

SEQUENCE LISTING

<110> Cold Spring Harbor Laboratory

<120> Methods For Treating Pancreatitis

<130> 2013237-0019

<140> US 62/729,354

<141> 2018-09-10

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> VH chain domain of clone 5B1

<400> 1

atggagtttg ggctgagctg gctttttctt gtggctatatt taaaaggcgt acagtgccag 60

gtgcagctgg tggagtctgg gggaggctcg gtgcagcctg gcaggccctt gagactctcc 120

tgtgaagcct ctggattcac ctttgaggcc tatgccatgc actgggtccg gcaacctcca 180

gggaagggcc tggagtgggt ctcaagtatt aattggaata gtggtcgcat agcctatgcg 240

gactctgtga agggccgatt caccatctcc agagacaacg ccaggaattc cctgtatctg 300

caaatgaaca gtctgagact tgaggacacg gccttctatt actgtgcaaa agatatacgg 360

aggttttagta ccgggggggc ggagtttgag tactggggcc aggggaaccct ggtcaccgtc 420

tcctca 426

<210> 2

<211> 142

<212> PRT

<213> Artificial Sequence

<220>

<223> VH chain domain of clone 5B1

<400> 2

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe
35 40 45

Glu Ala Tyr Ala Met His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ser Ile Asn Trp Asn Ser Gly Arg Ile Ala Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn
85 90 95

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

Tyr Tyr Cys Ala Lys Asp Ile Arg Arg Phe Ser Thr Gly Gly Ala Glu
115 120 125

Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

<210> 3
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> VL chain domain of clone 5B1

<400> 3
atggccggct tccctctcct cctcaccctc ctactcact gtgcagggtc ttgggccag 60
tctgtgctga ctgagccgcc ctgagcgtct gggacccccg ggcagagggt caccatctct 120

tgttctggaa gcagctccaa catcggaagt aattttgtat actggtacca gcagctccca	180
ggaacggccc ccaaactcct catatatagg aataatcagc ggccctcagg ggtccctgac	240
cgattctctg gctccaggtc tggcacctca gcctccctgg ccatcagtgg actccgggtcc	300
gaggatgagg ctgattatta ctgtgcagca tgggatgaca gcctgggagg ccattatgtc	360
ttcggaactg ggaccaaggt caccgtcctt	390

<210> 4
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL chain domain of clone 5B1

<400> 4

Met	Ala	Gly	Phe	Pro	Leu	Leu	Leu	Thr	Leu	Leu	Thr	His	Cys	Ala	Gly
1				5					10					15	

Ser	Trp	Ala	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly	Thr
			20					25					30		

Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	Ser	Gly	Ser	Ser	Ser	Asn	Ile
	35						40				45				

Gly	Ser	Asn	Phe	Val	Tyr	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro
50						55					60				

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

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

Gly	Leu	Arg	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Ala	Trp	Asp
			100					105					110		

Asp	Ser	Leu	Gly	Gly	His	Tyr	Val	Phe	Gly	Thr	Gly	Thr	Lys	Val	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Val Leu
130

<210> 5
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> VH chain domain of clone 9H3

<400> 5
atggagtttg ggctgagctg gctttttctt gtggctattt taaaaggcgt acagtgcgaa 60
gtgcagctgt tggagtctgg gggaggcttg gtacagcctg gcaggctccct gagactctcc 120
tgtgcggcct ctggatttac ctttgatgat tatgtcatgc actgggtccg gcaagctcca 180
gggaagggcc tggagtgggt ctcaagtatt agttggaata gtggtagcat aggctatgcg 240
gactctgtga agggccgatt catcatctcc agagacaacg ccaagaactc cctgtatctg 300
caaatgaaca gtctgagagc tgaggacacg gccttgtatt actgtgcaaa agatcgtcgt 360
attaggggtg actcgggggt cgagggtgac tactggggcc aggggaaccct ggtcaccgtc 420
tcctca 426

<210> 6
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> VH chain domain of clone 9H3

<400> 6

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Asp Asp Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ser Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

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

Tyr Tyr Cys Ala Lys Asp Arg Arg Ile Arg Gly Asp Ser Gly Phe Glu
115 120 125

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

<210> 7
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> VL chain domain of clone 9H3

<400> 7
atggccggct tccctctcct cctcaccctc ctcaactcact gtgcagggtc ttgggcccag 60
tctgtgttga cgcagccgcc ctacagctct gggacccccg ggcagagggt caccatctct 120
tgttctggaa gcagctccaa catcggaagt aattatgtat actggtacca gcagctccca 180
ggaacggccc ccaaactcct catctatagg aataatcagc ggccctcagg ggtccctgac 240
cgattctctg gctccaagtc tggcacctca gcctccctgg ccatcagtgg gctccgggtcc 300
gaggatgagg ctgattatta ctgtgcagca tgggatgcc a gcctgagtgg tgtggtattc 360

ggcggaggga ccaagctgac cgtccta

387

<210> 8

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> VL chain domain of clone 9H3

