

SEQUENCE LISTING

<110> cureab GmbH

<120> ANTI-GP73 ANTIBODIES AND IMMUNOCONJUGATES

<130> Z2254 PCT BS

<150> EP16 19 9882.8

<151> 2016-11-21

<160> 44

<170> BiSSAP 1.3.6

<210> 1

<211> 401

<212> PRT

<213> Homo sapiens

<220>

<223> GP73 UniProtKB Q8NBJ4

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Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val	Leu	Val	Asn	Asn	Ile	Thr	Thr
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Arg	Asn	Tyr	Gly	Arg	Leu	Gln	Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn
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Gln	Thr	Asn	Leu	Glu	Arg	Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile
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Asn	Gln	Met	Lys	Glu	Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu
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Val	Thr	Lys	Lys	Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu
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Asn	Asn	Asp	Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro
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	210					215					220				
Gly	Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
225					230					235					240
Glu	Val	Val	Leu	Asp	Ser	Lys	Arg	Gln	Val	Glu	Lys	Glu	Glu	Thr	Asn
			245						250					255	
Glu	Ile	Gln	Val	Val	Asn	Glu	Glu	Pro	Gln	Arg	Asp	Arg	Leu	Pro	Gln
			260					265					270		
Glu	Pro	Gly	Arg	Glu	Gln	Val	Val	Glu	Asp	Arg	Pro	Val	Gly	Gly	Arg
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	290					295					300				
Ala	Leu	Ser	Val	Ser	Gln	Glu	Asn	Pro	Glu	Met	Glu	Gly	Pro	Glu	Arg

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Asp	Gln	Leu	Val	Ile	Pro	Asp	Gly	Gln	Glu	Glu	Glu	Gln	Glu	Ala	Ala
				325					330					335	
Gly	Glu	Gly	Arg	Asn	Gln	Gln	Lys	Leu	Arg	Gly	Glu	Asp	Asp	Tyr	Asn
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Met	Asp	Glu	Asn	Glu	Ala	Glu	Ser	Glu	Thr	Asp	Lys	Gln	Ala	Ala	Leu
		355					360					365			
Ala	Gly	Asn	Asp	Arg	Asn	Ile	Asp	Val	Phe	Asn	Val	Glu	Asp	Gln	Lys
	370					375					380				
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Leu															

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-2 heavy chain variable region (VH)

<400> 2															
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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	Gly	Lys	Gly	Leu	Glu	Trp	Val
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Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	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	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Glu	Gly	Ser	Ala	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr
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Val	Thr	Val	Ser	Ser											
			115												

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 <213> Artificial Sequence

<220>
 <223> G2-2 light chain variable region (VL)

<400> 3															
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Ser	Ala	Ser	Leu	Thr	Cys	Thr	Leu	Arg	Ser	Asp	Ile	Ser	Val	Gly	Phe
		20						25					30		
His	Arg	Ile	Tyr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Pro	Pro	Gln	Tyr
		35				40						45			
Leu	Leu	Arg	Tyr	Lys	Ser	Asp	Ser	Asp	Lys	Gln	Gln	Gly	Ser	Gly	Val
	50					55				60					
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Lys	Asp	Ala	Ser	Ala	Asn	Ala	Gly	Ile
65					70				75					80	
Leu	Leu	Ile	Ser	Gly	Leu	Gln	Ser	Asp	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
			85					90					95		
Val	Ile	Trp	His	Thr	Ser	Gly	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Val

	100	105	110
--	-----	-----	-----

Glu Ile Lys
 115

<210> 4
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-2 HVR-H1

<400> 4
 Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

<210> 5
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-2 HVR-H2

<400> 5
 Ile Ser Tyr Asp Gly Ser Asn Lys
 1 5

<210> 6
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-2 HVR-H3

<400> 6
 Ala Arg Glu Gly Ser Ala Gly Met Asp Val
 1 5 10

<210> 7
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-2 HVR-L1

<400> 7
 Ser Asp Ile Ser Val Gly Phe His Arg
 1 5

<210> 8
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-2 HVR-L2

<400> 8
Tyr Lys Ser Asp Ser Asp Lys
1 5

<210> 9
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<212> PRT
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<223> G2-2 HVR-L3

<400> 9
Val Ile Trp His Thr Ser Gly Val Val
1 5

<210> 10
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> G2-1 heavy chain variable region (VH)

<400> 10
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Val Ile Ser Tyr Asp Gly Ser Asn Lys Ala 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 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Arg Ser Tyr Tyr Asp Ser Ser Gly Tyr Leu Phe Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 11
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<212> PRT
<213> Artificial Sequence

<220>
<223> G2-1 light chain variable region (VL)

