

SEQUENCE LISTING

<110> bluebird bio, Inc.
Friedman, Kevin

<120> COMPOSITIONS AND METHODS FOR TREATING CANCER

<130> BLUE-123.PC

<150> US 62/861,838

<151> 2019-06-14

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<151> 2020-03-18

<160> 97

<170> PatentIn version 3.5

<210> 1

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Anti-CD79A-01 CDRL1

<400> 1

Arg	Ser	Ser	Gln	Ser	Ile	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Glu
1				5					10					15	

<210> 2

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Anti-CD79A-01 CDRL2

<400> 2

Lys	Val	Ser	Asn	Arg	Phe	Ser
1				5		

<210> 3

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Anti-CD79A-01 CDRL3

<400> 3

Phe Gln Gly Ser His Val Pro Phe Thr
1 5

<210> 4

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Anti-CD79A-01 CDRH1

<400> 4

Gly Tyr Thr Phe Ser Thr Ser Trp Met Asn
1 5 10

<210> 5

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Anti-CD79A-01 CDRH2

<400> 5

Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
1 5 10 15

Gly

<210> 6

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Anti-CD79A-01 CDRH3

<400> 6

Phe Tyr Tyr Gly Asn Thr Phe Ala Met Asp Tyr
1 5 10

<210> 7

<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD79A-01 Light chain

<400> 7

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 8
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD79A-01 Heavy chain

<400> 8

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

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

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

Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

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

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

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

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 9
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Anti-CD79A-10 CDRL1

<400> 9

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 10
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Anti-CD79A-10 CDRL2

<400> 10

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 11

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

<220>
<223> Made in Lab - Anti-CD79A-10 CDRL3

<400> 11

Ser	Gln	Ser	Thr	His	Val	Pro	Pro	Tyr	Thr
1				5					10

<210> 12
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Anti-CD79A-19 CDRH1

<400> 12

Gly	Tyr	Ala	Phe	Ser	Phe	Ser	Trp	Met	Asn
1				5					10

<210> 13
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Anti-CD79A-10 CDRH2

<400> 13

Arg	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Asn	Tyr	Asn	Gly	Lys	Phe	Lys
1				5					10					15	

Gly

<210> 14
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Anti-CD79A-10 CDRH3

<400> 14

Trp Val Tyr Ser Gly Asn Asn Tyr Ala Val Asp Tyr
1 5 10

<210> 15
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD79A-10 Light chain

<400> 15

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 16
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD79A-10 Heavy chain

<400> 16

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

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

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

Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

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

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

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

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 17

<211> 492

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD79A-01_HL CAR construct

<400> 17

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
20 25 30

Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr

35

40

45

Thr Phe Ser Thr Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln
 50 55 60

Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn
 65 70 75 80

Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
 85 90 95

Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser
 100 105 110

Ala Val Tyr Phe Cys Glu Arg Phe Tyr Tyr Gly Asn Thr Phe Ala Met
 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Leu Met
 145 150 155 160

Thr Gln Ile Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser
 165 170 175

Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr
 180 185 190

Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu
 195 200 205

Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser
 210 215 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu
 225 230 235 240

Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro
 245 250 255

Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Thr Thr Thr
260 265 270

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
275 280 285

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
290 295 300

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
305 310 315 320

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
325 330 335

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
340 345 350

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
355 360 365

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
370 375 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
385 390 395 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr

465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 18
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD79A-01_LH CAR construct

<400> 18

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Val Leu Met Thr Gln Ile Pro Leu Ser Leu
20 25 30

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
35 40 45

Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
65 70 75 80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

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

Tyr Cys Phe Gln Gly Ser His Val Pro Phe Thr Phe Gly Ser Gly Thr
115 120 125

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

Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu

145		150		155		160
Val	Lys	Pro	Gly	Ala	Ser	Tyr
			165			175
Thr	Phe	Ser	Thr	Ser	Trp	Met
			180			185
Gly	Leu	Glu	Trp	Ile	Gly	Arg
			195			200
Tyr	Asn	Gly	Lys	Phe	Lys	Gly
			210			215
Ser	Asn	Thr	Ala	Tyr	Met	Gln
						230
Ala	Val	Tyr	Phe	Cys	Glu	Arg
						245
Asp	Tyr	Trp	Gly	Gln	Gly	Thr
						260
Pro	Ala	Pro	Arg	Pro	Pro	Thr
						275
Leu	Ser	Leu	Arg	Pro	Glu	Ala
						295
His	Thr	Arg	Gly	Leu	Asp	Phe
						310
Leu	Ala	Gly	Thr	Cys	Gly	Val
						325
Tyr	Cys	Lys	Arg	Gly	Arg	Lys
						340
Phe	Met	Arg	Pro	Val	Gln	Thr
						355
Thr	Gln	Glu	Glu	Asp	Gly	Cys
						360

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
370 375 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
385 390 395 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 19
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD79A-10_HL CAR construct

<400> 19

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
20 25 30

Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr
35 40 45

Ala Phe Ser Phe Ser Trp Met Asn Trp Val Lys Trp Gly Pro Gly Gln
50 55 60

Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr Asn
65 70 75 80

Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
85 90 95

Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser
100 105 110

Ala Val Tyr Phe Cys Ala Arg Trp Val Tyr Ser Gly Asn Asn Tyr Ala
115 120 125

Val Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val
145 150 155 160

Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala
165 170 175

Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn
180 185 190

Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu
195 200 205

Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
210 215 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
225 230 235 240

Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val
245 250 255

Pro Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr

260

265

270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
 275 280 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
 290 295 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
 305 310 315 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
 325 330 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
 340 345 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
 355 360 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
 370 375 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
 385 390 395 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
 405 410 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
 420 425 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
 435 440 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 450 455 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 20
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD79A-10_LH CAR construct

<400> 20

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
20 25 30

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
35 40 45

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
65 70 75 80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

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

Phe Cys Ser Gln Ser Thr His Val Pro Pro Tyr Thr Phe Gly Gly Gly
115 120 125

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

Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
145 150 155 160

Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr
165 170 175

Ala Phe Ser Phe Ser Trp Met Asn Trp Val Lys Trp Gly Pro Gly Gln
180 185 190

Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr Asn
195 200 205

Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
210 215 220

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

Ala Val Tyr Phe Cys Ala Arg Trp Val Tyr Ser Gly Asn Asn Tyr Ala
245 250 255

Val Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Thr Thr
260 265 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
275 280 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
290 295 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305 310 315 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
325 330 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
340 345 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
355 360 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys

370

375

380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385 390 395 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
405 410 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
420 425 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
435 440 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
450 455 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 21

<211> 1479

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD79A-01_HL CAR polynucleotide construct

<400> 21

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ccccaggtcc agcttcagca gtccggacca gagttggtga aacctggggc atcagtcaag 120

attagctgca aggcacagc gtacaccttc agcactagtt ggatgaattg ggtgaagcag 180

cggcctggcc aggggttgga gtggatcgga cgcacttacc caggggatgg cgatacaaac 240

tacaacggaa agtttaaagg taaggctact ttgaccgctg acaaatcatc aaacacggca 300

tatatgcaac tgtctagcct cacatctgtc gactctgccg tctacttttg cgagcgattc 360

tactatggca acacttttgc catggactac tgggggcagg ggacatcagt aacagttagt 420

tctggagggg gcggttccgg gggcggggga tccggagggg gaggcagtga tgtgctgatg	480
accagatac cgttgtcact cccggtctca ctgggtgacc aggcaagcat cagctgcagg	540
agcagccagt ccatcgtgca ctctaacgga aatacctacc tggagtggta tctgcagaaa	600
cctggccagt cccctaagtt gttgatttac aaagtttcaa accgatttag tggagttccc	660
gataggtttt ccggttccgg gagcgttaca gacttcaccc tgaagataag tcgggttgag	720
gctgaagacc tgggagtata ttattgcttt cagggcagcc acgtaccatt cacatttggg	780
agtggaacca aactggagat caaaagaacc acaacacctg ctccaaggcc cccacacccc	840
gctccaacta tagccagcca accattgagc ctacagacctg aagcttgacg gcccgagca	900
ggaggcgccg tccatacgcg aggcctggac ttgcgctgtg atatttatat ttggggcccct	960
ttggccggaa catgtgggggt gttgcttctc tcccttgtga tcaactctgta ttgtaagcgc	1020
gggagaaaga agctcctgta catcttcaag cagcctttta tgcgacctgt gcaaaccact	1080
caggaagaag atgggtgttc atgccgcttc cccgaggagg aagaaggagg gtgtgaactg	1140
agggtgaaat tttctagaag cgccgatgct cccgcatatc agcagggtca gaatcagctc	1200
tacaatgaat tgaatctcgg caggcgagaa gagtacgatg ttctggacaa gagacggggc	1260
agggatcccg agatgggggg aaagccccgg agaaaaaatc ctacaggagg gttgtacaat	1320
gagctgcaga aggacaagat ggctgaagcc tatagcgaga tcggaatgaa aggcgaaaga	1380
cgcagaggca aggggcatga cggctctgtac cagggtctct ctacagccac caaggacact	1440
tatgatgcgt tgcatatgca agccttgcca ccccgctaa	1479

<210> 22

<211> 1479

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD79A-01_LH CAR polynucleotide construct

