

SEQUENCE LISTING

<110> Agency for Science, Technology and Research
Tan Tock Seng Hospital

<120> AN APTAMER FOR DENGUE VIRUS AND RELATED METHODS AND PRODUCTS

<130> 2000474

<160> 57

<170> PatentIn version 3.5

<210> 1

<211> 352

<212> PRT

<213> Dengue virus

<400> 1

Asp	Ser	Gly	Cys	Val	Ile	Asn	Trp	Lys	Gly	Arg	Glu	Leu	Lys	Cys	Gly
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Ser	Gly	Ile	Phe	Val	Thr	Asn	Glu	Val	His	Thr	Trp	Thr	Glu	Gln	Tyr
			20					25					30		

Lys	Phe	Gln	Ala	Asp	Ser	Pro	Lys	Arg	Leu	Ser	Ala	Ala	Ile	Gly	Lys
		35					40					45			

Ala	Trp	Glu	Glu	Gly	Val	Cys	Gly	Ile	Arg	Ser	Ala	Thr	Arg	Leu	Glu
	50					55					60				

Asn	Ile	Met	Trp	Lys	Gln	Ile	Ser	Asn	Glu	Leu	Asn	His	Ile	Leu	Leu
65					70					75				80	

Glu	Asn	Asp	Met	Lys	Phe	Thr	Val	Val	Val	Gly	Asp	Val	Ser	Gly	Ile
				85					90					95	

Leu	Ala	Gln	Gly	Lys	Lys	Met	Ile	Arg	Pro	Gln	Pro	Met	Glu	His	Lys
			100					105					110		

Tyr	Ser	Trp	Lys	Ser	Trp	Gly	Lys	Ala	Lys	Ile	Ile	Gly	Ala	Asp	Val
		115					120					125			

Gln	Asn	Thr	Thr	Phe	Ile	Ile	Asp	Gly	Pro	Asn	Thr	Pro	Glu	Cys	Pro
	130					135					140				

Asp Asn Gln Arg Ala Trp Asn Ile Trp Glu Val Glu Asp Tyr Gly Phe
145 150 155 160

Gly Ile Phe Thr Thr Asn Ile Trp Leu Lys Leu Arg Asp Ser Tyr Thr
165 170 175

Gln Val Cys Asp His Arg Leu Met Ser Ala Ala Ile Lys Asp Ser Lys
180 185 190

Ala Val His Ala Asp Met Gly Tyr Trp Ile Glu Ser Glu Lys Asn Glu
195 200 205

Thr Trp Lys Leu Ala Arg Ala Ser Phe Ile Glu Val Lys Thr Cys Ile
210 215 220

Trp Pro Lys Ser His Thr Leu Trp Ser Asn Gly Val Leu Glu Ser Glu
225 230 235 240

Met Ile Ile Pro Lys Ile Tyr Gly Gly Pro Ile Ser Gln His Asn Tyr
245 250 255

Arg Pro Gly Tyr Phe Thr Gln Thr Ala Gly Pro Trp His Leu Gly Lys
260 265 270

Leu Glu Leu Asp Phe Asp Leu Cys Glu Gly Thr Thr Val Val Val Asp
275 280 285

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

Gly Lys Thr Ile His Glu Trp Cys Cys Arg Ser Cys Thr Leu Pro Pro
305 310 315 320

Leu Arg Phe Lys Gly Glu Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg
325 330 335