<400> 11
Asp Ile Gln Met Thr Gln Pro His Ser Val Ser Glu Ser Val Gly Lys
1 5 10 15
Thr Val Ile Ile Thr Cys Thr Gly Gly Gly Ser Ile Asp Thr Asn
20 25 30
Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Val Thr Leu
35 40 45
Ile Tyr Glu Asp Asp Gln Arg Pro Phe Gly Val Pro Asp Arg Phe Ser
50 55 60
Ala Ala Ile Asp Thr Ser Ser Ser Ser Ala Ser Leu Thr Ile Ser Gly

65		70		75		80									
Leu	Thr	Ala	Glu	Asp	Glu	Ala	Thr	Tyr	Tyr	Cys	Gln	Ser	Ser	His	Ser
				85					90					95	
Thr	Ala	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys		
			100					105					110		

<210> 12
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 <212> PRT
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<220>
 <223> G2-1 HVR-H1

<400> 12
 Gly Phe Thr Phe Ser Ser Tyr Ala
 1 5

<210> 13
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-1 HVR-H2

<400> 13
 Ile Ser Tyr Asp Gly Ser Asn Lys
 1 5

<210> 14
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-1 HVR-H3

<400> 14
 Ala Arg Gly Arg Ser Tyr Tyr Asp Ser Ser Gly Tyr Leu Phe Asp Tyr
 1 5 10 15

<210> 15
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-1 HVR-L1

<400> 15
 Gly Gly Ser Ile Asp Thr Asn Tyr
 1 5

<210> 16
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 <212> PRT
 <213> Artificial Sequence

<220>
<223> G2-1 HVR-L2

<400> 16
Glu Asp Asp
1

<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> G2-1 HVR-L3

<400> 17
Gln Ser Ser His Ser Thr Ala Val
1 5

<210> 18
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> G2-4 heavy chain variable region (VH)

<400> 18
Gln Val Gln Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr Asp Tyr
20 25 30
Tyr Met Ser Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu
35 40 45
Gly Phe Ile Arg Asn Lys Ala Lys Gly Tyr Thr Thr Glu Tyr Ser Ala
50 55 60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Gln Ser Ile
65 70 75 80
Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Ser Ala Thr Tyr
85 90 95
Tyr Cys Ala Arg Asp Pro Ser Thr Asn Tyr Trp Tyr Phe Asp Val Trp
100 105 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 19
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<212> PRT
<213> Artificial Sequence

<220>
<223> G2-4 light chain variable region (VL)

<400> 19
Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15
Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30
Arg Thr Arg 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	Thr		
65					70					75					80		
Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tyr	Tyr	Cys	Lys	Gln		
				85					90					95			
Ser	Tyr	Asn	Leu	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
			100					105					110				

Arg

<210> 20
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-4 HVR-H1

<400> 20
 Gly Phe Thr Phe Thr Asp Tyr
 1 5

<210> 21
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-4 HVR-H2

<400> 21
 Arg Asn Lys Ala Lys Gly Tyr Thr
 1 5

<210> 22
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-4 HVR-H3

<400> 22
 Asp Pro Ser Thr Asn Tyr Trp Tyr Phe Asp Val
 1 5 10

<210> 23
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-4 HVR-L1

<400> 23
 Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
 1 5 10 15
 Ala

<210> 24
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-4 HVR-L2

<400> 24
 Trp Ala Ser Thr Arg Glu Ser
 1 5

<210> 25
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G2-4 HVR-L3

<400> 25
 Lys Gln Ser Tyr Asn Leu Tyr Thr
 1 5

<210> 26
 <211> 330
 <212> PRT
 <213> Homo sapiens

<220>
 <223> G2-2/G2-1 heavy chain constant region (IgG1)

<400> 26
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205

Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
210						215					220				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
225					230					235					240
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
			245						250					255	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
			260					265					270		
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
		275					280					285			
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
	290					295					300				
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
305					310					315					320
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
			325						330						

<210> 27
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> G2-2/G2-1 light chain constant region (kappa)

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

<210> 28
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 <212> PRT
 <213> Mus musculus

<220>
 <223> mG2-2/mG2-1 heavy chain constant region (IgG2a)

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

Ile	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys		
			100					105					110				
Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro		
		115					120					125					
Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys		
		130				135					140						
Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp		
145					150					155					160		
Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Thr	His	Arg		
			165					170						175			
Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser	Ala	Leu	Pro	Ile	Gln		
		180						185					190				
His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn		
		195				200						205					
Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly		
	210					215					220						
Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu		
225					230					235					240		
Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met		
				245					250					255			
Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu		
			260					265					270				
Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe		
		275				280						285					
Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn		
	290					295					300						
Ser	Tyr	Ser	Cys	Ser	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr			
305					310				315					320			
Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys								
			325					330									