<400> 8

Met Ala Gly Phe Pro Leu Leu Leu Thr Leu Leu Thr His Cys Ala Gly
1 5 10 15

Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr
20 25 30

Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile
35 40 45

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

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

Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser
85 90 95

Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp
100 105 110

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

Leu

<210> 9

<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> VH chain domain of clone 5H11

<400> 9
atggagtttg ggctgagctg gctttttctt gtggctattt taaaaggcgt acagtgccag 60
gtgcagctgt tggagtctgg gggaggcttg gtacagcctg gcaggtcctt gagactctcc 120
tgtgcagcct ctggattcac ctttgatgaa tatgccatgc actgggtccg gcaagctcca 180
gggaagggcc tggagtgggt ctcaagtgtt agttggaata gtggtagcat aggctatgcg 240
gactctgtga agggccgatt caccatctcc agagacaacg ccaagaactc cctgtatcta 300
caaatgaaca gtctgagagc tgaggacacg gccttgtatt actgtgcaaa agatatacgg 360
acctatagca ccgggggggc ggagtttgcc tcctggggcc agggaaccct ggtcaccgcc 420
tcctca 426

<210> 10
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> VH chain domain of clone 5H11

<400> 10

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Asp Glu Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ser Val Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

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

Tyr Tyr Cys Ala Lys Asp Ile Arg Thr Tyr Ser Thr Gly Gly Ala Glu
115 120 125

Phe Ala Ser Trp Gly Gln Gly Thr Leu Val Thr Ala Ser Ser
130 135 140

<210> 11
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> VL chain domain of clone 5H11

<400> 11
atggccggct tccctctcct cctcaccctc ctcaactcact gtgcagggtc ttgggccag 60
tctgtgttga cgcagccgcc ctacagcgtct gggacccccg ggcagagggt caccatctct 120
tgttctggaa gcagctccaa catcggaagt aattatgtat actggtacca gcaggtccca 180
ggaacggccc ccaaactcct catctatagg aataatcagc ggccctcagg ggtccctgac 240
cgattctctg gctccaagtc tggcacctca gcctccctgg ccatcagtgg gctccgggtcc 300
gaggatgagg ctgattatta ctgtgcagca tgggatgaca gcctgagtgg ccattatgtc 360
ttcggaactg ggaccaaggt caccgtccta 390

<210> 12
<211> 130
<212> PRT
<213> Artificial Sequence

<220>

<223> VL chain domain of clone 5H11

<400> 12

Met Ala Gly Phe Pro Leu Leu Leu Thr Leu Leu Thr His Cys Ala Gly
1 5 10 15

Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr
20 25 30

Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile
35 40 45

Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro
50 55 60

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

Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser
85 90 95

Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp
100 105 110

Asp Ser Leu Ser Gly His Tyr Val Phe Gly Thr Gly Thr Lys Val Thr
115 120 125

Val Leu
130

<210> 13

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> VH chain domain of clone 7E3

<400> 13

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atggagtttg ggctgagctg gctttttctt gtggctattt taaaaggcgt acagtgccaa      60
gtgcagctgt tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc      120
tgtgcagcct ctggattcac cttcagtttc tatggcatgc actgggtccg ccaggctcca      180
ggcaaggggc tggagtgggt ggcagctata tcatatgatg gaagtaataa atactatgca      240
gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg      300
caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgaa aaggcccaac      360
caattttatt gtagtgatgg tagatgctac tccattgact actggggcca gggaaccctg      420
gtcaccgtct cctca                                                         435

```

<210> 14
 <211> 145
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH chain domain of clone 7E3

<400> 14

```

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1           5           10          15

```

```

Val Gln Cys Gln Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln
          20          25          30

```

```

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
          35          40          45

```

```

Ser Phe Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50           55           60

```

```

Glu Trp Val Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65           70           75           80

```

```

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

```

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

Tyr Tyr Cys Ala Lys Arg Pro Asn Gln Phe Tyr Cys Ser Asp Gly Arg
115 120 125

Cys Tyr Ser Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
130 135 140

Ser
145

<210> 15
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> VL chain domain of clone 7E3

<400> 15
atggacatga ggggtccccgc tcagctcctg gggctcctgc tactctggct ccgaggtgcc 60
cgggtgtgaaa ttgtaatgac gcagtctcca gccaccctgt ctgtgtctcc aggggagaga 120
gccaccctct cctgcagggc cagtcagagt gtagcagca acttagcctg gtaccagcag 180
aaacctggcc aggctcccag gctcctcatc tatggtgcat ccaccagggc cactggtatc 240
ccagccaggt tcagtggcag tgggtctggg acagacttca ctctcaccat cagcagcctg 300
cagtctgtag attctgcagt ttattactgt cagcagtata ataactggcc tccgtacact 360
tttgccagg ggaccaagct ggagatcaaa 390

<210> 16
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> VL chain domain of clone 7E3

<400> 16

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

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

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

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

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95

Ile Ser Ser Leu Gln Ser Val Asp Ser Ala Val Tyr Tyr Cys Gln Gln
100 105 110

Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu
115 120 125

Ile Lys
130

<210> 17
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> Diabody 5B1CysDb sequence

<400> 17
cagtctgtgc tgacgcagcc gccctcagcg tctgggaccc ccgggcagag ggtcaccatc 60
tcttgttctg gaagcagctc caacatcgga agtaattttg tatactggta ccagcagctc 120