<400> 22

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cccgacgtgt tgatgaccca aataccgctt agtctgcctg tatctcttgg ggaccaggct	120
agcatctcat gccgcagcag tcaatccatt gtgcactcaa atgggaacac ctatttggag	180
tggtatctgc aaaaaccggg acagtctccg aaactgctga tatacaaagt aagcaacagg	240

ttcagcggag ttcctgacag attcagcggg agcggttctg gaactgactt tacacttaag	300
atctctcgcg ttgaggcgga ggacctgggc gtgtattact gttttcaagg atcccacgtc	360
ccgtttacat tcggatcagg caccaagctg gagatcaagc gcggtggcgg gggttctggc	420
gggggcggat ccggaggcgg cggatcccag gtgcagctgc agcagtctgg accagaactg	480
gttaagcccc gagcttcagt taagatttcc tgtaaggctt caggctatac attttccact	540
tcttgatga actgggtgaa acagcgcctt ggccaggggc tggaatggat cggacggatc	600
tatccggcg atggagacac taattataac ggtaagttca aagggaaggc caccctcacg	660
gccgacaagt cctccaatac agcgtacatg caactcagtt ccctgaccag cgttgatagc	720
gcagtttact tctgtgagcg cttctattac ggaaacacct tcgctatgga ttactggggt	780
caggggacct ccgtgaccgt gtcctctacc acaacacctg ctccaaggcc cccacaccc	840
gctccaacta tagccagcca accattgagc ctgagacctg aagcttgcag gcccgagca	900
ggaggcgccg tccatacgcg aggcctggac ttcgcgtgtg atatttatat ttggggccct	960
ttggccggaa catgtggggt gttgcttctc tcccttgtga tcactctgta ttgtaagcgc	1020
gggagaaaga agctcctgta catcttcaag cagcctttta tgcgacctgt gcaaaccact	1080
caggaagaag atgggtgttc atgccgcttc cccgaggagg aagaaggagg gtgtgaactg	1140
agggtgaaat tttctagaag cgccgatgct cccgcatatc agcagggtca gaatcagctc	1200
tacaatgaat tgaatctcgg caggcgagaa gactacgatg ttctggacaa gagacggggc	1260
agggatcccg agatgggggg aaagccccgg agaaaaaatc ctgaggagg gttgtacaat	1320
gagctgcaga aggacaagat ggctgaagcc tatagcgaga tcggaatgaa aggcgaaaga	1380
cgagaggca aggggcatga cggctctgtac cagggtctct ctacagccac caaggacact	1440
tatgatgcgt tgcatatgca agccttgcca ccccgctaa	1479

<210> 23

<211> 1482

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD79A-10_HL CAR polynucleotide construct

<400> 23

atggctctgc cagtgactgc gctgctgctg cccctcgctc ttctgctgca cgccgctcgg	60
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ccacaggtcc aactgcaaca gagcggcccc gagctggtaa aaccggggc ctccgtaaaa	120
atatacctgca agaccagcgg ctatgccttt tcattctcct ggatgaactg ggtgaagtgg	180
ggacccggtc agggacttga gtggatcggg cgaatctatc ccggaaacgg ggacacgaat	240
tacaacggca aatttaaagg caaggctact ctgactgctg aaaaaagtag caacaccgcc	300
tacatgcagt tgtcctcttt gacatcagta gactctgcag tgtatTTTTg cgcccgggtg	360
gtttactccg gaaataacta cgcggttgac tattggggac agggcacctc cgtgacagt	420
tcttctggcg gcgggggatc aggtggcggc gggctctggg gtggaggagg cgacgtggtt	480
atgaccaga cccctttgag cctgcccgtg agccttggcg accaagcctc catctcttgc	540
cggctctctc aatcactggt gcacagtaac gggaatactt atctccactg gtatttgcaa	600
aagcccggtc agtctcctaa gcttctgac tataaggtgt ccaaccgctt ttctggagt	660
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gaagcggagg acttgggtgt ttatTTTTgt tcccagagta cccacgtgcc tccatacacg	780
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cccgctccaa ctatagccag ccaaccattg agcctcagac ctgaagcttg caggcccgc	900
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cctttggccg gaacatgtgg ggtgttgctt ctctcccttg tgatcactct gtattgtaag	1020
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aatgagctgc agaaggacaa gatggctgaa gcctatagcg agatcggaat gaaaggcgaa	1380
agacgcagag gcaaggggca tgacggtctg taccagggtc tctctacagc caccaaggac	1440
acttatgatg cgttgcatat gcaagccttg ccaccccgct aa	1482

<210> 24

<211> 1482

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD79A-10_LH CAR polynucleotide construct

<400> 24

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ccagatgtcg tgatgactca gacacctctt agcttgcccg tctccttggg tgatcaggct	120
agcatttcat gtagatcaag ccagagcttg gtacattcaa atggcaatac ctacctgcac	180
tggtatctcc agaaacctgg ccagagccca aaattgctta tctataaagt tagtaacaga	240
ttctccgggg tcccagatcg attttccggc tcaggctcag gcacggattt taccctgaag	300
atctcacgag tcgaggcaga agatcttggc gtgtactttt gttcccagag taccacgta	360
cccccttaca cattcggagg agggaccaag ttggagatca aaggaggggg gggcagtggg	420
gggggcggtt ccggaggggg aggaagccaa gtacaactgc aacaaagcgg acccgagctc	480
gtcaaacctg gtgctagcgt caaaatttcc tgtaagacca gcggctacgc ttttagcttt	540
tcttgatga actgggtgaa atgggggccc gggcagggcc tggagtggat aggacgaatt	600
tatcccggga atggggatac aaattacaat ggtaaattca aggggaaagc cacactgact	660
gcagataaaa gtcacaacac ggcatatcag cagctcagct ccctcacttc tgtggattct	720
gctgtttact tttgtgccag gtgggtttac tctggtaata actatgccgt ggattactgg	780
gggcaaggca cctctgttac agtgagttcc accacaacac ctgctccaag gccccccaca	840
cccgtccaa ctatagccag ccaaccattg agcctcagac ctgaagcttg caggcccgca	900
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cctttggccg gaacatgtgg ggtgttgctt ctctcccttg tgatcactct gtattgtaag	1020
cgcgggagaa agaagctcct gtacatcttc aagcagcctt ttatgcgacc tgtgcaaacc	1080
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ctgagggtga aattttctag aagcgccgat gctcccgcat atcagcaggg tcagaatcag	1200
ctctacaatg aattgaatct cggcaggcga gaagagtacg atgttctgga caagagacgg	1260
ggcagggatc ccgagatggg gggaaagccc cggagaaaaa atcctcagga ggggttgtag	1320
aatgagctgc agaaggacaa gatggctgaa gcctatagcg agatcggaat gaaaggcgaa	1380
agacgcagag gcaaggggca tgacggtctg taccagggtc tctctacagc caccaaggac	1440
acttatgatg cgttgcatat gcaagccttg ccaccccgct aa	1482

<210> 25
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Anti-CD20 CDRL1

<400> 25

Arg Ala Ser Ser Ser Val Asn Tyr Met Asp
1 5 10

<210> 26
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Anti-CD20 CDRL2

<400> 26

Ala Thr Ser Asn Leu Ala Ser
1 5

<210> 27
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Anti-CD20 CDRL3

<400> 27

Gln Gln Trp Ser Phe Asn Pro Pro Thr
1 5

<210> 28
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Anti-CD20 CDRH1

<400> 28

Gly Tyr Thr Phe Thr Ser Tyr Asn Met His

1 5 10

<210> 29
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Anti-CD20 CDRH2

<400> 29

Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 30
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Anti-CD20 CDRH3

<400> 30

Ser Asn Tyr Tyr Gly Ser Ser Tyr Trp Phe Phe Asp Val
1 5 10

<210> 31
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD20 Light chain

<400> 31

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
20 25 30

Asp Trp Tyr Gln Lys Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr

35

40

45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 32

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD20 Heavy chain

<400> 32

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

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

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

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

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

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

Ala Arg Ser Asn Tyr Tyr Gly Ser Ser Tyr Trp Phe Phe Asp Val Trp

100

105

110

Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 33

<211> 374

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD20 L-H CCR construct

<400> 33

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu
 20 25 30

Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln
 50 55 60

Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser
 65 70 75 80

Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
 85 90 95

Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser
 100 105 110

Ala Asp Tyr Tyr Cys Ala Arg Ser Asn Tyr Tyr Gly Ser Ser Tyr Trp
 115 120 125

Phe Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile

145		150		155		160									
Val	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys
				165					170					175	
Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	Asp	Trp
			180					185					190		
Tyr	Gln	Lys	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr
		195					200					205			
Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser
	210					215					220				
Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala
225					230					235					240
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly
				245					250					255	
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro
			260					265						270	
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro
		275					280					285			
Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu
	290					295					300				
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys
305					310					315					320
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Arg	Ser	Lys
				325					330					335	
Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg
			340					345					350		
Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp
		355					360					365			

Phe Ala Ala Tyr Arg Ser
370

<210> 34
<211> 1125
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD20 L-H CCR polynucleotide construct