Pro Val Lys Glu Lys Glu Glu Asn Leu Val Lys Ser Met Val Ser Ala
340 345 350

<210> 2
<211> 352
<212> PRT
<213> Dengue virus

<400> 2

Asp Ser Gly Cys Val Val Ser Trp Lys Asn Lys Glu Leu Lys Cys Gly
1 5 10 15

Ser Gly Ile Phe Ile Thr Asp Asn Val His Thr Trp Thr Glu Gln Tyr
20 25 30

Lys Phe Gln Pro Glu Ser Pro Ser Lys Leu Ala Ser Ala Ile Gln Lys
35 40 45

Ala His Glu Glu Gly Ile Cys Gly Ile Arg Ser Val Thr Arg Leu Glu
50 55 60

Asn Leu Met Trp Lys Gln Ile Thr Pro Glu Leu Asn His Ile Leu Ser
65 70 75 80

Glu Asn Glu Val Lys Leu Thr Ile Met Thr Gly Asp Ile Lys Gly Ile
85 90 95

Met Gln Ala Gly Lys Arg Ser Leu Arg Pro Gln Pro Thr Glu Leu Lys
100 105 110

Tyr Ser Trp Lys Thr Trp Gly Lys Ala Lys Met Leu Ser Thr Glu Ser
115 120 125

His Asn Gln Thr Phe Leu Ile Asp Gly Pro Glu Thr Ala Glu Cys Pro
130 135 140

Asn Thr Asn Arg Ala Trp Asn Ser Leu Glu Val Glu Asp Tyr Gly Phe
145 150 155 160

Gly Val Phe Thr Thr Asn Ile Trp Leu Lys Leu Lys Glu Lys Gln Asp
165 170 175

Val Phe Cys Asp Ser Lys Leu Met Ser Ala Ala Ile Lys Asp Asn Arg
180 185 190

Ala Val His Ala Asp Met Gly Tyr Trp Ile Glu Ser Ala Leu Asn Asp
195 200 205

Thr Trp Lys Ile Glu Lys Ala Ser Phe Ile Glu Val Lys Asn Cys His
210 215 220

Trp Pro Lys Ser His Thr Leu Trp Ser Asn Gly Val Leu Glu Ser Glu
225 230 235 240

Met Ile Ile Pro Lys Asn Leu Ala Gly Pro Val Ser Gln His Asn Tyr
245 250 255

Arg Pro Gly Tyr His Thr Gln Ile Thr Gly Pro Trp His Leu Gly Lys
260 265 270

Leu Glu Met Asp Phe Asp Phe Cys Asp Gly Thr Thr Val Val Val Thr
275 280 285

Glu Asp Cys Gly Asn Arg Gly Pro Ser Leu Arg Thr Thr Thr Ala Ser
290 295 300

Gly Lys Leu Ile Thr Glu Trp Cys Cys Arg Ser Cys Thr Leu Pro Pro
305 310 315 320

Leu Arg Tyr Arg Gly Glu Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg
325 330 335

Pro Leu Lys Glu Lys Glu Glu Asn Leu Val Asn Ser Leu Val Thr Ala
340 345 350

<210> 3
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<212> PRT
<213> Dengue virus