```

ccaggaacgg cccccaact cctcatatat aggaataatc agcggccctc aggggtccct      180
gaccgattct ctggctccag gtctggcacc tcagcctccc tggccatcag tggactccgg      240
tccgaggatg aggctgatta ttactgtgca gcatgggatg acagcctggg aggccattat      300
gtcttcggaa ctgggaccaa ggtcaccgtc ctttctggtg gtggtggtca ggtgcagctg      360
gtggagtctg ggggaggctc ggtgcagcct ggcagggtccc tgagactctc ctgtgaagcc      420
tctggattca cctttgaggc ctatgccatg cactgggtcc ggcaacctcc aggggaagggc      480
ctggagtggg tctcaagtat taattggaat agtggtcgca tagcctatgc ggactctgtg      540
aagggccgat tcaccatctc cagagacaac gccaggaatt ccctgtatct gcaaatgaac      600
agtctgagac ttgaggacac ggccttctat tactgtgcaa aagatatacg gaggtttagt      660
accggggggg cggagtttga gtactggggc cagggaaccc tggtcaccgt ctcctcaggt      720
tctcaccatc accatcacca tggcggttgc                                     750

```

<210> 18
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Diabody 5B1CysDb sequence

<400> 18

```

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

```

```

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
          20          25          30

```

```

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

```

```

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50          55          60

```

```

Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg

```

65		70		75		80									
Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Ala	Trp	Asp	Asp	Ser	Leu
			85					90						95	
Gly	Gly	His	Tyr	Val	Phe	Gly	Thr	Gly	Thr	Lys	Val	Thr	Val	Leu	Ser
			100					105					110		
Gly	Gly	Gly	Gly	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Ser	Val
			115				120						125		
Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Phe	Thr
			130				135					140			
Phe	Glu	Ala	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly
145					150					155					160
Leu	Glu	Trp	Val	Ser	Ser	Ile	Asn	Trp	Asn	Ser	Gly	Arg	Ile	Ala	Tyr
				165					170					175	
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Arg
			180					185					190		
Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Leu	Glu	Asp	Thr	Ala
		195					200					205			
Phe	Tyr	Tyr	Cys	Ala	Lys	Asp	Ile	Arg	Arg	Phe	Ser	Thr	Gly	Gly	Ala
	210					215					220				
Glu	Phe	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly
225					230					235					240
Ser	His	His	His	His	His	His	Gly	Gly	Cys						
			245						250						

<210> 19
 <211> 750
 <212> DNA

<213> Artificial Sequence

<220>

<223> Diabody 7E3CysDb sequence

<400> 19

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ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct      120
ggccaggctc ccaggctcct catctatggc gcatccacca gggccactgg tatcccagcc      180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct      240
gaagattctg cagtttatta ctgtcagcag tataataact ggcctccgta cacttttggc      300
caggggacca aggtggatat caaatctggc ggtgggtggc aagtgcagct ggtggagtct      360
gggggaggcg tgggtccagcc tgggaggtcc ctgagactct cctgtgcagc ctctggattc      420
accttcagtt tctatggcat gcactgggtc cgccaggctc caggcaaggg gctggagtgg      480
gtggcagcta tatcatatga tggaagtaat aaatactatg cagactccgt gaagggccga      540
ttcaccatct ccagagacaa ttccaagaac acgctgtatc tgcaaatgaa cagcctgaga      600
gctgaggaca cggctgtgta ttactgtgcg aaaaggccca accaatttta ttgtagtgat      660
ggtagatgct actccattga ctactggggc cagggaaccc tggtcaccgt ctctcaggt      720
tctcaccatc accatcacca tggcggttgc      750
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<210> 20

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Diabody 7E3CysDb sequence

<400> 20

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

```
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
          20           25           30
```

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

Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

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

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

Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Ser Gly Gly Gly Gly
100 105 110

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
115 120 125

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr
130 135 140

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
145 150 155 160

Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
165 170 175

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
180 185 190

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
195 200 205

Ala Lys Arg Pro Asn Gln Phe Tyr Cys Ser Asp Gly Arg Cys Tyr Ser
210 215 220

Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser

225

230

235

240

His His His His His His Gly Gly Cys
245