

SEQUENCE LISTING

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<120> CONJUGATES FOR TARGETED CELL SURFACE EDITING

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<160> 4

<170> PatentIn version 3.5

<210> 1

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 1

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
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Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Val	Asn	Thr	Ala
			20					25					30		

Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
			35				40					45			

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

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

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Thr	Thr	Pro	Pro
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
			100					105					110		

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 2
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 2

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 3

<211> 381

<212> PRT

<213> Salmonella typhimurium sialidase

<400> 3

Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe Thr
1 5 10 15

Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr Thr
20 25 30

Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr Ile
35 40 45

Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser Phe
50 55 60

Ile Asp Thr Ala Ala Ala Arg Ser Thr Asp Gly Gly Lys Thr Trp Asn
65 70 75 80

Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser Arg
85 90 95

Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu Thr
100 105 110

Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp Gly
115 120 125

Ala Tyr Arg Asp Lys Ala Pro Asp Thr Asp Trp Asp Leu Val Leu Tyr
130 135 140

Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn Ile
145 150 155 160

His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly Gly
165 170 175

Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro Val
180 185 190

Gln Met Val Arg Thr Lys Asn Ile Thr Thr Val Leu Asn Thr Ser Phe
195 200 205

Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr Cys

210

215

220

Glu Gly Phe Gly Ser Glu Asn Asn Ile Ile Glu Phe Asn Ala Ser Leu
 225 230 235 240

Val Asn Asn Ile Arg Asn Ser Gly Leu Arg Arg Ser Phe Glu Thr Lys
 245 250 255

Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys Val
 260 265 270

Asp Asn Arg Asn His Gly Val Gln Gly Ser Thr Ile Thr Ile Pro Ser
 275 280 285

Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn Asn
 290 295 300

Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr Ser
 305 310 315 320

Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn Ala
 325 330 335

Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp Lys
 340 345 350

Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe Gln
 355 360 365

Asp Leu Ser Arg His Leu Pro Val Ile Lys Ser Tyr Asn
 370 375 380

<210> 4

<211> 757

<212> PRT

<213> Vibrio cholerae sialidase

<400> 4

Ala Leu Phe Asp Tyr Asn Ala Thr Gly Asp Thr Glu Phe Asp Ser Pro
 1 5 10 15

Ala Lys Gln Gly Trp Met Gln Asp Asn Thr Asn Asn Gly Ser Gly Val
20 25 30

Leu Thr Asn Ala Asp Gly Met Pro Ala Trp Leu Val Gln Gly Ile Gly
35 40 45

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

Ala Ser Ser Phe Gly Trp Arg Met Thr Thr Glu Met Lys Val Leu Ser
65 70 75 80