<400> 3

Asp Met Gly Cys Val Ile Asn Trp Lys Gly Lys Glu Leu Lys Cys Gly
1 5 10 15

Ser Gly Ile Phe Val Thr Asn Glu Val His Thr Trp Thr Glu Gln Tyr
20 25 30

Lys Phe Gln Ala Asp Ser Pro Lys Arg Leu Ala Thr Ala Ile Ala Gly
35 40 45

Ala Trp Glu Asn Gly Val Cys Gly Ile Arg Ser Thr Thr Arg Met Glu
50 55 60

Asn Leu Leu Trp Lys Gln Ile Ala Asn Glu Leu Asn Tyr Ile Leu Trp
65 70 75 80

Glu Asn Asn Ile Lys Leu Thr Val Val Val Gly Asp Thr Leu Gly Val
85 90 95

Leu Glu Gln Gly Lys Arg Thr Leu Thr Pro Gln Pro Met Glu Leu Lys
100 105 110

Tyr Ser Trp Lys Thr Trp Gly Lys Ala Lys Ile Val Thr Ala Glu Thr
115 120 125

Gln Asn Ser Ser Phe Ile Ile Asp Gly Pro Asn Thr Pro Glu Cys Pro
130 135 140

Ser Ala Ser Arg Ala Trp Asn Val Trp Glu Val Glu Asp Tyr Gly Phe
145 150 155 160

Gly Val Phe Thr Thr Asn Ile Trp Leu Lys Leu Arg Glu Val Tyr Thr
165 170 175

Gln Leu Cys Asp His Arg Leu Met Ser Ala Ala Val Lys Asp Glu Arg
180 185 190

Ala Val His Ala Asp Met Gly Tyr Trp Ile Glu Ser Gln Lys Asn Gly
195 200 205

Ser Trp Lys Leu Glu Lys Ala Ser Leu Ile Glu Val Lys Thr Cys Thr
210 215 220

Trp Pro Lys Ser His Thr Leu Trp Thr Asn Gly Val Leu Glu Ser Asp
225 230 235 240

Met Ile Ile Pro Lys Ser Leu Ala Gly Pro Ile Ser Gln His Asn Tyr
245 250 255

Arg Pro Gly Tyr His Thr Gln Thr Ala Gly Pro Trp His Leu Gly Lys
260 265 270

Leu Glu Leu Asp Phe Asn Tyr Cys Glu Gly Thr Thr Val Val Ile Thr
275 280 285

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

Gly Lys Leu Ile His Glu Trp Cys Cys Arg Ser Cys Thr Leu Pro Pro
305 310 315 320

Leu Arg Tyr Met Gly Glu Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg
325 330 335

Pro Ile Ser Glu Lys Glu Glu Asn Met Val Lys Ser Leu Val Ser Ala
340 345 350

<210> 4
<211> 352
<212> PRT
<213> Dengue virus

<400> 4

Asp Met Gly Cys Val Ala Ser Trp Ser Gly Lys Glu Leu Lys Cys Gly
1 5 10 15

Ser Gly Ile Phe Val Val Asp Asn Val His Thr Trp Thr Glu Gln Tyr
20 25 30

Lys Phe Gln Pro Glu Ser Pro Ala Arg Leu Ala Ser Ala Ile Leu Asn
35 40 45

Ala His Lys Asp Gly Val Cys Gly Ile Arg Ser Thr Thr Arg Leu Glu
50 55 60

Asn Val Met Trp Lys Gln Ile Thr Asn Glu Leu Asn Tyr Val Leu Trp
65 70 75 80

Glu Gly Gly His Asp Leu Thr Val Val Ala Gly Asp Val Lys Gly Val
85 90 95

Leu Thr Lys Gly Lys Arg Ala Leu Thr Pro Pro Val Ser Asp Leu Lys
100 105 110

Tyr Ser Trp Lys Thr Trp Gly Lys Ala Lys Ile Phe Thr Pro Glu Ala
115 120 125

Arg Asn Ser Thr Phe Leu Ile Asp Gly Pro Asp Thr Ser Glu Cys Pro
130 135 140

Asn Glu Arg Arg Ala Trp Asn Ser Leu Glu Val Glu Asp Tyr Gly Phe
145 150 155 160

Gly Met Phe Thr Thr Asn Ile Trp Met Lys Phe Arg Glu Gly Ser Ser
165 170 175

Glu Val Cys Asp His Arg Leu Met Ser Ala Ala Ile Lys Asp Gln Lys
180 185 190

Ala Val His Ala Asp Met Gly Tyr Trp Ile Glu Ser Ser Lys Asn Gln
195 200 205

Thr Trp Gln Ile Glu Lys Ala Ser Leu Ile Glu Val Lys Thr Cys Leu
210 215 220

Trp Pro Lys Thr His Thr Leu Trp Ser Asn Gly Val Leu Glu Ser Gln
225 230 235 240

Met Leu Ile Pro Lys Ser Tyr Ala Gly Pro Phe Ser Gln His Asn Tyr
245 250 255

Arg Gln Gly Tyr Ala Thr Gln Thr Val Gly Pro Trp His Leu Gly Lys
260 265 270

Leu Glu Ile Asp Phe Gly Glu Cys Pro Gly Thr Thr Val Thr Ile Gln
275 280 285

Glu Asp Cys Asp His Arg Gly Pro Ser Leu Arg Thr Thr Thr Ala Ser

290

295

300

Gly Lys Leu Val Thr Gln Trp Cys Cys Arg Ser Cys Thr Met Pro Pro
 305 310 315 320

Leu Arg Phe Leu Gly Glu Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg
 325 330 335