<400> 34
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atgtcatgta aagcctcagg atatactttt acttcataca atatgcactg ggtgaagcag 180
acaccgggtc agggacttga gtggatcggc gcaatatacc ccggaaatgg agacaccagc 240
tacaaccaga aatttaaggg aaaagccacc ctgacagccg ataaatcctc cagtacggct 300
tacatgcaat tgagctcact gactagcgag gactccgcag attattattg tgctagaagt 360
aactactacg gcagctccta ttggtttttt gacgtgtggg gggcgggcac caccgttaca 420
gtcagcagtg gcggcggagg ttcaggtggg gggggctctg gaggcggtgg gtctgatatc 480
gtcttgactc aaagcccagc gatattgtca gcctcccctg gagagaaagt gactatgacc 540
tgcagggcta gcagctctgt taattatatg gattgggtatc agaagaaacc tggcagctcc 600
cctaagccct ggatttatgc tacatcaaat ctgcctcag gggtgccagc caggttcagt 660
ggatccggca gtggcaccag ctatagcctg acaatctcaa gggtcgaagc agaggacgcc 720
gcaacatatt attgtcagca atggagcttt aatcccccca ctttggcgg aggaaccaag 780
ttggagatca agaccacgac cccggcaccc cggccaccta caccagcccc tacaattgct 840
agccagcccc tgagccttag gccagaagcc tgtagaccgc ccgccggcgg tgcggttcac 900
acccggggac tcgacttcgc ctgtgatata tatatctggg caccctggc cggcacatgt 960
ggagtgcctt tgctgtcctt ggtcattacc ctctactgca gatctaaaag atccagactg 1020
cttcattctg actatatgaa tatgactcct agacggcctg ggcccaccag gaagcactac 1080
cagccatacg ccccaccag agattttgcc gcttatcggg cctaa 1125

<210> 35

<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD20 H-L CCR construct

<400> 35

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Leu
20 25 30

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

Ser Val Asn Tyr Met Asp Trp Tyr Gln Lys Lys Pro Gly Ser Ser Pro
50 55 60

Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
85 90 95

Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
100 105 110

Phe Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
130 135 140

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val
145 150 155 160

Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met
165 170 175

His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly Ala

180

185

190

Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly
 195 200 205

Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
 210 215 220

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Asp Tyr Tyr Cys Ala Arg
 225 230 235 240

Ser Asn Tyr Tyr Gly Ser Ser Tyr Trp Phe Phe Asp Val Trp Gly Ala
 245 250 255

Gly Thr Thr Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro
 260 265 270

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
 275 280 285

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
 290 295 300

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
 305 310 315 320

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys
 325 330 335

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
 340 345 350

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
 355 360 365

Phe Ala Ala Tyr Arg Ser
 370

<210> 36

<211> 1125

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD20 H-L CCR polynucleotide construct

<400> 36

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actatgacct gcagggctag cagctctgtt aattatatgg attggtatca gaagaaacct      180
ggcagctccc ctaagccctg gatttatgct acatcaaadc tcgcctcagg ggtgccagcc      240
aggttcagtg gatccggcag tggcaccagc tatagcctga caatctcaag ggtcgaagca      300
gaggacgccg caacatatta ttgtcagcaa tggagcttta atccccccac atttggcgga      360
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aagatgtcat gtaaagcctc aggatatact tttacttcat acaatatgca ctgggtgaag      540
cagacaccgg gtcagggact tgagtggatc ggcgcaatat accccggaag tggagacacc      600
agctacaacc agaaatttaa gggaaaagcc accctgacag ccgataaatc ctccagtacg      660
gcttacatgc aattgagctc actgactagc gaggactccg cagattatta ttgtgctaga      720
agtaactact acggcagctc ctattggttt tttgacgtgt gggggggcggg caccaccgtt      780
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ggagtgcctt tgctgtcctt ggtcattacc ctctactgca gatctaaaag atccagactg     1020
cttcattctg actatatgaa tatgactcct agacggcctg ggcccaccag gaagcactac     1080
cagccatacg ccccaccacg agattttgcc gcttatcggt cctaa                       1125
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<210> 37

<211> 887

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD79A-01_LH CAR - T2A - anti-CD20 CCR construct

<400> 37

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Val Leu Met Thr Gln Ile Pro Leu Ser Leu
20 25 30

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
35 40 45

Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
65 70 75 80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

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

Tyr Cys Phe Gln Gly Ser His Val Pro Phe Thr Phe Gly Ser Gly Thr
115 120 125

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

Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
145 150 155 160

Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
165 170 175

Thr Phe Ser Thr Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln
180 185 190

Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn
195 200 205

Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
210 215 220

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

Ala Val Tyr Phe Cys Glu Arg Phe Tyr Tyr Gly Asn Thr Phe Ala Met
245 250 255

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr
260 265 270

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
275 280 285

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
290 295 300

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
305 310 315 320

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
325 330 335

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
340 345 350

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
355 360 365

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
370 375 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
385 390 395 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu
485 490 495

Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly
500 505 510

Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
515 520 525

Leu His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Ala Glu
530 535 540

Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
545 550 555 560

Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly
565 570 575

Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr
580 585 590

Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
595 600 605

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
610 615 620

Ser Ala Asp Tyr Tyr Cys Ala Arg Ser Asn Tyr Tyr Gly Ser Ser Tyr
625 630 635 640

Trp Phe Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
645 650 655

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
660 665 670

Ile Val Leu Thr Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu
675 680 685

Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met Asp
690 695 700

Trp Tyr Gln Lys Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala
705 710 715 720

Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
725 730 735

Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu Asp
740 745 750

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr Phe
755 760 765

Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
770 775 780

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
785 790 795 800

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
805 810 815

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
820 825 830

Cys Gly Val Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser
835 840 845

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
850 855 860

Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg
865					870					875					880

Asp	Phe	Ala	Ala	Tyr	Arg	Ser
					885	

<210> 38
 <211> 2664
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in Lab - anti-CD79A-01_LH CAR - T2A - CD20 CCR
 polynucleotide construct

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agcatctcat gccgcagcag tcaatccatt gtgcactcaa atgggaacac ctatttggag	180
tggtatctgc aaaaaccggg acagtctccg aaactgctga tatacaaagt aagcaacagg	240
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gctccaacta tagccagcca accattgagc ctcagacctg aagcttgcag gcccgcagca	900
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ttggccggaa catgtggggt gttgcttctc tcccttgtga tcactctgta ttgtaagcgc	1020

gggagaaaga agctcctgta catcttcaag cagcctttta tgcgacctgt gcaaaccact	1080
caggaagaag atgggtgttc atgccgcttc cccgaggagg aagaaggagg gtgtgaactg	1140
agggtgaaat tttctagaag cgccgatgct cccgcatatc agcagggtca gaatcagctc	1200
tacaatgaat tgaatctcgg caggcgagaa gagtacgatg ttctggacaa gagacggggc	1260
agggatcccc agatgggggg aaagccccgg agaaaaaatc ctcaggaggg gttgtacaat	1320
gagctgcaga aggacaagat ggctgaagcc tatagcgaga tcggaatgaa aggcgaaaga	1380
cgcagaggca aggggcatga cggctctgtac cagggtctct ctacagccac caaggacact	1440
tatgatgcgt tgcatatgca agccttgcca ccccgcggtt ccggtgaggg acgaggatct	1500
ctgttaacgt gtggcgatgt cgaggaaaat cctggcccaa tggcgctccc tgtcacagca	1560
ctgctccttc cgctggctct gcttctgcac gctgctaggc cagaagttca actccagcag	1620
agcggcgag agctcgtgaa gcccggagct tcagtgaaga tgtcatgtaa agcctcagga	1680
tatactttta cttcatacaa tatgactgg gtgaagcaga caccgggtca gggacttgag	1740
tggatcggcg caatataccc cggaaatgga gacaccagct acaaccagaa atttaaggga	1800
aaagccaccc tgacagccga taaatcctcc agtacggctt acatgcaatt gagctcactg	1860
actagcgagg actccgcaga ttattattgt gctagaagta actactacgg cagctcctat	1920
tggttttttg acgtgtgggg ggcgggcacc accgttacag tcagcagtgg cggcggagg	1980
tcagggtgggg ggggctctgg aggcggtggg tctgatatcg tcttgactca aagcccagcg	2040
atattgtcag cctcccctgg agagaaagt actatgacct gcagggctag cagctctgtt	2100
aattatatgg attggtatca gaagaaacct ggcagctccc ctaagccctg gatttatgct	2160
acatcaaadc tcgcctcagg ggtgccagcc aggttcagtg gatccggcag tggcaccagc	2220
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tggagcttta atccccccac atttggcgga ggaaccaagt tggagatcaa gaccacgacc	2340
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tgtgatatat atatctgggc acccctggcc ggcacatgtg gagtgttct gctgtccttg	2520
gtcattaccc tctactgcag atctaaaaga tccagactgc ttcatctga ctatatgaat	2580
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gattttgccg cttatcggtc ctaa

2664

<210> 39

<211> 888

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD79A-10_HL CAR - T2A - anti-CD20 CCR
construct