<210> 29
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 <213> Mus musculus

<220>
 <223> GP73 UniProt Q91XA2

<400> 29

Met	Met	Gly	Leu	Gly	Asn	Gly	Arg	Arg	Ser	Met	Lys	Ser	Pro	Pro	Leu		
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Ile	Leu	Ala	Ala	Leu	Val	Ala	Cys	Val	Ile	Val	Leu	Gly	Phe	Asn	Tyr		
		20					25					30					
Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Glu	Leu	Gln	Thr	Arg	Ile	Val	Glu		
		35				40					45						
Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg	Gly	Ala	Val	Glu		
	50					55				60							
Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Gln	Lys	Gln	Arg	Glu	Gln		
65				70					75					80			
Leu	Asp	Arg	Ile	Gln	Ser	Ser	His	Ser	Phe	Gln	Leu	Glu	Asn	Val	Asn		
			85					90					95				
Lys	Leu	His	Gln	Asp	Glu	Lys	Ala	Val	Leu	Val	Asn	Asn	Ile	Thr	Thr		
		100					105						110				
Gly	Glu	Lys	Leu	Ile	Arg	Asp	Leu	Gln	Asp	Gln	Leu	Lys	Ala	Leu	Gln		
		115				120						125					
Arg	Ser	Tyr	Ser	Ser	Leu	Gln	Asp	Ile	Phe	Gln	Phe	Gln	Lys	Asn			
	130				135					140							
Gln	Thr	Ser	Leu	Glu	Lys	Lys	Phe	Ser	Tyr	Asp	Leu	Asn	Gln	Cys	Ile		
145				150						155				160			
Ser	Gln	Met	Thr	Glu	Val	Lys	Glu	Gln	Cys	Asp	Glu	Arg	Ile	Glu	Glu		
			165						170					175			
Val	Ile	Arg	Lys	Arg	Asn	Glu	Ala	Pro	Gly	Ser	Arg	Asp	Leu	Ala	Glu		

			180					185					190				
Thr	Asn	Asn	Gln	His	Gln	Gln	Ala	Leu	Lys	Pro	Gln	Pro	Lys	Leu	Gln		
		195					200					205					
Glu	Glu	Val	Pro	Ser	Glu	Glu	Gln	Met	Pro	Gln	Glu	Lys	Gly	Asp	Val		
	210					215					220						
Pro	Arg	Asn	Lys	Ser	Gln	Ile	Pro	Ala	Pro	Asn	Ser	Glu	Ser	Leu	Gly		
225					230					235					240		
Leu	Lys	Pro	Gln	Val	Gln	Asn	Glu	Glu	Thr	Asn	Glu	Ile	Gln	Ala	Val		
				245					250					255			
Gly	Glu	Glu	His	Gln	Gln	Ala	Ser	Ile	Gln	Gly	Gln	Ala	Val	Ala	Asp		
			260					265					270				
Gly	Thr	Arg	Val	Gly	Ala	Glu	Lys	Leu	Asp	Gln	His	Thr	Gln	Leu	Pro		
	275						280					285					
Ala	Gly	Leu	Leu	Ala	Arg	Pro	Glu	Glu	Asp	Ser	Gln	Tyr	Pro	Glu	Arg		
	290					295					300						
Glu	Gln	Leu	Val	Ile	Arg	Asp	Arg	Gln	Glu	Gln	Gln	Arg	Ala	Ser	Glu		
305				310				315							320		
Glu	Gly	Gly	Gly	Gln	Lys	Asn	Pro	Gly	Asp	Glu	Tyr	Asp	Met	Asp	Glu		
				325				330						335			
Asn	Glu	Ala	Glu	Ser	Glu	Arg	Glu	Lys	Gln	Ala	Ala	Leu	Ala	Gly	Asn		
			340					345					350				
Asp	Arg	Asn	Ile	Asn	Val	Leu	Asn	Ala	Asp	Ala	Gln	Lys	Arg	Gly	Ile		
	355					360						365					
Ile	Asn	Val	Pro	Val	Gly	Ser	Glu	Arg	Gln	Ser	His	Ile	Leu	Asn	Gln		
	370				375						380						
Val	Gly	Ile	His	Ile	Pro	Gln	Gln	Ala									
385					390												

<210> 30
 <211> 20
 <212> PRT
 <213> Homo sapiens

<220>
 <223> GP73 aa 36 to 55 UniProt Q8NBJ4

<400> 30																	
Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg	Ile	Met	Glu	Leu	Glu	Gly		
1			5					10					15				
Arg	Val	Arg	Arg														
			20														