Pro Leu Ser Glu Lys Glu Glu Asn Met Val Lys Ser Gln Val Thr Ala
 340 345 350

<210> 5

<211> 352

<212> PRT

<213> Dengue virus

<400> 5

Asp Ser Gly Cys Val Ile Asn Trp Lys Gly Arg Glu Leu Lys Cys Gly
 1 5 10 15

Ser Gly Ile Phe Val Thr Asn Glu Val His Thr Trp Thr Glu Gln Tyr
 20 25 30

Lys Phe Gln Ala Asp Ser Pro Lys Arg Leu Ser Ala Ala Ile Gly Lys
 35 40 45

Ala Trp Glu Glu Gly Val Cys Gly Ile Arg Ser Ala Thr Arg Leu Glu
 50 55 60

Asn Ile Met Trp Lys Gln Ile Ser Asn Glu Leu Asn His Ile Leu Leu
 65 70 75 80

Glu Asn Asp Met Lys Phe Thr Val Val Val Gly Asp Ala Asn Gly Ile
 85 90 95

Leu Thr Gln Gly Lys Lys Met Ile Arg Pro Gln Pro Met Glu His Lys
 100 105 110

Tyr Ser Trp Lys Ser Trp Gly Lys Ala Lys Ile Ile Gly Ala Asp Thr
 115 120 125

Gln Asn Thr Thr Phe Ile Ile Asp Gly Pro Asp Thr Pro Glu Cys Pro
130 135 140

Asp Asp Gln Arg Ala Trp Asn Ile Trp Glu Val Glu Asp Tyr Gly Phe
145 150 155 160

Gly Val Phe Thr Thr Asn Ile Trp Leu Lys Leu Arg Asp Ser Tyr Thr
165 170 175

Gln Met Cys Asp His Arg Leu Met Ser Ala Ala Ile Lys Asp Ser Lys
180 185 190

Ala Val His Ala Asp Met Gly Tyr Trp Ile Glu Ser Glu Lys Asn Glu
195 200 205

Thr Trp Lys Leu Ala Arg Ala Ser Phe Ile Glu Val Lys Thr Cys Ile
210 215 220

Trp Pro Arg Ser His Thr Leu Trp Ser Asn Gly Val Leu Glu Ser Glu
225 230 235 240

Met Ile Ile Pro Lys Ile Tyr Gly Gly Pro Ile Ser Gln His Asn Tyr
245 250 255

Arg Pro Gly Tyr Phe Thr Gln Thr Ala Gly Pro Trp His Leu Gly Lys
260 265 270

Leu Glu Leu Asp Phe Asn Leu Cys Glu Gly Thr Thr Val Val Val Asp
275 280 285

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

Gly Lys Ile Ile His Glu Trp Cys Cys Arg Ser Cys Thr Leu Pro Pro
305 310 315 320

Leu Arg Phe Arg Gly Glu Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg
325 330 335

