SEQUENCE LISTING

<110> Singapore General Hospital Pte Ltd
Xiao, Zhi-Cheng

<120> Central nervous system damage

<130> CMD/FP6186654

<150> US 60/431,620
<151> 2002-12-06

<160> 35

<170> PatentIn version 3.1

<210> 1
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 1

Tyr Leu Thr Gln Pro Gln Ser
1 5

<210> 2
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 2

Gly Ser Leu Pro His Ser Leu
1 5

<210> 3
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 3

Thr Gln Leu Phe Pro Pro Gln
1 5

<210> 4
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 4

His Ser Ile Pro Asp Asn Ile
1 5

<210> 5
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 5

His His Met Pro His Asp Lys
1 5

<210> 6
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 6

Tyr Thr Thr Pro Pro Ser Pro
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<210> 7
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 7

Gln Leu Pro Leu Met Pro Arg
1 5

<210> 8
<211> 508
<212> PRT
<213> Rattus norvegicus

<400> 8

Met Ile Phe Leu Thr Thr Leu Pro Leu Phe Trp Ile Met Ile Ser Ala
1 5 10 15

Ser Arg Gly Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala
20 25 30

Phe Glu Gly Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp
35 40 45

Glu Leu Arg Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro
50 55 60

Tyr Pro Lys Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val
65 70 75 80

Val His Glu Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly
85 90 95

Leu Arg Asn Cys Thr Leu Leu Leu Ser Thr Leu Ser Pro Glu Leu Gly
100 105 110

Gly Lys Tyr Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr
115 120 125

Phe Ser Glu His Ser Val Leu Asp Ile Ile Asn Thr Pro Asn Ile Val
130 135 140

Val Pro Pro Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met
145 150 155 160

Val Pro Asp Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly
165 170 175

His Glu Gly Leu Gly Glu Pro Thr Val Leu Gly Arg Leu Arg Glu Asp
180 185 190

Glu Gly Thr Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg
195 200 205

Glu Ala Asn Gly His Arg Leu Gly Cys Gln Ala Ala Phe Pro Asn Thr
210 215 220

Thr Leu Gln Phe Glu Gly Tyr Ala Ser Leu Asp Val Lys Tyr Pro Pro
225 230 235 240

Val Ile Val Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His
245 250 255

Val Ser Leu Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr

260 265 270

Trp Met Arg Asp Gly Met Val Leu Arg Glu Ala Val Ala Glu Ser Leu
275 280 285

Tyr Leu Asp Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Ile Tyr Ala
290 295 300

Cys Leu Ala Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Glu Leu
305 310 315 320

Ser Val Met Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Val Val
325 330 335

Ala Val Glu Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn
340 345 350

Pro Asp Pro Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ala Thr
355 360 365

Val Ile Tyr Glu Ser Gln Leu Gln Leu Glu Leu Pro Ala Val Thr Pro
370 375 380

Glu Asp Asp Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln
385 390 395 400

Arg Ala Thr Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Ile Ile Leu
405 410 415

Leu Glu Ser His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys
420 425 430

Val Val Lys Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser
435 440 445

Arg Asn Val Thr Val Asn Glu Thr Glu Arg Glu Phe Val Tyr Ser Glu
450 455 460

Arg Ser Gly Leu Leu Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala
465 470 475 480

