

SEQUENCE LISTING

<110> Univeritätsklinikum Hamburg Eppendorf
Forschungszentrum Borstel

<120> Antibodies binding mannose 6-phosphate

<130> P 77448

<160> 12

<170> PatentIn version 3.4

<210> 1

<211> 12

<212> PRT

<213> Oryctolagus cuniculus

<400> 1

Gln Ser Ser Gln Ser Val Tyr Asn Asn Arg Leu Ala
1 5 10

<210> 2

<211> 7

<212> PRT

<213> Oryctolagus cuniculus

<400> 2

Ser Ala Ser Thr Leu Ala Ser
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<210> 3

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His Gly Gly Tyr Arg Ser Asn Asp Asp Arg Tyr Ala
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<213> Oryctolagus cuniculus

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Trp Tyr Thr Met Asn
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<211> 17
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<213> Oryctolagus cuniculus

<400> 5

Cys Ile Gly Ala Gly Val Tyr Gly Ser Asn Tyr Tyr Ala Ser Trp Ala
1 5 10 15

Lys

<210> 6
<211> 9
<212> PRT
<213> Oryctolagus cuniculus

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Asp Gly Ile Asn Gly Gly Tyr Asp Ile
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<210> 7
<211> 111
<212> PRT
<213> Oryctolagus cuniculus

<400> 7

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

Gly Thr Val Thr Ile Lys Cys Gln Ser Ser Gln Ser Val Tyr Asn Asn
20 25 30

Arg Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Arg Pro Lys Leu Leu
35 40 45

Ile Tyr Ser Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys
50 55 60

Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Asp Leu Glu
65 70 75 80

Trp Gly Asp Ala Ala Thr Tyr Tyr Cys His Gly Gly Tyr Arg Ser Asn
85 90 95

Asp Asp Arg Tyr Ala Phe Ser Gly Gly Thr Glu Leu Glu Ile Leu
100 105 110

<210> 8
 <211> 117
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 8

Gln	Ser	Val	Lys	Glu	Ser	Glu	Gly	Asp	Leu	Val	Lys	Pro	Gly	Ala	Ser
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Leu	Thr	Leu	Thr	Cys	Lys	Ala	Ser	Gly	Phe	Asp	Phe	Thr	Trp	Tyr	Thr
			20					25					30		
Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Ala
		35					40					45			
Cys	Ile	Gly	Ala	Gly	Val	Tyr	Gly	Ser	Asn	Tyr	Tyr	Ala	Ser	Trp	Ala
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Ala	Ser	Ser	Thr	Thr	Val	Thr	Leu
65					70					75					80
Gln	Met	Thr	Ser	Leu	Thr	Val	Ala	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala
				85					90					95	
Arg	Asp	Gly	Ile	Asn	Gly	Gly	Tyr	Asp	Ile	Trp	Gly	Pro	Gly	Thr	Leu
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Val	Thr	Val	Ser	Ser											
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<210> 9
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 <212> DNA
 <213> artificial sequence

<220>
 <223> antibody construct

<220>
 <221> CDS
 <222> (1)..(870)

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1				5				10					15			
acc	gtg	gcc	cag	gcg	gcc	gag	ctc	gtg	atg	acc	cag	act	gaa	tcg	ccc	96
Thr	Val	Ala	Gln	Ala	Ala	Glu	Leu	Val	Met	Thr	Gln	Thr	Glu	Ser	Pro	
			20					25					30			
gtg	tct	gca	gct	gtg	gga	ggc	aca	gtt	acc	atc	aag	tgc	cag	tcc	agt	144
Val	Ser	Ala	Ala	Val	Gly	Gly	Thr	Val	Thr	Ile	Lys	Cys	Gln	Ser	Ser	