Pro Val Lys Glu Lys Glu Glu Asn Leu Val Arg Ser Met Val Ser Ala
340 345 350

<210> 6
<211> 352
<212> PRT
<213> Dengue virus

<400> 6

Asp Ser Gly Cys Val Ile Asn Trp Lys Gly Arg Glu Leu Lys Cys Gly
1 5 10 15

Ser Gly Ile Phe Val Thr Asn Glu Val His Thr Trp Thr Glu Gln Tyr
20 25 30

Lys Phe Gln Ala Asp Ser Pro Lys Arg Leu Ser Ala Ala Ile Gly Lys
35 40 45

Ala Trp Glu Glu Gly Val Cys Gly Ile Arg Ser Ala Thr Arg Leu Glu
50 55 60

Asn Ile Met Trp Lys Gln Ile Ser Asn Glu Leu Asn His Ile Leu Leu
65 70 75 80

Glu Asn Asp Met Lys Phe Thr Val Val Val Gly Asp Val Ala Gly Ile
85 90 95

Leu Ala Gln Gly Lys Lys Met Ile Arg Pro Gln Pro Met Glu His Lys
100 105 110

Tyr Ser Trp Lys Ser Trp Gly Lys Ala Lys Ile Ile Gly Ala Asp Val
115 120 125

Gln Asn Thr Thr Phe Ile Ile Asp Gly Pro Asn Thr Pro Glu Cys Pro
130 135 140

Asp Asp Gln Arg Ala Trp Asn Ile Trp Glu Val Glu Asp Tyr Gly Phe
145 150 155 160

Gly Ile Phe Thr Thr Asn Ile Trp Leu Lys Leu Arg Asp Ser Tyr Thr
165 170 175

Gln Val Cys Asp His Arg Leu Met Ser Ala Ala Ile Lys Asp Ser Lys

180

185

190

Ala Val His Ala Asp Met Gly Tyr Trp Ile Glu Ser Glu Lys Asn Glu
 195 200 205

Thr Trp Lys Leu Ala Arg Ala Ser Phe Ile Glu Val Lys Thr Cys Ile
 210 215 220

Trp Pro Lys Ser His Thr Leu Trp Ser Asn Gly Val Leu Glu Ser Glu
 225 230 235 240

Met Ile Ile Pro Lys Ile Tyr Gly Gly Pro Ile Ser Gln His Asn Tyr
 245 250 255

Arg Pro Gly Tyr Phe Thr Gln Thr Ala Gly Pro Trp His Leu Gly Lys
 260 265 270

Leu Glu Leu Asp Phe Asp Leu Cys Glu Gly Thr Thr Val Val Val Asp
 275 280 285

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

Gly Lys Ile Ile His Glu Trp Cys Cys Arg Ser Cys Thr Leu Pro Pro
 305 310 315 320

Leu Arg Phe Arg Gly Glu Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg
 325 330 335

Pro Val Lys Glu Lys Glu Glu Asn Leu Val Lys Ser Met Val Ser Ala
 340 345 350

<210> 7

<211> 358

<212> PRT

<213> Artificial Sequence

<220>

<223> modified NS1

<400> 7

Asp Ser Gly Cys Val Ile Asn Trp Lys Gly Arg Glu Leu Lys Cys Gly

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

Trp Pro Lys Ser His Thr Leu Trp Ser Asn Gly Val Leu Glu Ser Glu
225 230 235 240

Met Ile Ile Pro Lys Ile Tyr Gly Gly Pro Ile Ser Gln His Asn Tyr
245 250 255

Arg Pro Gly Tyr Phe Thr Gln Thr Ala Gly Pro Trp His Leu Gly Lys
260 265 270

Leu Glu Leu Asp Phe Asp Leu Cys Glu Gly Thr Thr Val Val Val Asp
275 280 285

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

Gly Lys Thr Ile His Glu Trp Cys Cys Arg Ser Cys Thr Leu Pro Pro
305 310 315 320

Leu Arg Phe Lys Gly Glu Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg
325 330 335

