

SEQUENCE LISTING

<110> SHANGHAI REINOVAX BIOLOGICS CO., LTD
SHANGHAI MICRODOM BIOTECH CO., LTD

<120> POLYSACCHARIDE PROTEIN CONJUGATE AND APPLICATION THEREOF

<130> 0180-PA-003

<160> 8

<170> PatentIn version 3.5

<210> 1

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> TTD-1

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Lys Lys Leu Glu Ser Lys Ile Asn Lys Val Phe Ser Thr Pro Ile Pro
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Phe Ser Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp
35 40 45

Ile Asp Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn
50 55 60

Asn Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr
65 70 75 80

Tyr Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His
85 90 95

Leu Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp
100 105 110

Ile Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu
115 120 125

Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn
 130 135 140

Glu Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly
 145 150 155 160

Ser Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu
 165 170 175

Lys Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro
 180 185 190

Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile
 195 200 205

Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu
 210 215 220

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

Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val
 245 250 255

Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu
 260 265 270

Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp
 275 280 285

Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro
 290 295 300

Val Ala Ser Ser Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr
 305 310 315 320

Met Tyr Leu Thr Asn Ala Pro Ser Tyr Thr Asn Gly Lys Leu Asn Ile
 325 330 335

Tyr Tyr Arg Arg Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg Tyr

340

345

350

Thr Pro Asn Asn Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile
 355 360 365

Lys Leu Tyr Val Ser Tyr Asn Asn Asn Glu His Ile Val Gly Tyr Pro
 370 375 380

Lys Asp Gly Asn Ala Phe Asn Asn Leu Asp Arg Ile Leu Arg Val Gly
 385 390 395 400

Tyr Asn Ala Pro Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys
 405 410 415

Leu Arg Asp Leu Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp
 420 425 430

Lys Asn Ala Ser Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly
 435 440 445

Asn Asp Pro Asn Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn
 450 455 460

His Leu Lys Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr
 465 470 475 480

Asp Glu Gly Trp Thr Asn Asp
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<210> 2

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<213> Artificial Sequence

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Gly Ile Thr Glu Leu Lys Lys Leu Glu Ser Lys Ile Asn Lys Val Phe
 1 5 10 15

Ser Thr Pro Ile Pro Phe Ser Tyr Ser Lys Asn Leu Asp Cys Trp Val

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Asp	Asn	Glu	Glu	Asp	Ile	Asp	Val	Ile	Leu	Lys	Lys	Ser	Thr	Ile	Leu
	35						40					45			
Asn	Leu	Asp	Ile	Asn	Asn	Asp	Ile	Ile	Ser	Asp	Ile	Ser	Gly	Phe	Asn
	50					55					60				
Ser	Ser	Val	Ile	Thr	Tyr	Pro	Asp	Ala	Gln	Leu	Val	Pro	Gly	Ile	Asn
65					70					75					80
Gly	Lys	Ala	Ile	His	Leu	Val	Asn	Asn	Glu	Ser	Ser	Glu	Val	Ile	Val
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His	Lys	Ala	Met	Asp	Ile	Glu	Tyr	Asn	Asp	Met	Phe	Asn	Asn	Phe	Thr
			100					105					110		
Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu
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Gln	Tyr	Gly	Thr	Asn	Glu	Tyr	Ser	Ile	Ile	Ser	Ser	Met	Lys	Lys	His
	130					135					140				
Ser	Leu	Ser	Ile	Gly	Ser	Gly	Trp	Ser	Val	Ser	Leu	Lys	Gly	Asn	Asn
145					150					155					160
Leu	Ile	Trp	Thr	Leu	Lys	Asp	Ser	Ala	Gly	Glu	Val	Arg	Gln	Ile	Thr
				165					170					175	
Phe	Arg	Asp	Leu	Pro	Asp	Lys	Phe	Asn	Ala	Tyr	Leu	Ala	Asn	Lys	Trp
			180					185					190		
Val	Phe	Ile	Thr	Ile	Thr	Asn	Asp	Arg	Leu	Ser	Ser	Ala	Asn	Leu	Tyr
		195					200					205			
Ile	Asn	Gly	Val	Leu	Met	Gly	Ser	Ala	Glu	Ile	Thr	Gly	Leu	Gly	Ala
	210					215					220				
Ile	Arg	Glu	Asp	Asn	Asn	Ile	Thr	Leu	Lys	Leu	Asp	Arg	Cys	Asn	Asn
225					230					235					240