<400> 39

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
20 25 30

Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr
35 40 45

Ala Phe Ser Phe Ser Trp Met Asn Trp Val Lys Trp Gly Pro Gly Gln
50 55 60

Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr Asn
65 70 75 80

Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
85 90 95

Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser
100 105 110

Ala Val Tyr Phe Cys Ala Arg Trp Val Tyr Ser Gly Asn Asn Tyr Ala
115 120 125

Val Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Arg Ser Asp Val Val
145 150 155 160

Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala
165 170 175

Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn
180 185 190

Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu
195 200 205

Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
210 215 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
225 230 235 240

Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val
245 250 255

Pro Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr
260 265 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
275 280 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
290 295 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305 310 315 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
325 330 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
340 345 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
355 360 365

Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
370 375 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385 390 395 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
405 410 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
420 425 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
435 440 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
450 455 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly
485 490 495

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
500 505 510

Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu
515 520 525

Leu Leu His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Ala
530 535 540

Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser
545 550 555 560

Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro
565 570 575

Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp
580 585 590

Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
595 600 605

Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu
610 615 620

Asp Ser Ala Asp Tyr Tyr Cys Ala Arg Ser Asn Tyr Tyr Gly Ser Ser
625 630 635 640

Tyr Trp Phe Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser
645 650 655

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
660 665 670

Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
675 680 685

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
690 695 700

Asp Trp Tyr Gln Lys Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
705 710 715 720

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
725 730 735

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
740 745 750

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr
755 760 765

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro
770 775 780

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
785 790 795 800

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
805 810 815

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
820 825 830

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
835 840 845

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
850 855 860

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
865 870 875 880

Arg Asp Phe Ala Ala Tyr Arg Ser
885

<210> 40
<211> 2667
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD79A-10_HL CAR - T2A - anti-CD20 CCR
polynucleotide construct

<400> 40
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atatcctgca agaccagcgg ctatgccttt tcattctcct ggatgaactg ggtgaagtgg 180
ggacccggtc agggacttga gtggatcggg cgaatctatc ccggaaacgg ggacacgaat 240
tacaacggca aatttaaagg caaggctact ctgactgctg aaaaaagtag caacaccgcc 300
tacatgcagt tgtcctcttt gacatcagta gactctgcag tgtatTTTTTg cgcccgggtg 360
gtttactccg gaaataacta cgcggttgac tattggggac agggcacctc cgtgacagtg 420
tcttctggcg gcgggggatc aggtggcggc gggctctgggg gtggaaggag cgacgtggtt 480
atgaccaga cccctttgag cctgcccgtg agccttggcg accaagcctc catctcttgc 540
cggctctctc aatcactggt gcacagtaac gggaatactt atctccactg gtatttgcaa 600
aagcccgtc agtctcctaa gcttctgac tataaggtgt ccaaccgtt ttctggagtg 660

cccgatagat tttccggatc tggatccggg acagacttca cattgaagat tagtagagtc	720
gaagcggagg acttgggtgt ttatTTTTgt tcccagagta cccacgtgcc tccatacacg	780
tttggagggtg gaaccaaact tgaaattaag accacaacac ctgctccaag gccccccaca	840
cccgctccaa ctatagccag ccaaccattg agcctcagac ctgaagcttg caggccccgca	900
gcaggaggcg ccgtccatac gcgaggcctg gacttcgcgt gtgatattta tatttgggcc	960
cctttggccg gaacatgtgg ggtgttgctt ctctcccttg tgatcactct gtattgtaag	1020
cgcgggagaa agaagctcct gtacatcttc aagcagcctt ttatgcgacc tgtgcaaacc	1080
actcaggaag aagatgggtg ttcattgccg tccccgagg aggaagaagg aggggtgtgaa	1140
ctgagggtga aattttctag aagcgccgat gctcccgcat atcagcaggg tcagaatcag	1200
ctctacaatg aattgaatct cggcaggcga gaagagtacg atgttctgga caagagacgg	1260
ggcagggatc ccgagatggg gggaaagccc cggagaaaaa atcctcagga ggggttgtag	1320
aatgagctgc agaaggacaa gatggctgaa gcctatagcg agatcggaat gaaaggcgaa	1380
agacgcagag gcaaggggca tgacggtctg taccagggtc tctctacagc caccaaggac	1440
acttatgatg cgttgcatat gcaagccttg ccaccccgcg ggtccggtga gggacgagga	1500
tctctgttaa cgtgtggcga tgtcgaggaa aatcctggcc caatggcgct ccctgtcaca	1560
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cagagcggcg cagagctcgt gaagcccgga gcttcagtga agatgtcatg taaagcctca	1680
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ggaaaagcca ccctgacagc cgataaatcc tccagtacgg cttacatgca attgagctca	1860
ctgactagcg aggactccgc agattattat tgtgctagaa gtaactacta cggcagctcc	1920
tattggTTTT ttgacgtgtg gggggcgggc accaccgtta cagtcagcag tggcggcgga	1980
ggttcagggtg gggggggctc tggaggcggg gggcttgata tcgtcttgac tcaaagccca	2040
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gttaattata tggattggta tcagaagaaa cctggcagct cccctaagcc ctggatttat	2160
gctacatcaa atctcgcctc aggggtgcca gccaggttca gtggatccgg cagtggcacc	2220
agctatagcc tgacaatctc aagggtcgaa gcagaggacg ccgcaacata ttattgtcag	2280

caatggagct ttaatcccc cacatttggc ggaggaacca agttggagat caagaccacg 2340
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 ttggtcatta ccctctactg cagatctaaa agatccagac tgcttcattc tgactatatg 2580
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<210> 41
 <211> 999
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - anti-CD79A-01_LH CAR-T2A-anti-CD20 CD28z CAR
 construct

<400> 41

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Asp Val Leu Met Thr Gln Ile Pro Leu Ser Leu
 20 25 30

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
 35 40 45

Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln
 50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 65 70 75 80

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95

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

Tyr Cys Phe Gln Gly Ser His Val Pro Phe Thr Phe Gly Ser Gly Thr
115 120 125

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

Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
145 150 155 160

Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
165 170 175

Thr Phe Ser Thr Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln
180 185 190

Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn
195 200 205

Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
210 215 220

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

Ala Val Tyr Phe Cys Glu Arg Phe Tyr Tyr Gly Asn Thr Phe Ala Met
245 250 255

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr
260 265 270

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
275 280 285

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
290 295 300

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
305 310 315 320

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
325 330 335

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
340 345 350

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
355 360 365

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
370 375 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
385 390 395 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu
485 490 495

Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly
500 505 510

Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
515 520 525

Leu His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Ala Glu
530 535 540

Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
545 550 555 560

Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly
565 570 575

Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr
580 585 590

Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
595 600 605

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
610 615 620

Ser Ala Asp Tyr Tyr Cys Ala Arg Ser Asn Tyr Tyr Gly Ser Ser Tyr
625 630 635 640

Trp Phe Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
645 650 655

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
660 665 670

Ile Val Leu Thr Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu
675 680 685

Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met Asp
690 695 700

Trp Tyr Gln Lys Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala
705 710 715 720

Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
725 730 735

Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu Asp
740 745 750

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr Phe
755 760 765

Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
770 775 780

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
785 790 795 800

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
805 810 815

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
820 825 830

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser
835 840 845

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
850 855 860

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
865 870 875 880

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
885 890 895

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
900 905 910

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
915 920 925

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
930 935 940

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
945 950 955 960

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
965 970 975

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
 980 985 990

Met Gln Ala Leu Pro Pro Arg
 995

<210> 42

<211> 3000

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD79A-01_LH CAR-T2A-anti-CD20 CD28z CAR
 polynucleotide construct

<400> 42

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agcatctcat gccgcagcag tcaatccatt gtgcactcaa atgggaacac ctatttggag	180
tggtatctgc aaaaaccggg acagtctccg aaactgctga tatacaaagt aagcaacagg	240
ttcagcggag ttcctgacag attcagcggg agcggttctg gaactgactt tacacttaag	300
atctctcgcg ttgaggcgga ggacctgggc gtgtattact gttttcaagg atcccacgtc	360
ccgtttacat tcggatcagg caccaagctg gagatcaagc gcggtggcgg gggttctggc	420
ggggggcgga ccggaggcgg cggatcccag gtgcagctgc agcagtctgg accagaactg	480
gttaagcccg gagcttcagt taagatttcc tgtaaggctt caggctatac attttccact	540
tcttgatga actgggtgaa acagcgccct ggccaggggc tggaatggat cggacggatc	600
tatcccggcg atggagacac taattataac ggtaagttca aagggaaggc caccctcacg	660
gccgacaagt cctccaatac agcgtacatg caactcagtt ccctgaccag cgttgatagc	720
gcagtttact tctgtgagcg cttctattac ggaaacacct tcgctatgga ttactggggt	780
caggggacct ccgtgaccgt gtcctctacc acaacacctg ctccaaggcc cccacaccc	840
gctccaacta tagccagcca accattgagc ctgagacctg aagcttgcag gcccgcagca	900
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ttggccggaa catgtggggt gttgcttctc tcccttgtga tcactctgta ttgtaagcgc	1020
gggagaaaga agctcctgta catcttcaag cagcctttta tgcgacctgt gcaaaccact	1080

caggaagaag atgggtgttc atgccgcttc cccgaggagg aagaaggagg gtgtgaactg	1140
agggtgaaat tttctagaag cgccgatgct cccgcatatc agcagggtca gaatcagctc	1200
tacaatgaat tgaatctcgg caggcgagaa gagtacgatg ttctggacaa gagacggggc	1260
agggatcccc agatgggggg aaagccccgg agaaaaaatc ctcaggaggg gttgtacaat	1320
gagctgcaga aggacaagat ggctgaagcc tatagcgaga tcggaatgaa aggcgaaaga	1380
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ctgttaacgt gtggcgatgt cgaggaaaat cctggcccaa tggcgctccc tgtcacagca	1560
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atattgtcag cctcccctgg agagaaagt actatgacct gcagggctag cagctctggt	2100
aattatatgg attggtatca gaagaaacct ggcagctccc ctaagccctg gatttatgct	2160
acatcaaatac tcgcctcagg ggtgccagcc aggttcagtg gatccggcag tggcaccagc	2220
tatagcctga caatctcaag ggtcgaagca gaggacgccg caacatatta ttgtcagcaa	2280
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<210> 43