<210> 31
 <211> 20
 <212> PRT
 <213> Mus musculus

<220>
 <223> GP73 aa 36 to 55 UniProt Q91XA2

<400> 31																	
Ser	Ser	Arg	Ser	Val	Glu	Leu	Gln	Thr	Arg	Ile	Val	Glu	Leu	Glu	Gly		
1			5					10					15				
Arg	Val	Arg	Arg														
			20														

<210> 32
 <211> 20
 <212> PRT
 <213> Canis

<220>

<223> GP73 aa 36 to 55 UniProt E2RLA5

<400> 32

Ser Ser Arg Ser Val Asp Leu Gln Thr Arg Ile Val Glu Leu Glu Gly
1 5 10 15
Arg Val Arg Arg
20

<210> 33

<211> 11

<212> PRT

<213> Homo Sapiens

<220>

<223> epitope of antibodies of the invention

<400> 33

Arg Ile Met Glu Leu Glu Gly Arg Val Arg Arg
1 5 10

<210> 34

<211> 6

<212> PRT

<213> Homo Sapiens

<220>

<223> epitope of antibodies of the invention

<400> 34

Glu Gly Arg Val Arg Arg
1 5

<210> 35

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> G2-2opti (IgG1) and G2-2opti (IgG2a) heavy chain variable region (VH)

<400> 35

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
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 His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys 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 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Ser Ala Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110
Val Thr Val Ser Ser
115

<210> 36

<211> 115
<212> PRT
<213> Artificial Sequence

<220>

<223> G2-2opti (IgG1) and G2-2opti (IgG2a) light chain variable region
(VL)

<400> 36

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

<210> 37
<211> 123
<212> PRT
<213> Artificial Sequence

<220>

<223> G2-1opti (IgG1) and G2-1opti (IgG2a) heavy chain variable region
(VH)

<400> 37

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

<210> 38
<211> 110
<212> PRT
<213> Artificial Sequence

<220>

<223> G2-1opti (IgG1) and G2-1opti (IgG2a) light chain variable region
(VL)

<400> 38

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

<210> 39

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> G2-2opti (IgG2a)/ G2-1opti (IgG2a) heavy chain constant region (IgG2a)

<400> 39

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

<210> 41
 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GP73 aa 36 to 401 (R52A)-His (GP73-His AVRR)

<400> 41
 Ser Ser Arg Ser Val Asp Leu Gln Thr Arg Ile Met Glu Leu Glu Gly
 1 5 10 15
 Ala Val Arg Arg Ala Ala Ala Glu Arg Gly Ala Val Glu Leu Lys Lys
 20 25 30
 Asn Glu Phe Gln Gly Glu Leu Glu Lys Gln Arg Glu Gln Leu Asp Lys
 35 40 45
 Ile Gln Ser Ser His Asn Phe Gln Leu Glu Ser Val Asn Lys Leu Tyr
 50 55 60
 Gln Asp Glu Lys Ala Val Leu Val Asn Asn Ile Thr Thr Gly Glu Arg
 65 70 75 80
 Leu Ile Arg Val Leu Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr
 85 90 95
 Gly Arg Leu Gln Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn
 100 105 110
 Leu Glu Arg Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met
 115 120 125
 Lys Glu Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys
 130 135 140
 Lys Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
 145 150 155 160
 Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu Gln
 165 170 175
 Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly Asn Val
 180 185 190
 Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser Glu Val Val
 195 200 205
 Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr Asn Glu Ile Gln
 210 215 220
 Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu Pro Gln Glu Pro Gly
 225 230 235 240
 Arg Glu Gln Val Val Glu Asp Arg Pro Val Gly Gly Arg Gly Phe Gly
 245 250 255
 Gly Ala Gly Glu Leu Gly Gln Thr Pro Gln Val Gln Ala Ala Leu Ser
 260 265 270
 Val Ser Gln Glu Asn Pro Glu Met Glu Gly Pro Glu Arg Asp Gln Leu
 275 280 285
 Val Ile Pro Asp Gly Gln Glu Glu Glu Gln Glu Ala Ala Gly Glu Gly
 290 295 300
 Arg Asn Gln Gln Lys Leu Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu
 305 310 315 320
 Asn Glu Ala Glu Ser Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn
 325 330 335
 Asp Arg Asn Ile Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr
 340 345 350
 Ile Asn Leu Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu Ala His
 355 360 365
 His His His His His His His His
 370 375

<210> 42
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Endosomal escape domain (EED)

<400> 42

Met Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly
1 5 10 15
Gly Ile Val Gly Ser
20

<210> 43

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> EED Linker

<400> 43

Ser Ala Ala Ala Gly Thr
1 5

<210> 44

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> G2-1 HVR-L3 variant

<400> 44

Gln Ser Ser His Ser Thr Ala Val Val
1 5