Gln Ala Pro Pro Arg Val Ile Cys Thr Ser Arg Asn Leu Tyr Gly Thr
485 490 495

Gln Ser Leu Glu Leu Pro Phe Gln Gly Ala His Arg
500 505

<210> 9
<211> 205
<212> PRT
<213> Homo sapiens

<400> 9

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

Ala Asn Cys Cys Gln Glu Ser Ala Ala Thr Gly Gln Leu Asp Tyr Ile
35 40 45

Pro His Cys Ser Gly His Gly Asn Phe Ser Phe Glu Ser Cys Gly Cys
50 55 60

Ile Cys Asn Glu Gly Trp Phe Gly Lys Asn Cys Ser Glu Pro Tyr Cys
65 70 75 80

Pro Leu Gly Cys Ser Ser Arg Gly Val Cys Val Asp Gly Gln Cys Ile
85 90 95

Cys Asp Ser Glu Tyr Ser Gly Asp Asp Cys Ser Glu Leu Arg Cys Pro
100 105 110

Thr Asp Cys Ser Ser Arg Gly Leu Cys Val Asp Gly Glu Cys Val Cys
115 120 125

Glu Glu Pro Tyr Thr Gly Glu Asp Cys Arg Glu Leu Arg Cys Pro Gly
130 135 140

Asp Cys Ser Gly Lys Gly Arg Cys Ala Asn Gly Thr Cys Leu Cys Glu
145 150 155 160

Glu Gly Tyr Val Gly Glu Asp Cys Gly Gln Arg Gln Cys Leu Asn Ala
165 170 175

Cys Ser Gly Arg Gly Gln Cys Glu Glu Gly Leu Cys Val Cys Glu Glu
180 185 190

Gly Tyr Gln Gly Pro Asp Cys Ser Ala Val Ala Pro Pro
195 200 205

<210> 10
<211> 185

<212> PRT
<213> Homo sapiens

<400> 10

Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro
1 5 10 15

Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
20 25 30

Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
35 40 45

Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
50 55 60

Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65 70 75 80

Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
100 105 110

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

Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
130 135 140

Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
145 150 155 160

Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
165 170 175

Lys Arg Arg Gly Ser Ser Gly Ser Val
180 185

<210> 11
<211> 66
<212> PRT
<213> Homo sapiens

<400> 11

Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
1 5 10 15

His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu
20 25 30

Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr
35 40 45

Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser
50 55 60

Leu Lys
65

<210> 12
<211> 973
<212> PRT
<213> Artificial sequence

<220>
<223> Fusion protein

<220>
<221> VARIANT
<222> (509)..(511)
<223> Polyalanine linker.

<220>
<221> VARIANT
<222> (717)..(719)
<223> Polyalanine linker.

<220>
<221> VARIANT
<222> (905)..(907)
<223> Polyalanine linker.

<400> 12

Met Ile Phe Leu Thr Thr Leu Pro Leu Phe Trp Ile Met Ile Ser Ala
1 5 10 15

Ser Arg Gly Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala
20 25 30

Phe Glu Gly Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp
35 40 45

Glu Leu Arg Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro
50 55 60

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Tyr Pro Lys Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val
65                  70                  75                  80

Val His Glu Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly
                85                  90                  95

Leu Arg Asn Cys Thr Leu Leu Leu Ser Thr Leu Ser Pro Glu Leu Gly
            100                 105                 110

Gly Lys Tyr Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr
        115                 120                 125

Phe Ser Glu His Ser Val Leu Asp Ile Ile Asn Thr Pro Asn Ile Val
    130                 135                 140

Val Pro Pro Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met
145                 150                 155                 160

Val Pro Asp Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly
                165                 170                 175

His Glu Gly Leu Gly Glu Pro Thr Val Leu Gly Arg Leu Arg Glu Asp
            180                 185                 190

Glu Gly Thr Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg
        195                 200                 205

Glu Ala Asn Gly His Arg Leu Gly Cys Gln Ala Ala Phe Pro Asn Thr
    210                 215                 220

Thr Leu Gln Phe Glu Gly Tyr Ala Ser Leu Asp Val Lys Tyr Pro Pro
225                 230                 235                 240

Val Ile Val Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His
                245                 250                 255

Val Ser Leu Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr
            260                 265                 270

Trp Met Arg Asp Gly Met Val Leu Arg Glu Ala Val Ala Glu Ser Leu
        275                 280                 285

Tyr Leu Asp Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Ile Tyr Ala
    290                 295                 300

Cys Leu Ala Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Glu Leu
305                 310                 315                 320
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Ser Val Met Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Val Val
325 330 335

Ala Val Glu Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn
340 345 350

Pro Asp Pro Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ala Thr
355 360 365

Val Ile Tyr Glu Ser Gln Leu Gln Leu Glu Leu Pro Ala Val Thr Pro
370 375 380

Glu Asp Asp Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln
385 390 395 400

Arg Ala Thr Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Ile Ile Leu
405 410 415

Leu Glu Ser His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys
420 425 430

Val Val Lys Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser
435 440 445

Arg Asn Val Thr Val Asn Glu Thr Glu Arg Glu Phe Val Tyr Ser Glu
450 455 460

Arg Ser Gly Leu Leu Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala
465 470 475 480