Pro Val Lys Glu Lys Glu Glu Asn Leu Val Lys Ser Met Val Ser Ala
340 345 350

His His His His His His
355

<210> 8
<211> 358
<212> PRT
<213> Artificial Sequence

<220>
<223> modified NS1

<400> 8

Asp Ser Gly Cys Val Val Ser Trp Lys Asn Lys Glu Leu Lys Cys Gly
1 5 10 15

Ser Gly Ile Phe Ile Thr Asp Asn Val His Thr Trp Thr Glu Gln Tyr
20 25 30

Lys Phe Gln Pro Glu Ser Pro Ser Lys Leu Ala Ser Ala Ile Gln Lys
35 40 45

Ala His Glu Glu Gly Ile Cys Gly Ile Arg Ser Val Thr Arg Leu Glu
50 55 60

Asn Leu Met Trp Lys Gln Ile Thr Pro Glu Leu Asn His Ile Leu Ser
65 70 75 80

Glu Asn Glu Val Lys Leu Thr Ile Met Thr Gly Asp Ile Lys Gly Ile
85 90 95

Met Gln Ala Gly Lys Arg Ser Leu Arg Pro Gln Pro Thr Glu Leu Lys
100 105 110

Tyr Ser Trp Lys Thr Trp Gly Lys Ala Lys Met Leu Ser Thr Glu Ser
115 120 125

His Asn Gln Thr Phe Leu Ile Asp Gly Pro Glu Thr Ala Glu Cys Pro
130 135 140

Asn Thr Asn Arg Ala Trp Asn Ser Leu Glu Val Glu Asp Tyr Gly Phe
145 150 155 160

Gly Val Phe Thr Thr Asn Ile Trp Leu Lys Leu Lys Glu Lys Gln Asp
165 170 175

Val Phe Cys Asp Ser Lys Leu Met Ser Ala Ala Ile Lys Asp Asn Arg
180 185 190

Ala Val His Ala Asp Met Gly Tyr Trp Ile Glu Ser Ala Leu Asn Asp
195 200 205

Thr Trp Lys Ile Glu Lys Ala Ser Phe Ile Glu Val Lys Asn Cys His
210 215 220

Trp Pro Lys Ser His Thr Leu Trp Ser Asn Gly Val Leu Glu Ser Glu
225 230 235 240

Met Ile Ile Pro Lys Asn Leu Ala Gly Pro Val Ser Gln His Asn Tyr

245

250

255

Arg Pro Gly Tyr His Thr Gln Ile Thr Gly Pro Trp His Leu Gly Lys
 260 265 270

Leu Glu Met Asp Phe Asp Phe Cys Asp Gly Thr Thr Val Val Val Thr
 275 280 285

Glu Asp Cys Gly Asn Arg Gly Pro Ser Leu Arg Thr Thr Thr Ala Ser
 290 295 300

Gly Lys Leu Ile Thr Glu Trp Cys Cys Arg Ser Cys Thr Leu Pro Pro
 305 310 315 320

Leu Arg Tyr Arg Gly Glu Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg
 325 330 335

Pro Leu Lys Glu Lys Glu Glu Asn Leu Val Asn Ser Leu Val Thr Ala
 340 345 350

His His His His His His
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<210> 9