Gly Gly Met Ile Thr Asn Tyr Tyr Ala Asn Gly Thr Gln Arg Val Leu
85 90 95

Pro Ile Ile Ser Leu Asp Ser Ser Gly Asn Leu Val Val Glu Phe Glu
100 105 110

Gly Gln Thr Gly Arg Thr Val Leu Ala Thr Gly Thr Ala Ala Thr Glu
115 120 125

Tyr His Lys Phe Glu Leu Val Phe Leu Pro Gly Ser Asn Pro Ser Ala
130 135 140

Ser Phe Tyr Phe Asp Gly Lys Leu Ile Arg Asp Asn Ile Gln Pro Thr
145 150 155 160

Ala Ser Lys Gln Asn Met Ile Val Trp Gly Asn Gly Ser Ser Asn Thr
165 170 175

Asp Gly Val Ala Ala Tyr Arg Asp Ile Lys Phe Glu Ile Gln Gly Asp
180 185 190

Val Ile Phe Arg Gly Pro Asp Arg Ile Pro Ser Ile Val Ala Ser Ser
195 200 205

Val Thr Pro Gly Val Val Thr Ala Phe Ala Glu Lys Arg Val Gly Gly
210 215 220

Gly Asp Pro Gly Ala Leu Ser Asn Thr Asn Asp Ile Ile Thr Arg Thr
225 230 235 240

Ser Arg Asp Gly Gly Ile Thr Trp Asp Thr Glu Leu Asn Leu Thr Glu
245 250 255

Gln Ile Asn Val Ser Asp Glu Phe Asp Phe Ser Asp Pro Arg Pro Ile
260 265 270

Tyr Asp Pro Ser Ser Asn Thr Val Leu Val Ser Tyr Ala Arg Trp Pro
275 280 285

Thr Asp Ala Ala Gln Asn Gly Asp Arg Ile Lys Pro Trp Met Pro Asn
290 295 300

Gly Ile Phe Tyr Ser Val Tyr Asp Val Ala Ser Gly Asn Trp Gln Ala
305 310 315 320

Pro Ile Asp Val Thr Asp Gln Val Lys Glu Arg Ser Phe Gln Ile Ala
325 330 335

Gly Trp Gly Gly Ser Glu Leu Tyr Arg Arg Asn Thr Ser Leu Asn Ser
340 345 350

Gln Gln Asp Trp Gln Ser Asn Ala Lys Ile Arg Ile Val Asp Gly Ala
355 360 365

Ala Asn Gln Ile Gln Val Ala Asp Gly Ser Arg Lys Tyr Val Val Thr
370 375 380

Leu Ser Ile Asp Glu Ser Gly Gly Leu Val Ala Asn Leu Asn Gly Val
385 390 395 400

Ser Ala Pro Ile Ile Leu Gln Ser Glu His Ala Lys Val His Ser Phe
405 410 415

His Asp Tyr Glu Leu Gln Tyr Ser Ala Leu Asn His Thr Thr Thr Leu
420 425 430

Phe Val Asp Gly Gln Gln Ile Thr Thr Trp Ala Gly Glu Val Ser Gln
435 440 445

Glu Asn Asn Ile Gln Phe Gly Asn Ala Asp Ala Gln Ile Asp Gly Arg
450 455 460

Leu His Val Gln Lys Ile Val Leu Thr Gln Gln Gly His Asn Leu Val
465 470 475 480

Glu Phe Asp Ala Phe Tyr Leu Ala Gln Gln Thr Pro Glu Val Glu Lys
485 490 495

Asp Leu Glu Lys Leu Gly Trp Thr Lys Ile Lys Thr Gly Asn Thr Met
500 505 510

Ser Leu Tyr Gly Asn Ala Ser Val Asn Pro Gly Pro Gly His Gly Ile
515 520 525

Thr Leu Thr Arg Gln Gln Asn Ile Ser Gly Ser Gln Asn Gly Arg Leu
530 535 540

Ile Tyr Pro Ala Ile Val Leu Asp Arg Phe Phe Leu Asn Val Met Ser
545 550 555 560

Ile Tyr Ser Asp Asp Gly Gly Ser Asn Trp Gln Thr Gly Ser Thr Leu
565 570 575

Pro Ile Pro Phe Arg Trp Lys Ser Ser Ser Ile Leu Glu Thr Leu Glu
580 585 590

Pro Ser Glu Ala Asp Met Val Glu Leu Gln Asn Gly Asp Leu Leu Leu
595 600 605

Thr Ala Arg Leu Asp Phe Asn Gln Ile Val Asn Gly Val Asn Tyr Ser
610 615 620

Pro Arg Gln Gln Phe Leu Ser Lys Asp Gly Gly Ile Thr Trp Ser Leu
625 630 635 640

Leu Glu Ala Asn Asn Ala Asn Val Phe Ser Asn Ile Ser Thr Gly Thr
645 650 655

Val Asp Ala Ser Ile Thr Arg Phe Glu Gln Ser Asp Gly Ser His Phe
660 665 670

Leu Leu Phe Thr Asn Pro Gln Gly Asn Pro Ala Gly Thr Asn Gly Arg
675 680 685

Gln Asn Leu Gly Leu Trp Phe Ser Phe Asp Glu Gly Val Thr Trp Lys
690 695 700

Gly Pro Ile Gln Leu Val Asn Gly Ala Ser Ala Tyr Ser Asp Ile Tyr
705 710 715 720

Gln Leu Asp Ser Glu Asn Ala Ile Val Ile Val Glu Thr Asp Asn Ser
725 730 735

Asn Met Arg Ile Leu Arg Met Pro Ile Thr Leu Leu Lys Gln Lys Leu
740 745 750

Thr Leu Ser Gln Asn
755