	His	His		
145					150				155							