<211> 358

<212> PRT

<213> Artificial Sequence

<220>

<223> modified NS1

<400> 9

Asp Met Gly Cys Val Ile Asn Trp Lys Gly Lys Glu Leu Lys Cys Gly
 1 5 10 15

Ser Gly Ile Phe Val Thr Asn Glu Val His Thr Trp Thr Glu Gln Tyr
 20 25 30

Lys Phe Gln Ala Asp Ser Pro Lys Arg Leu Ala Thr Ala Ile Ala Gly
 35 40 45

Ala Trp Glu Asn Gly Val Cys Gly Ile Arg Ser Thr Thr Arg Met Glu

50

55

60

Asn Leu Leu Trp Lys Gln Ile Ala Asn Glu Leu Asn Tyr Ile Leu Trp
 65 70 75 80

Glu Asn Asn Ile Lys Leu Thr Val Val Val Gly Asp Thr Leu Gly Val
 85 90 95

Leu Glu Gln Gly Lys Arg Thr Leu Thr Pro Gln Pro Met Glu Leu Lys
 100 105 110

Tyr Ser Trp Lys Thr Trp Gly Lys Ala Lys Ile Val Thr Ala Glu Thr
 115 120 125

Gln Asn Ser Ser Phe Ile Ile Asp Gly Pro Asn Thr Pro Glu Cys Pro
 130 135 140

Ser Ala Ser Arg Ala Trp Asn Val Trp Glu Val Glu Asp Tyr Gly Phe
 145 150 155 160

Gly Val Phe Thr Thr Asn Ile Trp Leu Lys Leu Arg Glu Val Tyr Thr
 165 170 175

Gln Leu Cys Asp His Arg Leu Met Ser Ala Ala Val Lys Asp Glu Arg
 180 185 190

Ala Val His Ala Asp Met Gly Tyr Trp Ile Glu Ser Gln Lys Asn Gly
 195 200 205

Ser Trp Lys Leu Glu Lys Ala Ser Leu Ile Glu Val Lys Thr Cys Thr
 210 215 220

Trp Pro Lys Ser His Thr Leu Trp Thr Asn Gly Val Leu Glu Ser Asp
 225 230 235 240

Met Ile Ile Pro Lys Ser Leu Ala Gly Pro Ile Ser Gln His Asn Tyr
 245 250 255

Arg Pro Gly Tyr His Thr Gln Thr Ala Gly Pro Trp His Leu Gly Lys
 260 265 270

Leu Glu Leu Asp Phe Asn Tyr Cys Glu Gly Thr Thr Val Val Ile Thr
275 280 285

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

Gly Lys Leu Ile His Glu Trp Cys Cys Arg Ser Cys Thr Leu Pro Pro
305 310 315 320

Leu Arg Tyr Met Gly Glu Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg
325 330 335

Pro Ile Ser Glu Lys Glu Glu Asn Met Val Lys Ser Leu Val Ser Ala
340 345 350

His His His His His His
355

<210> 10
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<223> modified NS1

<400> 10

Asp Met Gly Cys Val Ala Ser Trp Ser Gly Lys Glu Leu Lys Cys Gly
1 5 10 15

Ser Gly Ile Phe Val Val Asp Asn Val His Thr Trp Thr Glu Gln Tyr
20 25 30

Lys Phe Gln Pro Glu Ser Pro Ala Arg Leu Ala Ser Ala Ile Leu Asn
35 40 45

Ala His Lys Asp Gly Val Cys Gly Ile Arg Ser Thr Thr Arg Leu Glu
50 55 60

Asn Val Met Trp Lys Gln Ile Thr Asn Glu Leu Asn Tyr Val Leu Trp
65 70 75 80

Glu Gly Gly His Asp Leu Thr Val Val Ala Gly Asp Val Lys Gly Val
85 90 95

Leu Thr Lys Gly Lys Arg Ala Leu Thr Pro Pro Val Ser Asp Leu Lys
100 105 110

Tyr Ser Trp Lys Thr Trp Gly Lys Ala Lys Ile Phe Thr Pro Glu Ala
115 120 125

Arg Asn Ser Thr Phe Leu Ile Asp Gly Pro Asp Thr Ser Glu Cys Pro
130 135 140

Asn Glu Arg Arg Ala Trp Asn Ser Leu Glu Val Glu Asp Tyr Gly Phe
145 150 155 160

Gly Met Phe Thr Thr Asn Ile Trp Met Lys Phe Arg Glu Gly Ser Ser
165 170 175

Glu Val Cys Asp His Arg Leu Met Ser Ala Ala Ile Lys Asp Gln Lys
180 185 190

Ala Val His Ala Asp Met Gly Tyr Trp Ile Glu Ser Ser Lys Asn Gln
195 200 205

Thr Trp Gln Ile Glu Lys Ala Ser Leu Ile Glu Val Lys Thr Cys Leu
210 215 220

Trp Pro Lys Thr His Thr Leu Trp Ser Asn Gly Val Leu Glu Ser Gln
225 230 235 240

Met Leu Ile Pro Lys Ser Tyr Ala Gly Pro Phe Ser Gln His Asn Tyr
245 250 255

Arg Gln Gly Tyr Ala Thr Gln Thr Val Gly Pro Trp His Leu Gly Lys
260 265 270

Leu Glu Ile Asp Phe Gly Glu Cys Pro Gly Thr Thr Val Thr Ile Gln
275 280 285

Glu Asp Cys Asp His Arg Gly Pro Ser Leu Arg Thr Thr Thr Ala Ser

290

295

300

Gly Lys Leu Val Thr Gln Trp Cys Cys Arg Ser Cys Thr Met Pro Pro
 305 310 315 320

Leu Arg Phe Leu Gly Glu Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg
 325 330 335