Asn Asn Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala
 245 250 255

Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile
 260 265 270

Thr Phe Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu
 275 280 285

Tyr Tyr Leu Ile Pro Val Ala Ser Ser Ser Lys Asp Val Gln Leu Lys
 290 295 300

Asn Ile Thr Asp Tyr Met Tyr Leu Thr Asn Ala Pro Ser Tyr Thr Asn
 305 310 315 320

Gly Lys Leu Asn Ile Tyr Tyr Arg Arg Leu Tyr Asn Gly Leu Lys Phe
 325 330 335

Ile Ile Lys Arg Tyr Thr Pro Asn Asn Glu Ile Asp Ser Phe Val Lys
 340 345 350

Ser Gly Asp Phe Ile Lys Leu Tyr Val Ser Tyr Asn Asn Asn Glu His
 355 360 365

Ile Val Gly Tyr Pro Lys Asp Gly Asn Ala Phe Asn Asn Leu Asp Arg
 370 375 380

Ile Leu Arg Val Gly Tyr Asn Ala Pro Gly Ile Pro Leu Tyr Lys Lys
 385 390 395 400

Met Glu Ala Val Lys Leu Arg Asp Leu Lys Thr Tyr Ser Val Gln Leu
 405 410 415

Lys Leu Tyr Asp Asp Lys Asn Ala Ser Leu Gly Leu Val Gly Thr His
 420 425 430

Asn Gly Gln Ile Gly Asn Asp Pro Asn Arg Asp Ile Leu Ile Ala Ser
 435 440 445

Asn Trp Tyr Phe Asn His Leu Lys Asp Lys Ile Leu Gly Cys Asp Trp

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455

460

Tyr Phe Val Pro Thr Asp Glu Gly Trp Thr Asn Asp
 465 470 475

<210> 3

<211> 451

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<213> Artificial Sequence

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<223> TTD-3

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Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile
 20 25 30

Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala
 35 40 45

Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val Asn Asn
 50 55 60

Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu Tyr Asn
 65 70 75 80

Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys
 85 90 95

Val Ser Ala Ser His Leu Glu Gln Tyr Asp Thr Asn Glu Tyr Ser Ile
 100 105 110

Ile Ser Ser Met Lys Lys Tyr Ser Leu Ser Ile Gly Ser Gly Trp Ser
 115 120 125

Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala
 130 135 140

Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Ser Asp Lys Phe Asn

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

Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu
 370 375 380

Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys Asp Ala Ser
 385 390 395 400

Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn Asp Pro Asn
 405 410 415

Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His Leu Lys Asp
 420 425 430

Lys Thr Leu Thr Cys Asp Trp Tyr Phe Val Pro Thr Asp Glu Gly Trp
 435 440 445

Thr Asn Asp
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 <213> Artificial Sequence

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 tgggttgata atgaagaaga tatagatggt atattaaaaa agagtacaat tttaaattta 180
 gatattaata atgatattat atcagatata tctgggttta attcatctgt aataacatat 240
 ccagatgctc aattgggtgcc cggaataaat ggcaaagcaa tacatttagt aaacaatgaa 300
 tcttctgaag ttatagtgc taaagctatg gatattgaat ataatgatat gtttaataat 360
 tttaccgtta gcttttggtt gagggttcct aaagtatctg ctagtcattt agaacaatat 420
 ggcacaaatg agtattcaat aattagctct atgaaaaaac atagtctatc aataggatct 480
 ggttgagtg tatcacttaa aggtaataac ttaatatgga ctttaaaaga ttccgcggga 540
 gaagttagac aaataacttt tagggattta cctgataaat ttaatgctta tttagcaa 600

aaatggggtt ttataactat tactaatgat agattatctt ctgctaattt gtatataaat	660
ggagtactta tgggaagtgc agaaattact ggtttaggag ctattagaga ggataataat	720
ataacattaa aactagatag atgtaataat aataatcaat acgtttctat tgataaattt	780
aggatatattt gcaaagcatt aaatccaaaa gagattgaaa aattatacac aagttattta	840
tctataacct ttttaagaga cttctgggga aaccctttac gatatgatac agaatattat	900
ttaataccag tagcttctag ttctaaagat gttcaattga aaaatataac agattatatg	960
tatttgacaa atgcgccatc gtataactaac ggaaaattga atatataatta tagaaggtta	1020
tataatggac taaaatttat tataaaaaaga tatacaccta ataatgaaat agattctttt	1080
gttaaatcag gtgattttat taaattatat gtatcatata acaataatga gcacattgta	1140
ggttatccga aagatggaaa tgcctttaat aatcttgata gaattctaag agtaggttat	1200
aatgccccag gtatccctct ttataaaaaa atggaagcag taaaattgcg tgatttaaaa	1260
acctattctg tacaacttaa attatatgat gataaaaatg catctttagg actagtaggt	1320
acccataatg gtcaaataagg caacgatcca aatagggata tattaattgc aagcaactgg	1380
tactttaatc atttaaaaaga taaaatttta ggatgtgatt ggtactttgt acctacagat	1440
gaaggatgga caaatgat	1458