<211> 1000

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD79A-10_HL CAR-T2A-anti-CD20 CD28z CAR construct

<400> 43

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu
			20					25					30		

Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Thr	Ser	Gly	Tyr
		35					40					45			

Ala	Phe	Ser	Phe	Ser	Trp	Met	Asn	Trp	Val	Lys	Trp	Gly	Pro	Gly	Gln
	50					55					60				

Gly	Leu	Glu	Trp	Ile	Gly	Arg	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Asn
65					70					75					80

Tyr	Asn	Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser
			85						90					95	

Ser	Asn	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Val	Asp	Ser
			100					105					110		

Ala	Val	Tyr	Phe	Cys	Ala	Arg	Trp	Val	Tyr	Ser	Gly	Asn	Asn	Tyr	Ala
		115					120					125			

Val Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Arg Ser Asp Val Val
145 150 155 160

Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala
165 170 175

Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn
180 185 190

Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu
195 200 205

Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
210 215 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
225 230 235 240

Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val
245 250 255

Pro Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr
260 265 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
275 280 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
290 295 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305 310 315 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
325 330 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
340 345 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
355 360 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
370 375 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385 390 395 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
405 410 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
420 425 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
435 440 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
450 455 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly
485 490 495

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
500 505 510

Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu
515 520 525

Leu Leu His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Ala
530 535 540

Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser
545 550 555 560

Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro
565 570 575

Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp
580 585 590

Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
595 600 605

Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu
610 615 620

Asp Ser Ala Asp Tyr Tyr Cys Ala Arg Ser Asn Tyr Tyr Gly Ser Ser
625 630 635 640

Tyr Trp Phe Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser
645 650 655

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
660 665 670

Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
675 680 685

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
690 695 700

Asp Trp Tyr Gln Lys Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
705 710 715 720

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
725 730 735

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
740 745 750

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr
755 760 765

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro
770 775 780

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
785 790 795 800

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
805 810 815

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
820 825 830

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
835 840 845

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
850 855 860

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
865 870 875 880

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala
885 890 895

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
900 905 910

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
915 920 925

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
930 935 940

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
945 950 955 960

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
965 970 975

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
980 985 990

His Met Gln Ala Leu Pro Pro Arg
995 1000

<210> 44
<211> 3003
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in Lab - anti-CD79A-10_HL CAR-T2A-anti-CD20 CD28z CAR
polynucleotide construct

<400> 44
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atatcctgca agaccagcgg ctatgccttt tcattctcct ggatgaactg ggtgaagtgg 180
ggacccggtc agggacttga gtggatcggg cgaatctatc ccggaaacgg ggacacgaat 240
tacaacggca aatttaaagg caaggctact ctgactgctg aaaaaagtag caacaccgcc 300
tacatgcagt tgtcctcttt gacatcagta gactctgcag tgtatttttg cgcccgggtg 360
gtttactccg gaaataacta cgcggttgac tattggggac agggcacctc cgtgacagtg 420
tcttctggcg gcgggggatc aggtggcggc gggctctgggg gtggaaggag cgacgtggtt 480
atgaccaga cccctttgag cctgcccgtg agccttggcg accaagcctc catctcttgc 540
cggtcctctc aatcactggt gcacagtaac gggaatactt atctccactg gtatttgcaa 600
aagcccggtc agtctcctaa gcttctgatc tataaggtgt ccaaccgctt ttctggagtg 660
cccgatagat tttccggatc tggatccggg acagacttca cattgaagat tagtagagtc 720
gaagcggagg acttgggtgt ttattttttgt tcccagagta cccacgtgcc tccatacacg 780
tttggaggtg gaaccaaact tgaaattaag accacaacac ctgctccaag gccccccaca 840
cccgctccaa ctatagccag ccaaccattg agcctcagac ctgaagcttg caggcccgca 900
gcaggaggcg ccgtccatac gcgaggcctg gacttcgcgt gtgatattta tatttgggcc 960
cctttggccg gaacatgtgg ggtgttgctt ctctcccttg tgatcactct gtattgtaag 1020
cgcgggagaa agaagctcct gtacatcttc aagcagcctt ttatgcgacc tgtgcaaacc 1080
actcaggaag aagatgggtg ttcatgccgc ttccccgagg aggaagaagg aggggtgtgaa 1140
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ctctacaatg aattgaatct cggcaggcga gaagagtacg atgttctgga caagagacgg	1260
ggcaggggatc ccgagatggg gggaaagccc cggagaaaaa atcctcagga ggggttgtac	1320
aatgagctgc agaaggacaa gatggctgaa gcctatagcg agatcggaat gaaaggcgaa	1380
agacgcagag gcaaggggca tgacggtctg taccagggtc tctctacagc caccaaggac	1440
acttatgatg cgttgcatat gcaagccttg ccaccccgcg ggtccggtga gggacgagga	1500
tctctgttaa cgtgtggcga tgtcgaggaa aatcctggcc caatggcgct ccctgtcaca	1560
gcactgctcc ttccgctggc tctgcttctg cacgctgcta ggccagaagt tcaactccag	1620
cagagcggcg cagagctcgt gaagcccgga gcttcagtga agatgtcatg taaagcctca	1680
ggatatactt ttacttcata caatatgcac tgggtgaagc agacaccggg tcagggaactt	1740
gagtggatcg gcgcaatata ccccggaat ggagacacca gctacaacca gaaatttaag	1800
ggaaaagcca ccctgacagc cgataaatcc tccagtacgg cttacatgca attgagctca	1860
ctgactagcg aggactccgc agattattat tgtgctagaa gtaactacta cggcagctcc	1920
tattggtttt ttgacgtgtg gggggcgggc accaccgtta cagtcagcag tggcggcgga	1980
ggttcagggtg gggggggctc tggaggcggt gggcttgata tcgtcttgac tcaaagccca	2040
gcgatattgt cagcctcccc tggagagaaa gtgactatga cctgcagggc tagcagctct	2100
gttaattata tggattggta tcagaagaaa cctggcagct cccctaagcc ctggatttat	2160
gctacatcaa atctcgctc aggggtgcca gccaggttca gtggatccgg cagtggcacc	2220
agctatagcc tgacaatctc aagggtcgaa gcagaggacg ccgcaacata ttattgtcag	2280
caatggagct ttaatcccc cacatttggc ggaggaacca agttggagat caagaccacg	2340
accccggcac cccggccacc tacaccagcc cctacaattg ctagccagcc cctgagcctt	2400
aggccagaag cctgtagacc cgccgccggc ggtgcggttc acaccgggg actcgacttc	2460
gcctgtgata tatatatctg ggcaccctg gccggcacat gtggagtgtc tctgctgtcc	2520
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aatatgactc ctagacggcc tgggcccacc aggaagcact accagccata cgccccacca	2640
cgagattttg ccgcttatcg gtcccgggtt aaattttcta ggagcgccga cgcgccagca	2700
taccagcagg gccagaacca gctctacaac gagctcaacc tggggcgag ggaggagtat	2760
gacgtgcttg acaagaggag aggccgggat ccagagatgg gcgggaagcc taggcggaaa	2820

aaccacagg aggggttgta caacgagctt caaaaggaca aaatggccga agcctactct	2880
gaaataggca tgaagggcga acgcagacga ggcaaaggcc acgacggact gtatcaagga	2940
ttgtctaccg ctacaaagga tacctacgac gcaactgcata tgcaggccct gcctcctagg	3000
taa	3003

<210> 45
 <211> 1000
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - anti-CD79A-01_LH CAR-T2A-anti-CD20 BBz CAR construct

<400> 45

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Asp	Val	Leu	Met	Thr	Gln	Ile	Pro	Leu	Ser	Leu
			20					25					30		

Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln
		35					40					45			

Ser	Ile	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Glu	Trp	Tyr	Leu	Gln
	50					55					60				

Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg
65					70					75				80	

Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
			85						90					95	

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

Tyr	Cys	Phe	Gln	Gly	Ser	His	Val	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr
		115					120					125			

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

Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
145 150 155 160

Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
165 170 175

Thr Phe Ser Thr Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln
180 185 190

Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn
195 200 205

Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
210 215 220

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

Ala Val Tyr Phe Cys Glu Arg Phe Tyr Tyr Gly Asn Thr Phe Ala Met
245 250 255

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr
260 265 270

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
275 280 285

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
290 295 300

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
305 310 315 320

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
325 330 335

Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
340 345 350

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
355 360 365

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
370 375 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
385 390 395 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu
485 490 495

Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly
500 505 510

Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
515 520 525

Leu His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Ala Glu
530 535 540

Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
545 550 555 560

Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly
565 570 575

Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr
580 585 590

Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
595 600 605

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
610 615 620

Ser Ala Asp Tyr Tyr Cys Ala Arg Ser Asn Tyr Tyr Gly Ser Ser Tyr
625 630 635 640

Trp Phe Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
645 650 655

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
660 665 670

Ile Val Leu Thr Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu
675 680 685

Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met Asp
690 695 700

Trp Tyr Gln Lys Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala
705 710 715 720

Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
725 730 735

Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu Asp
740 745 750

Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr Phe
755 760 765

Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
770 775 780

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
785 790 795 800

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
805 810 815

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
820 825 830

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
835 840 845

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
850 855 860

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
865 870 875 880

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
885 890 895

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
900 905 910

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
915 920 925

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
930 935 940

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
945 950 955 960

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
965 970 975

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
980 985 990

His Met Gln Ala Leu Pro Pro Arg
995 1000

<210> 46
<211> 3003
<212> DNA
<213> Artificial Sequene

<220>
<223> Made in Lab - anti-CD79A-01_LH CAR-T2A-anti-CD20 BBz CAR
polynucleotide construct

<400> 46
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agcatctcat gccgcagcag tcaatccatt gtgcactcaa atgggaacac ctatttggag 180
tggtatctgc aaaaaccggg acagtctccg aaactgctga tatacaaagt aagcaacagg 240
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atctctcgcg ttgaggcggg ggacctgggc gtgtattact gttttcaagg atcccacgtc 360
ccgtttacat tcggatcagg caccaagctg gagatcaagc gcggtggcgg gggttctggc 420
gggggcggat ccggaggcgg cggatcccag gtgcagctgc agcagtctgg accagaactg 480
gttaagcccg gagcttcagt taagatttcc tgtaaggctt caggctatac attttccact 540
tcttgatga actgggtgaa acagcgccct ggccaggggc tggaatggat cggacggatc 600
tatccggcg atggagacac taattataac ggtaagttca aagggaaggc caccctcacg 660
gccgacaagt cctccaatac agcgtacatg caactcagtt ccctgaccag cgttgatagc 720
gcagtttact tctgtgagcg cttctattac ggaaacacct tcgctatgga ttactggggg 780
caggggacct ccgtgaccgt gtcctctacc acaacacctg ctccaaggcc cccacacccc 840
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tacaatgaat tgaatctcgg caggcgagaa gagtacgatg ttctggacaa gagacggggc 1260

agggatccccg agatgggggg aaagccccgg agaaaaaatc ctcaggaggg gttgtacaat	1320
gagctgcaga aggacaagat ggctgaagcc tatagcgaga tcggaatgaa aggcgaaaga	1380
cgagaggca aggggcatga cggctctgtac cagggtctct ctacagccac caaggacact	1440
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ctgttaacgt gtggcgatgt cgaggaaaat cctggcccaa tggcgctccc tgtcacagca	1560
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aaagccaccc tgacagccga taaatcctcc agtacggctt acatgcaatt gagctcactg	1860
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tggttttttg acgtgtgggg ggccgggcacc accgttacag tcagcagtgg cggcggaggt	1980
tcaggtgggg ggggctctgg aggcggtggg tctgatatcg tcttgactca aagcccagcg	2040
atattgtcag cctcccctgg agagaaagt actatgacct gcagggctag cagctctgtt	2100
aattatatgg attggtatca gaagaaacct ggcagctccc ctaagccctg gatttatgct	2160
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taccagcagg gccagaacca gctctacaac gagctcaacc tggggcgag ggaggagtat	2760
gacgtgcttg acaagaggag aggccgggat ccagagatgg gcgggaagcc taggcgga	2820
aaccacagg aggggttgta caacgagctt caaaaggaca aaatggccga agcctactct	2880

gaaataggca tgaagggcga acgcagacga ggcaaaggcc acgacggact gtatcaagga 2940
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 taa 3003

<210> 47
 <211> 1001
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - anti-CD79A-10_HL CAR-T2A-anti-CD20 BBz CAR
 construct

<400> 47

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
 20 25 30

Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr
 35 40 45

Ala Phe Ser Phe Ser Trp Met Asn Trp Val Lys Trp Gly Pro Gly Gln
 50 55 60

Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr Asn
 65 70 75 80

Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
 85 90 95

Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser
 100 105 110

Ala Val Tyr Phe Cys Ala Arg Trp Val Tyr Ser Gly Asn Asn Tyr Ala
 115 120 125

Val Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly
 130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Arg Ser Asp Val Val
145 150 155 160

Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala
165 170 175

Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn
180 185 190

Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu
195 200 205

Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
210 215 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
225 230 235 240

Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val
245 250 255

Pro Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr
260 265 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
275 280 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
290 295 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305 310 315 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
325 330 335

Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
340 345 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
355 360 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
370 375 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385 390 395 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
405 410 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
420 425 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
435 440 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
450 455 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly
485 490 495

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
500 505 510

Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu
515 520 525

Leu Leu His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Ala
530 535 540

Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser
545 550 555 560

Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro
565 570 575

Gly Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp
580 585 590

Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
595 600 605

Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu
610 615 620

Asp Ser Ala Asp Tyr Tyr Cys Ala Arg Ser Asn Tyr Tyr Gly Ser Ser
625 630 635 640

Tyr Trp Phe Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser
645 650 655

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
660 665 670

Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
675 680 685

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
690 695 700

Asp Trp Tyr Gln Lys Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
705 710 715 720

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
725 730 735

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
740 745 750

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr
755 760 765

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro
770 775 780

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
785 790 795 800

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
805 810 815

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
820 825 830

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
835 840 845

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
850 855 860

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
865 870 875 880

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
885 890 895

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
900 905 910

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
915 920 925

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
930 935 940

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
945 950 955 960

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
965 970 975

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
980 985 990

Leu His Met Gln Ala Leu Pro Pro Arg
995 1000

<210> 48
<211> 3006
<212> DNA
<213> Artificial Sequence

<220>

<223> Made in Lab - anti-CD79A-10_HL CAR-T2A-anti-CD20 BBz CAR
polynucleotide construct

<400> 48

atggctctgc cagtgactgc gctgctgctg cccctcgctc ttctgctgca cgccgctcgg	60
ccacaggtcc aactgcaaca gagcggcccc gagctggtaa aaccgggggc ctccgtaaaa	120
atatcctgca agaccagcgg ctatgccttt tcattctcct ggatgaactg ggtgaagtgg	180
ggacccggtc agggacttga gtggatcggg cgaatctatc ccggaaacgg ggacacgaat	240
tacaacggca aatttaaagg caaggctact ctgactgctg aaaaaagtag caacaccgcc	300
tacatgcagt tgtcctcttt gacatcagta gactctgcag tgtatttttg cgcccgggtg	360
gtttactccg gaaataacta cgcggttgac tattggggac agggcacctc cgtgacagtg	420
tcttctggcg gcgggggatc aggtggcggc gggctctgggg gtggaaggag cgacgtggtt	480
atgaccaga cccctttgag cctgcccgtg agccttggcg accaagcctc catctcttgc	540
cggctctctc aatcactggt gcacagtaac gggaatactt atctccactg gtatttgcaa	600
aagcccggtc agtctcctaa gcttctgac tataaggtgt ccaaccgctt ttctggagtg	660
cccgatagat tttccggatc tggatccggg acagacttca cattgaagat tagtagagtc	720
gaagcggagg acttgggtgt ttatttttgt tcccagagta cccacgtgcc tccatacacg	780
tttggagggtg gaaccaaact tgaaattaag accacaacac ctgctccaag gccccccaca	840
cccgctccaa ctatagccag ccaaccattg agcctcagac ctgaagcttg caggcccgca	900
gcaggaggcg ccgtccatac gcgaggcctg gacttcgcgt gtgatattta tatttgggcc	960
cctttggccg gaacatgtgg ggtgttgctt ctctcccttg tgatcactct gtattgtaag	1020
cgcgggagaa agaagctcct gtacatcttc aagcagcctt ttatgcgacc tgtgcaaacc	1080
actcaggaag aagatgggtg ttcatgccgc ttccccgagg aggaagaagg aggggtgtgaa	1140
ctgagggtga aattttctag aagcgccgat gctcccgcat atcagcaggg tcagaatcag	1200
ctctacaatg aattgaatct cggcaggcga gaagagtacg atgttctgga caagagacgg	1260
ggcagggatc ccgagatggg gggaaagccc cgagaaaaa atcctcagga ggggttgtag	1320