Gln Ala Pro Pro Arg Val Ile Cys Thr Ser Arg Asn Leu Tyr Gly Thr
485 490 495

Gln Ser Leu Glu Leu Pro Phe Gln Gly Ala His Arg Ala Ala Ala Cys
500 505 510

Pro Cys Ala Ser Ser Ala Gln Val Leu Gln Glu Leu Leu Ser Arg Ile
515 520 525

Glu Met Leu Glu Arg Glu Val Ser Val Leu Arg Asp Gln Cys Asn Ala
530 535 540

Asn Cys Cys Gln Glu Ser Ala Ala Thr Gly Gln Leu Asp Tyr Ile Pro
545 550 555 560

His Cys Ser Gly His Gly Asn Phe Ser Phe Glu Ser Cys Gly Cys Ile
565 570 575

Cys Asn Glu Gly Trp Phe Gly Lys Asn Cys Ser Glu Pro Tyr Cys Pro
580 585 590

Leu Gly Cys Ser Ser Arg Gly Val Cys Val Asp Gly Gln Cys Ile Cys
595 600 605

Asp Ser Glu Tyr Ser Gly Asp Asp Cys Ser Glu Leu Arg Cys Pro Thr
610 615 620

Asp Cys Ser Ser Arg Gly Leu Cys Val Asp Gly Glu Cys Val Cys Glu
625 630 635 640

Glu Pro Tyr Thr Gly Glu Asp Cys Arg Glu Leu Arg Cys Pro Gly Asp
645 650 655

Cys Ser Gly Lys Gly Arg Cys Ala Asn Gly Thr Cys Leu Cys Glu Glu
660 665 670

Gly Tyr Val Gly Glu Asp Cys Gly Gln Arg Gln Cys Leu Asn Ala Cys
675 680 685

Ser Gly Arg Gly Gln Cys Glu Glu Gly Leu Cys Val Cys Glu Glu Gly
690 695 700

Tyr Gln Gly Pro Asp Cys Ser Ala Val Ala Pro Pro Ala Ala Ala Met
705 710 715 720

Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro Pro
725 730 735

Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu Asp
740 745 750

Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp Leu
755 760 765

Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser Ala
770 775 780

Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp Phe
785 790 795 800

Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala Ala
805 810 815

Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro Val
820 825 830

Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val Ser
835 840 845

Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro
850 855 860

Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr Pro
865 870 875 880

Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro Lys
885 890 895

Arg Arg Gly Ser Ser Gly Ser Val Ala Ala Ala Arg Ile Tyr Lys Gly
900 905 910

Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala
915 920 925

Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr
930 935 940

Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg
945 950 955 960

Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys
965 970

<210> 13
<211> 1524
<212> DNA
<213> Rattus norvegicus

<400> 13
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ccctgccgtt tcgacttccc ggatgagctc agaccggctg tggtacatgg cgtctggtat 180

ttcaacagtc cctaccccaa gaactacccg ccagtggtct tcaagtcccg cacacaagtg 240

gtccacgaga gcttccaggg ccgtagccgc ctgttgggag acctgggcct acgaaactgc 300

accctgcttc tcagcacgct gagccctgag ctgggaggga aatactattt ccgaggtgac 360

ctgggcggct acaaccagta caccttctcg gagcacagcg tcctggacat catcaacacc 420

cccaacatcg tggtgccccc agaagtggtg gcaggaacgg aagtagaggt cagctgcatg 480

gtgccggaca actgcccaga gctgcgccct gagctgagct ggctgggcca cgaggggcta 540

ggggagccca ctgttctggg tcggctgcgg gaggatgaag gcacctgggt gcaggtgtca 600

ctgctacact tcgtgcctac tagagaggcc aacggccacc gtctgggctg tcaggctgcc 660

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gtgattgtgg agatgaattc ctctgtggag gccattgagg gctcccacgt cagcctgctc 780

tgtggggctg acagcaaccc gccaccgctg ctgacttgga tgcgggatgg gatggtgttg 840

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gtgtactcag agcgcagcgg cctcctgctc accagcatcc tcacgctccg gggtcaggcc 1440

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ctgcctttcc agggagcaca ccga 1524

<210> 14
<211> 615
<212> DNA
<213> Homo sapiens

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gccacaggac aactggacta tatccctcac tgcagtggcc acggcaactt tagctttgag 180

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tacagcgggg atgactgttc cgaactccgg tgcccaacag actgcagctc ccgggggctc 360

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gcagttgccc ctcca 615

<210> 15
<211> 555
<212> DNA
<213> Homo sapiens

<400> 15
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tcctcgggct cagtg 555

<210> 16
<211> 198
<212> DNA
<213> Homo sapiens

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ttagttgatt ctctgaag 198

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<212> DNA
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<220>
<223> PCR primer MAG1

<400> 17
cgggatccat gatattcctt accaccct 28

<210> 18
<211> 28

<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer MAG2

<400> 18
tccccgcggc tcggtgtgct ccctggaa 28

<210> 19
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer TNR1

<400> 19
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<210> 20
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<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer TNR2

<400> 20
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<210> 21
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<212> DNA
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<220>
<223> PCR primer NogoN1

<400> 21
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<210> 22
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<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer NogoN2

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aaactgcagc cactgagccc gaggagcccc t 31

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<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer Nogo66-1

<400> 23
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<210> 24
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer Nogo66-2

<400> 24
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<210> 25
<211> 2934
<212> DNA
<213> Artificial sequence

<220>
<223> Construct resulting from sequentially connected PCR products

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