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cctttctcgt atagtaaaaa ccttgactgc tgggtggata acgaagagga catcgacgtc	120
atattgaaaa aatcgactat tttaaattta gacattaaca atgacattat ttcggacatt	180
tcaggcttta actcatcagt aataacttat cctgacgcac aattgggtccc tggaatcaac	240
ggtaaagcca tccatctggg gaacaacgaa agttccgaag tgattgtcca taaagctatg	300
gacattgagt ataacgatat gtttaataat ttcactgtga gtttttggct gcgtgtccct	360
aaagtatctg ccagtcactt agagcaatat ggtacgaacg aatactcgat aatttcactt	420

atgaaaaaac atagcttgtc aatcggctca ggctgggtccg tctcactgaa gggcaataat	480
cttatctgga ccctgaagga ctctgcgggt gaagtacggc agatcacgtt tagagatcctt	540
ccggataaat ttaacgctta tttagcgaac aaatgggtct ttatcactat cacaaatgat	600
cgtctgtcga gcgccaacct ttatattaac ggagtactga tgggtagtgc tgagattacc	660
ggacttggag cgattcggga agacaacaac atcaccctta aacttgatcg ttgtaacaat	720
aataatcagt acgtgagcat cgacaagttt cggatatctt gtaaggcgtt aaatccgaag	780
gaaattgaaa aattatatac atcgtatctg tcaatcactt tcttgcggga tttctggggg	840
aatcctcttc ggtatgatac cgaatactat cttatacctg tggcatctag tagtaaggat	900
gtacagttga agaacattac agattatatg tatcttacca atgcaccag ttacacaaac	960
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tacactccca acaacgagat agattctttt gtcaagagcg gagacttcat taagttatat	1080
gtcagctaca acaacaatga gcacatagtt ggctacccaa aggacggaaa cgcgtttaac	1140
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atggaagcag taaaattgcg cgacttgaag acgtactccg tacaacttaa actttacgac	1260
gacaaaaatg cgagtcttgg attgggttgg acgcacaacg gacagatcgg gaatgatccg	1320
aaccgtgaca tcttaattgc atcaaattgg tactttaatc atttgaaaga caaaatcctt	1380
ggctgcgatt ggtatcttgt tccgactgat gaggggtgga cgaacgac	1428

<210> 6

<211> 1353

<212> DNA

<213> Artificial Sequence

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<223> TTD-6

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tcagtaataa cttatcctga cgcacaattg gtccctggaa tcaacggtaa agccatccat	180
ctggatgaaca acgaaagttc cgaagtgtt gtccataaag ctatggacat tgagtataac	240
gatatgttta ataatttcac tgtgagtttt tggctgcgtg tccctaaagt atctgccagt	300

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cacttagagc aatatggtac gaacgaatac tcgataatth catctatgaa aaaacatagc      360
ttgtcaatcg gctcaggctg gtccgtctca ctgaaggga ataatcttat ctggaccctg      420
aaggactctg cgggtgaagt acggcagatc acgttttagag atcttccgga taaatttaac      480
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aacctttata ttaacggagt actgatgggt agtgctgaga ttaccggact tggagcgatt      600
cgggaagaca acaacatcac ccttaaactt gatcgttgta acaataataa tcagtacgtg      660
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tatacatcgt atctgtcaat cactttcttg cgggatttct gggggaatcc tcttcggtat      780
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attacagatt atatgtatct taccaatgca cccagttaca caaacggcaa gttaaataac      900
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gagatagatt cttttgtcaa gagcggagac ttcattaagt tatatgtcag ctacaacaac     1020
aatgagcaca tagttggcta ccaaaggac ggaaacgcgt ttaacaacct ggatcgtata     1080
ctgcgggtgg gctataacgc gcctgggatt cccttgata aaaagatgga agcagtaaaa     1140
ttgcgcgact tgaagacgta ctccgtacaa cttaaacttt acgacgaaa aaatgcgagt     1200
cttgattgg ttggtacgca caacggacag atcgggaatg atccgaaccg tgacatctta     1260
attgcatcaa attggtactt taatcatttg aaagacaaaa tccttggtg cgattggtat     1320
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<210> 7

<211> 36

<212> PRT

<213> Artificial Sequence

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<223> The amino acid sequence 07 of the translocation region

<400> 7

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

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Phe Ser Tyr Ser
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<210> 8

<211> 25

<212> PRT

<213> Artificial Sequence

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<223> The amino acid sequence 08 of the translocation region

<400> 8

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1				5				10						15	

Ser	Thr	Pro	Ile	Pro	Phe	Ser	Tyr	Ser
			20					25