35	40	45	
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caa cgt ccc aag ctc ctg atc tat tct gca tcc act ctg gca tct ggg Gln Arg Pro Lys Leu Leu Ile Tyr Ser Ala Ser Thr Leu Ala Ser Gly 65 70 75 80			240
gtc cca tcg cgg ttc aaa ggc agt gga tct ggg aca cag ttc act ctc Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu 85 90 95			288
acc atc agc gac ctg gag tgg ggc gat gct gcc act tac tac tgt cat Thr Ile Ser Asp Leu Glu Trp Gly Asp Ala Ala Thr Tyr Tyr Cys His 100 105 110			336
ggc ggt tac cgt agt aat gat gat aga tat gct ttc agc gga ggg acc Gly Gly Tyr Arg Ser Asn Asp Asp Arg Tyr Ala Phe Ser Gly Gly Thr 115 120 125			384
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aag ggg ctg gag tgg atc gca tgc att ggt gct ggt gtt tat ggt agc Lys Gly Leu Glu Trp Ile Ala Cys Ile Gly Ala Gly Val Tyr Gly Ser 195 200 205			624
aat tac tac gcg agc tgg gcg aaa ggc cgg ttc acc atc tcc aaa gcc Asn Tyr Tyr Ala Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Ala 210 215 220			672
tcg tcg acc acg gtg acc ctg caa atg acc agt ctg aca gtc gcg gac Ser Ser Thr Thr Val Thr Leu Gln Met Thr Ser Leu Thr Val Ala Asp 225 230 235 240			720
acg gcc acc tat ttc tgt gcg aga gat ggt att aat ggt ggt tat gac Thr Ala Thr Tyr Phe Cys Ala Arg Asp Gly Ile Asn Gly Gly Tyr Asp 245 250 255			768
atc tgg ggc cca ggc acc ctg gtc acc gtc tcc tca aga tct gaa cag			816

Ile Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Arg Ser Glu Gln
260 265 270

aag cta atc agt gag gaa gat ttg aag gga tcc cat cac cat cac cat 864
Lys Leu Ile Ser Glu Glu Asp Leu Lys Gly Ser His His His His His
275 280 285

tag tga 870

<210> 10
<211> 288
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic Construct

<400> 10

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
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Thr Val Ala Gln Ala Ala Glu Leu Val Met Thr Gln Thr Glu Ser Pro
20 25 30

Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ser Ser
35 40 45

Gln Ser Val Tyr Asn Asn Arg Leu Ala Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Arg Pro Lys Leu Leu Ile Tyr Ser Ala Ser Thr Leu Ala Ser Gly
65 70 75 80

Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu
85 90 95

Thr Ile Ser Asp Leu Glu Trp Gly Asp Ala Ala Thr Tyr Tyr Cys His
100 105 110

Gly Gly Tyr Arg Ser Asn Asp Asp Arg Tyr Ala Phe Ser Gly Gly Thr
115 120 125

Glu Leu Glu Ile Leu Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Gly Gly Ser Ser Arg Ser Ser Gln Ser Val Lys Glu Ser Glu Gly Asp
145 150 155 160

Leu Val Lys Pro Gly Ala Ser Leu Thr Leu Thr Cys Lys Ala Ser Gly
165 170 175

Phe Asp Phe Thr Trp Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly
180 185 190

Lys Gly Leu Glu Trp Ile Ala Cys Ile Gly Ala Gly Val Tyr Gly Ser
195 200 205

Asn Tyr Tyr Ala Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Ala
210 215 220

Ser Ser Thr Thr Val Thr Leu Gln Met Thr Ser Leu Thr Val Ala Asp
225 230 235 240

Thr Ala Thr Tyr Phe Cys Ala Arg Asp Gly Ile Asn Gly Gly Tyr Asp
245 250 255

Ile Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Arg Ser Glu Gln
260 265 270

Lys Leu Ile Ser Glu Glu Asp Leu Lys Gly Ser His His His His His
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<210> 11
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<212> DNA
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<223> PCR oligonucleotide primer

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37

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<212> DNA
<213> Artificial

<220>
<223> PCR oligonucleotide primer

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60

gaccagggt

69