aatgagctgc agaaggacaa gatggctgaa gcctatagcg agatcggaat gaaaggcgaa	1380
agacgcagag gcaaggggca tgacgggtctg taccagggtc tctctacagc caccaaggac	1440
acttatgatg cgttgcatat gcaagccttg ccaccccgcg ggtccggtga gggacgagga	1500
tctctgttaa cgtgtggcga tgtcgaggaa aatcctggcc caatggcgct ccctgtcaca	1560
gcactgctcc ttccgctggc tctgcttctg cacgctgcta ggccagaagt tcaactccag	1620
cagagcggcg cagagctcgt gaagcccgga gcttcagtga agatgtcatg taaagcctca	1680
ggatatactt ttacttcata caatatgcac tgggtgaagc agacaccggg tcagggactt	1740
gagtggatcg gcgcaatata ccccggaat ggagacacca gctacaacca gaaatttaag	1800
ggaaaagcca ccctgacagc cgataaatcc tccagtacgg cttacatgca attgagctca	1860
ctgactagcg aggactccgc agattattat tgtgctagaa gtaactacta cggcagctcc	1920
tattggtttt ttgacgtgtg gggggcgggc accaccgtta cagtcagcag tggcggcgga	1980
ggttcaggtg gggggggctc tggaggcggt gggctctgata tcgtcttgac tcaaagccca	2040
gcgatattgt cagcctcccc tggagagaaa gtgactatga cctgcagggc tagcagctct	2100
gttaattata tggattggta tcagaagaaa cctggcagct cccctaagcc ctggatttat	2160
gtacatcaa atctgcctc aggggtgcca gccaggttca gtggatccgg cagtggcacc	2220
agctatagcc tgacaatctc aagggtcgaa gcagaggacg ccgcaacata ttattgtcag	2280
caatggagct ttaatcccc cacatttggc ggaggaacca agttggagat caagaccagc	2340
acccggcac cccggccacc tacaccagcc cctacaattg ctagccagcc cctgagcctt	2400
aggccagaag cctgtagacc cgccgccggc ggtgcggttc acaccgggg actcgacttc	2460
gcctgtgata tatatatctg ggcaccctg gccggcacat gtggagtgtc tctgctgtcc	2520
ttggtcatta ccctctactg caaacgcggt cggaagaagc ttctgtacat cttcaaacaa	2580
cccttcatga ggcctgtgca gacaacacag gaggaggatg gctgtagttg cagattccct	2640
gaagaagagg aagggtggctg cgagctccgg gttaaatttt ctaggagcgc cgacgcgcca	2700
gcataccagc agggccagaa ccagctctac aacgagctca acctggggcg cagggaggag	2760
tatgacgtgc ttgacaagag gagaggccgg gatccagaga tgggcgggaa gcctaggcgg	2820
aaaaaccac aggaggggtt gtacaacgag cttcaaaagg acaaaatggc cgaagcctac	2880
tctgaaatag gcatgaaggg cgaacgcaga cgaggcaaag gccacgacgg actgtatcaa	2940

ggattgtcta ccgctacaaa ggatacctac gacgcactgc atatgcaggc cctgcctcct 3000
 aggtaa 3006

<210> 49
 <211> 303
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - PDCD-1 I-OnuI LHE variant

<220>
 <221> MOD_RES
 <222> (1)..(4)
 <223> Xaa is any amino acid or absent

<220>
 <221> MOD_RES
 <222> (302)..(303)
 <223> Xaa is any amino acid or absent

<400> 49

Xaa Xaa Xaa Xaa Ser Arg Arg Glu Ser Ile Asn Pro Trp Thr Leu Thr
 1 5 10 15

Gly Phe Ala Asp Ala Glu Gly Ser Phe Gly Leu Ser Ile Leu Asn Arg
 20 25 30

Asn Arg Gly Thr Ala Arg Tyr His Thr Arg Leu Ser Phe Thr Ile Met
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
 50 55 60

Lys Val Gly Ser Ile Leu Asn Asn Gly Asp His Tyr Val Ser Leu Val
 65 70 75 80

Val Tyr Ala Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
 85 90 95

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
 100 105 110

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
130 135 140

Glu Leu Lys Lys Ala Phe Pro Glu Val Ile Ser Arg Glu Arg Pro Leu
145 150 155 160

Ile Asn Lys Asn Ile Pro Asn Gly Lys Trp Leu Ala Gly Phe Thr Ser
165 170 175

Gly Asp Gly Ser Phe Phe Val Arg Leu Arg Lys Ser Asn Val Asn Ala
180 185 190

Arg Val Arg Val Gln Leu Val Phe Glu Ile Ser Gln His Ile Arg Asp
195 200 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly His Ile
210 215 220

Tyr Glu Gly Asn Lys Ser Glu Arg Ser Trp Leu Gln Phe Arg Val Glu
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Met Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
275 280 285

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Arg Arg Xaa Xaa
290 295 300

<210> 50

<211> 944

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - PDCD-1 megaTAL construct

<400> 50

Met Gly Ser Cys Arg Pro Pro Lys Lys Lys Arg Lys Val Val Asp Leu
1 5 10 15

Arg Thr Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys
20 25 30

Val Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly
35 40 45

Phe Thr His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu
50 55 60

Gly Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu
65 70 75 80

Ala Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala
85 90 95

Arg Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro
100 105 110

Pro Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly
115 120 125

Gly Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr
130 135 140

Gly Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser
145 150 155 160

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
165 170 175

Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
180 185 190

Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
195 200 205

Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val
210 215 220

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
225 230 235 240

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
245 250 255

Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr
260 265 270

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
275 280 285

Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu
290 295 300

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu
305 310 315 320

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln
325 330 335

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His
340 345 350

Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly
355 360 365

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
370 375 380

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp
385 390 395 400

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
405 410 415

Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser
420 425 430

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
435 440 445

Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
450 455 460

Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
465 470 475 480

Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val
485 490 495

Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
500 505 510

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
515 520 525

Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr
530 535 540

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
545 550 555 560

Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu
565 570 575

Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala
580 585 590

Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro
595 600 605

Ala Met Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile
610 615 620

Arg Arg Val Asn Arg Arg Ile Gly Glu Arg Thr Ser His Arg Val Ala
625 630 635 640

Ile Ser Arg Val Gly Gly Ser Ser Arg Arg Glu Ser Ile Asn Pro Trp
645 650 655

Thr Leu Thr Gly Phe Ala Asp Ala Glu Gly Ser Phe Gly Leu Ser Ile
660 665 670

Leu Asn Arg Asn Arg Gly Thr Ala Arg Tyr His Thr Arg Leu Ser Phe
675 680 685

Thr Ile Met Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln
690 695 700

Ser Thr Trp Lys Val Gly Ser Ile Leu Asn Asn Gly Asp His Tyr Val
705 710 715 720

Ser Leu Val Val Tyr Ala Phe Glu Asp Leu Lys Val Ile Ile Asp His
725 730 735

Phe Glu Lys Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu
740 745 750

Phe Lys Gln Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu
755 760 765

Asn Gly Ile Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly
770 775 780

Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro Glu Val Ile Ser Arg Glu
785 790 795 800

Arg Pro Leu Ile Asn Lys Asn Ile Pro Asn Gly Lys Trp Leu Ala Gly
805 810 815

Phe Thr Ser Gly Asp Gly Ser Phe Phe Val Arg Leu Arg Lys Ser Asn
820 825 830

Val Asn Ala Arg Val Arg Val Gln Leu Val Phe Glu Ile Ser Gln His
835 840 845

Ile Arg Asp Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys
850 855 860

Gly His Ile Tyr Glu Gly Asn Lys Ser Glu Arg Ser Trp Leu Gln Phe
865 870 875 880

Arg Val Glu Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe
885 890 895

Gln Glu Asn Thr Leu Ile Gly Met Lys Leu Glu Asp Phe Glu Asp Trp
900 905 910

Cys Lys Val Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser
915 920 925

Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Arg Arg
930 935 940

<210> 51
<211> 22
<212> DNA
<213> Homo sapiens

<400> 51
ggcatgcaga tccacaggc gc

22

<210> 52
<211> 37
<212> DNA
<213> Homo sapiens

<400> 52
ggtggggctg ctccaggcat gcagatccca caggcgc

37

<210> 53
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - CBLB I-OnuI LHE variant

<220>
<221> MOD_RES
<222> (1)..(4)

<223> Xaa is any amino acid or absent

<220>

<221> MOD_RES

<222> (302)..(306)

<223> Xaa is any amino acid or absent

<400> 53

Xaa	Xaa	Xaa	Xaa	Ser	Arg	Arg	Glu	Ser	Ile	Asn	Pro	Trp	Ile	Leu	Thr
1				5					10					15	

Gly	Phe	Ala	Asp	Ala	Glu	Gly	Cys	Phe	Arg	Leu	Asp	Ile	Arg	Asn	Ala
			20					25					30		

Asn	Asp	Leu	Arg	Ala	Gly	Tyr	Arg	Thr	Arg	Leu	Ala	Phe	Glu	Ile	Val
		35					40					45			

Leu	His	Asn	Lys	Asp	Lys	Ser	Ile	Leu	Glu	Asn	Ile	Gln	Ser	Thr	Trp
	50					55					60				

Lys	Val	Gly	Thr	Ile	Tyr	Asn	Ala	Gly	Asp	Asn	Ala	Val	Arg	Leu	Gln
65					70					75				80	

Val	Thr	Arg	Phe	Glu	Asp	Leu	Lys	Val	Ile	Ile	Asp	His	Phe	Glu	Lys
				85					90					95	

Tyr	Pro	Leu	Ile	Thr	Gln	Lys	Leu	Gly	Asp	Tyr	Lys	Leu	Phe	Lys	Gln
			100					105					110		