Pro Leu Ser Glu Lys Glu Glu Asn Met Val Lys Ser Gln Val Thr Ala
 340 345 350

His His His His His His His His His
 355 360

<210> 11
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Aptamer

<220>
 <221> misc_feature
 <222> (19)..(19)
 <223> n = dDs

<220>
 <221> misc_feature
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 <223> n = dDs

<220>
 <221> misc_feature
 <222> (44)..(44)
 <223> n = Biotin-dT

<400> 11
 cccagacgg actggtgtnc tcggnatggc cgtctggggc gcgnagcg

48

<210> 12
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Aptamer

<220>
<221> misc_feature
<222> (11)..(11)
<223> n = dDs

<220>
<221> misc_feature
<222> (23)..(23)
<223> n = dDs

<220>
<221> misc_feature
<222> (35)..(35)
<223> n = Diol1-dPa

<220>
<221> misc_feature
<222> (68)..(68)
<223> n = Biotin-dT

<400> 12
ggctggtccg nctgggaaca agnggcggga ggganggggtg tgggtgacgac aagcggacca 60

gcccgcgnag cg 72

<210> 13
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Aptamer

<220>
<221> misc_feature
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<223> n = dDs

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<222> (55)..(55)
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<400> 13
ccgcttggtca tctancctgg ccntgtggta ctgtaacggc tgacaagcgg cgcgnagcg 59

<210> 14
<211> 57
<212> DNA
<213> Artificial Sequence

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<221> misc_feature
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<223> n = dDs

<220>
<221> misc_feature
<222> (53)..(53)
<223> n = Biotin-dT

<400> 14
cggcggagac gtaacgcnta tcaaatcnaa acagcttagg gtccgccgcg cgnagcg

57

<210> 15
<211> 97
<212> DNA
<213> Artificial Sequence

<220>
<223> Aptamer

<220>
<221> misc_feature
<222> (1)..(1)
<223> n = Biotin

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<221> misc_feature
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<221> misc_feature
<222> (61)..(61)
<223> n = dDs

<400> 15
ntttcgcaact ccatgatatg gtctactgag cgagacgatg ctgctaaant acgccgtggt 60

nacgaagaca gacaagcgga gtagttagac cgtgaaa 97

<210> 16
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<222> (56)..(56)
<223> n = dDs

<220>
<221> misc_feature
<222> (84)..(84)
<223> n = Biotin-dT

<400> 16
gcactccatg atatggtcta ctgagcgaga cgatgctgct aaantacgcc gtggtnacga 60

agacagacaa gcggagtgtc gcgnagcg 88

<210> 17
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Aptamer

<220>
<221> misc_feature
<222> (1)..(1)
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<220>
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<222> (21)..(21)
<223> n = dDs

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aagcggagta gttagacc                                                             78

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aagcggagta gttagacc                                                    78

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aagcggagta gttagacc 78

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<400> 29
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aagcggagta gttagacc 78

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<400> 32
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<210> 33
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<400> 33
cgtgcgacga ngccaacca gtccaatcn acaagtcgca cgcgcgnagc g

51

<210> 34
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<210> 35
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<210> 38
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<400> 38

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48

<210> 39

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<222> (46)..(46)

<223> n = dDs

<400> 39

nactccatga tatggtctac tgatagtact ccngtttaac tctganactt gacgtccatt

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aagcggagta gtttagacc 78

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aagcggagta gtttagacc 78

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ggccgcgcgn agcg 74

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28