Ala	Phe	Ser	Val	Met	Glu	Asn	Lys	Glu	His	Leu	Lys	Glu	Asn	Gly	Ile
		115					120					125			

Lys	Glu	Leu	Val	Arg	Ile	Lys	Ala	Lys	Met	Asn	Trp	Gly	Leu	Asn	Asp
	130					135					140				

Glu	Leu	Lys	Lys	Ala	Phe	Pro	Glu	Asn	Ile	Ser	Lys	Glu	Arg	Ser	Leu
145					150					155					160

Ile	Asn	Lys	Asn	Ile	Pro	Asn	Leu	Lys	Trp	Leu	Ala	Gly	Phe	Thr	Ser
				165					170					175	

Gly	Asp	Gly	Ser	Phe	Val	Val	Glu	Leu	Lys	Lys	Arg	Arg	Ser	Pro	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

180

185

190

Lys Val Gly Val Arg Leu Arg Phe Ser Ile Thr Gln His Ile Arg Asp
 195 200 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
 210 215 220

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
 225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
 245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
 260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
 275 280 285

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa Xaa
 290 295 300

Xaa Xaa
 305

<210> 54
 <211> 915
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - CBLB megaTAL construct

<400> 54

Met Gly Ser Cys Arg Pro Pro Lys Lys Lys Arg Lys Val Val Asp Leu
 1 5 10 15

Arg Thr Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys
 20 25 30

Val Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly

35

40

45

Phe Thr His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu
 50 55 60

Gly Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu
 65 70 75 80

Ala Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala
 85 90 95

Arg Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro
 100 105 110

Pro Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly
 115 120 125

Gly Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr
 130 135 140

Gly Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser
 145 150 155 160

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
 165 170 175

Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
 180 185 190

Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
 195 200 205

Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val
 210 215 220

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
 225 230 235 240

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
 245 250 255

Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr
260 265 270

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
275 280 285

Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu
290 295 300

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu
305 310 315 320

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln
325 330 335

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His
340 345 350

Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly
355 360 365

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
370 375 380

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile
385 390 395 400

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
405 410 415

Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser
420 425 430

Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
435 440 445

Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
450 455 460

Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu

465		470		475		480									
Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val
			485						490					495	
Ala	Ile	Ala	Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln
			500					505					510		
Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln
		515					520					525			
Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Ser
	530					535					540				
Ile	Val	Ala	Gln	Leu	Ser	Arg	Pro	Asp	Pro	Ala	Leu	Ala	Ala	Leu	Thr
545					550					555					560
Asn	Asp	His	Leu	Val	Ala	Leu	Ala	Cys	Leu	Gly	Gly	Arg	Pro	Ala	Met
			565						570					575	
Asp	Ala	Val	Lys	Lys	Gly	Leu	Pro	His	Ala	Pro	Glu	Leu	Ile	Arg	Arg
			580					585					590		
Val	Asn	Arg	Arg	Ile	Gly	Glu	Arg	Thr	Ser	His	Arg	Val	Ala	Ile	Ser
		595					600					605			
Arg	Val	Gly	Gly	Ser	Ser	Arg	Arg	Glu	Ser	Ile	Asn	Pro	Trp	Ile	Leu
	610					615					620				
Thr	Gly	Phe	Ala	Asp	Ala	Glu	Gly	Cys	Phe	Arg	Leu	Asp	Ile	Arg	Asn
625					630					635					640
Ala	Asn	Asp	Leu	Arg	Ala	Gly	Tyr	Arg	Thr	Arg	Leu	Ala	Phe	Glu	Ile
				645					650					655	
Val	Leu	His	Asn	Lys	Asp	Lys	Ser	Ile	Leu	Glu	Asn	Ile	Gln	Ser	Thr
			660					665					670		
Trp	Lys	Val	Gly	Thr	Ile	Tyr	Asn	Ala	Gly	Asp	Asn	Ala	Val	Arg	Leu
		675					680					685			

Gln Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu
690 695 700

Lys Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys
705 710 715 720

Gln Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly
725 730 735

Ile Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn
740 745 750

Asp Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Ser
755 760 765

Leu Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr
770 775 780

Ser Gly Asp Gly Ser Phe Val Val Glu Leu Lys Lys Arg Arg Ser Pro
785 790 795 800

Val Lys Val Gly Val Arg Leu Arg Phe Ser Ile Thr Gln His Ile Arg
805 810 815

Asp Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg
820 825 830

Ile Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val
835 840 845

Thr Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu
850 855 860

Asn Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys
865 870 875 880

Val Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu
885 890 895

Asp Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe

900

905

910

Ser Gly Arg
915

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ctgtaagata ttcccatccc ca 22

<210> 56
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ttgttatgag gtatggtctg taagatattc ccatcccca 39

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Asp Gly Gly Gly Ser
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<400> 58

Thr Gly Glu Lys Pro
1 5

<210> 59

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<400> 59

Gly Gly Arg Arg
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<400> 60

Gly Gly Gly Gly Ser
1 5

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<211> 14
<212> PRT
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<400> 61

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Val Asp
1 5 10

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<400> 62

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

Leu Asp

<210> 63
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<400> 63

Gly Gly Arg Arg Gly Gly Gly Ser
1 5

<210> 64
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Leu Arg Gln Arg Asp Gly Glu Arg Pro
1 5

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Leu Arg Gln Lys Asp Gly Gly Gly Ser Glu Arg Pro
1 5 10

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

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<211> 18

<212> PRT

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Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

<210> 68

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<222> (5)..(5)

<223> Xaa is any amino acid

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<222> (7)..(7)

<223> Xaa = Gly or Ser

<400> 68

Glu Xaa Xaa Tyr Xaa Gln Xaa
1 5

<210> 69
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Glu Asn Leu Tyr Phe Gln Gly
1 5

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<220>
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<400> 70

Glu Asn Leu Tyr Phe Gln Ser
1 5

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Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
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Glu Glu Asn Pro Gly Pro
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<400> 72

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 73

<211> 14

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<400> 73

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

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<211> 21

<212> PRT

<213> Artificial Sequence

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<400> 74

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
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Glu Asn Pro Gly Pro
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<210> 75

<211> 18

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Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro

1 5 10 15

Gly Pro

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<211> 13
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<400> 76

Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
1 5 10

<210> 77
<211> 23
<212> PRT
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<400> 77

Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp
1 5 10 15

Val Glu Ser Asn Pro Gly Pro
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<210> 78
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<400> 78

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro

<210> 79
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 <212> PRT
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<400> 79

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

<210> 80
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<220>
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Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
 1 5 10 15

Gly Asp Val Glu Ser Asn Pro Gly Pro
 20 25

<210> 81
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<400> 81

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
 1 5 10 15

Glu Ser Asn Pro Gly Pro
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<210> 82

<211> 14
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<400> 82

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

<210> 83
<211> 19
<212> PRT
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<220>

<223> Self-cleaving polypeptide comprising 2A site

<400> 83

Leu Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn
1 5 10 15

Pro Gly Pro

<210> 84
<211> 19
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<400> 84

Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn
1 5 10 15

Pro Gly Pro

<210> 85
<211> 14
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<400> 85

Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
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<210> 86

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<223> Self-cleaving polypeptide comprising 2A site

<400> 86

Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly
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Pro

<210> 87

<211> 20

<212> PRT

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

Asn Pro Gly Pro
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<211> 24

<212> PRT

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<223> Self-cleaving polypeptide comprising 2A site

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Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
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Asp Val Glu Ser Asn Pro Gly Pro
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<210> 89
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<400> 89

Val Thr Glu Leu Leu Tyr Arg Met Lys Arg Ala Glu Thr Tyr Cys Pro
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Arg Pro Leu Leu Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys
20 25 30

Ile Val Ala Pro Val Lys Gln Thr
35 40

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<223> Self-cleaving polypeptide comprising 2A site

<400> 90

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

Gly Pro

<210> 91
<211> 40
<212> PRT
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<223> Self-cleaving polypeptide comprising 2A site

<400> 91

Leu Leu Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys Ile Val
1 5 10 15

Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
20 25 30

Asp Val Glu Ser Asn Pro Gly Pro
35 40

<210> 92

<211> 33

<212> PRT

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<223> Self-cleaving polypeptide comprising 2A site

<400> 92

Glu Ala Arg His Lys Gln Lys Ile Val Ala Pro Val Lys Gln Thr Leu
1 5 10 15

Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly
20 25 30

Pro

<210> 93

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<212> DNA

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gccrccatgg

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<210> 94

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<223> Exemplary rule for determining heavy chain CDR-H1motif

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Cys Xaa Xaa Xaa

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<211> 5

<212> PRT

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<223> Exemplary rule for determining heavy chain CDR-H2 motif

<400> 95

Leu Glu Trp Ile Gly

1 5

<210> 96

<211> 4

<212> PRT

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<223> Exemplary rule for determining heavy chain CDR-H3 motif

<220>

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<223> Xaa is any amino acid

<400> 96

Trp Gly Xaa Gly

1

<210> 97

<211> 4

<212> PRT

<213> Artificial Sequence

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<222> (3)..(3)

<223> Xaa is any amino acid

<400> 97

Phe Gly Xaa Gly

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