SEQUENCE LISTING

<110> The University Court of the University of Aberdeen
Wright, Matthew
Porter, Andy

<120> Specific Binding Members Against Synaptophysin

<130> SMK/6287585

<140> PCT/GB2005/001190
<141> 2005-03-29

<150> GB 0407059.5
<151> 2004-03-29

<150> GB 0416402.6
<151> 2004-07-22

<160> 27

<170> PatentIn version 3.1

<210> 1
<211> 356
<212> DNA
<213> Homo sapiens

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gccaggctcc agggaagggg ctggagtggg tctcaactat tgctgcgtcg ggtccttcta 180

cagggtacgc agactccgtg aagggccggt tcaccatctc cagagacaat tccaagaaca 240

cgctgtatct gcaaatgaac agcctgagag ccgaggacac ggccgtatat tactgtgcga 300

aaactacggc gaagtttgac tactggggcc agggaaccct ggtcaccgtc tcgagc 356

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<211> 118
<212> PRT
<213> Homo sapiens

<400> 2

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Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

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

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

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

Tyr Cys Ala Lys Thr Thr Ala Lys Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 3
<211> 339
<212> DNA
<213> Homo sapiens

<400> 3
acggacatcc agatgaccca gtctccatcc tccctgtctg catctgtagg agacagagtc 60

accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa 120

ccagggaaag cccctaagct cctgatctat tctgcatccc gattgcaaag tggggtccca 180

tcaaggttca atggcagtgg atctgggaca gatttcactc tcaccatcag cagtctgcaa 240

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caagggacca aggtggaaat caaacgggcg gccgctgca 339

<210> 4
<211> 113
<212> PRT
<213> Homo sapiens

<400> 4

Thr Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
20 25 30

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Gln Arg Lys Pro
85 90 95

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

Ala

<210> 5
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> C1-3 linker encoding nucleotide sequence

<400> 5
ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggtcg 45

<210> 6
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> C1-3 linker amino acid sequence

<400> 6

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 7
<211> 758
<212> DNA
<213> Artificial sequence

<220>
<223> C1-3 encoding nucleotide sequence

<400> 7
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tgagactctc ctgtgcagcc tctggattca cctttagcag ctatgccatg agctgggtcc 120

gccaggctcc agggaagggg ctggagtggg tctcaactat tgctgcgtcg ggtccttcta 180

cagggtacgc agactccgtg aagggccggt tcaccatctc cagagacaat tccaagaaca 240

cgctgtatct gcaaatgaac agcctgagag ccgaggacac ggccgtatat tactgtgcga 300

aaactacggc gaagtttgac tactggggcc agggaaccct ggtcaccgtc tcgagcggtg 360

gaggcggttc aggcggaggt ggcagcggcg gtggcgggtc gacggacatc cagatgaccc 420

agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcact tgccgggcaa 480

gtcagagcat tagcagctat ttaaattggt atcagcagaa accagggaaa gcccctaagc 540

tcctgatcta ttctgcatcc cgattgcaaa gtggggtccc atcaaggttc aatggcagtg 600

gatctgggac agatttcact ctcaccatca gcagtctgca acctgaagat tttgcaactt 660

actactgtca acagctgcag aggaagccta cgacgttcgg ccaagggacc aaggtggaaa 720

tcaaacgggc ggccgctgca ccatctgtct tcatcttt 758

<210> 8
<211> 252
<212> PRT

<213> Artificial sequence

<220>
<223> C1-3 amino acid sequence

<400> 8

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Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30

Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

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

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

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

Tyr Cys Ala Lys Thr Thr Ala Lys Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Arg Leu Gln Ser Gly Val
            180                 185                 190

Pro Ser Arg Phe Asn Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Leu Gln Arg Lys Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225                 230                 235                 240

Lys Arg Gly Ala Ala Ala Pro Ser Val Phe Ile Phe
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245 250

<210> 9
<211> 15
<212> PRT
<213> Homo sapiens

<400> 9

Tyr Pro Phe Arg Leu His Gln Val Tyr Phe Asp Ala Pro Ser Cys
1 5 10 15

<210> 10
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(15)

<400> 10
agc tat gcc atg agc 15
Ser Tyr Ala Met Ser
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<210> 11
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(51)

<400> 11
act att gct gcg tcg ggt cct tct aca ggg tac gca gac tcc gtg aag 48
Thr Ile Ala Ala Ser Gly Pro Ser Thr Gly Tyr Ala Asp Ser Val Lys
1 5 10 15

ggc 51
Gly

<210> 12
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(21)

<400> 12
act acg gcg aag ttt gac tac 21
Thr Thr Ala Lys Phe Asp Tyr
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<210> 13
<211> 33
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (1)..(33)

<400> 13
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Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 14
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(21)

<400> 14
tct gca tcc cga ttg caa agt 21
Ser Ala Ser Arg Leu Gln Ser
1 5

<210> 15
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(27)

<400> 15
caa cag ctg cag agg aag cct acg acg 27
Gln Gln Leu Gln Arg Lys Pro Thr Thr
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<210> 16
<211> 110
<212> PRT
<213> Artificial sequence

<220>
<223> Entire amino acid sequence for the Human constant kappa domain and 6 Histidine residue purification tag

<400> 16

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
1 5 10 15

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
20 25 30

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
35 40 45

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
50 55 60

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
65 70 75 80

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
85 90 95

Lys Ser Phe Asn Arg Gly Glu Ser His His His His His His
100 105 110

<210> 17
<211> 339
<212> DNA
<213> Homo sapiens

<400> 17
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accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa 120

ccagggaaag cccctaagct cctgatctat tctgcatccc gattgcaaag tggggtccca 180

tcaaggttca gtggcagtgg atctgggaca gatttcactc tcaccatcag cagtgtgcaa 240

cctgaagatt ttgcaactta ctactgtcaa cagctgcaga ggaagctacg acgttcggcc 300

aagggaccag gtggaaatca aacgggcggc cgctgcaca 339

<210> 18
<211> 113
<212> PRT
<213> Homo sapiens

<400> 18

Thr Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
20 25 30

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Gln Arg Lys Leu
85 90 95

Arg Arg Ser Ala Lys Gly Pro Gly Gly Asn Gln Thr Gly Gly Arg Cys
100 105 110

Thr

<210> 19
<211> 755
<212> DNA
<213> Artificial sequence

<220>
<223> An earlier version of the C1-3 encoding nucleotide sequence

<400> 19
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tgagactctc ctgtgcagcc tctggattca cctttagcag ctatgccatg agctgggtcc 120

gccaggctcc agggaagggg ctggagtggg tctcaactat tgctgcgtcg ggtccttcta 180

cagggtacgc agactccgtg aagggccggt tcaccatctc cagagacaat tccaagaaca 240

cgctgtatct gcaaatgaac agcctgagag ccgaggacac ggccgtatat tactgtgcga 300

aaactacggc gaagtttgac tactggggcc agggaaccct ggtcaccgtc tcgagcggtg 360

gaggcggttc aggcggaggt ggcagcggcg gtggcgggtc gacggacatc cagatgaccc 420

agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcact tgccgggcaa 480

gtcagagcat tagcagctat ttaaattggt atcagcagaa accagggaaa gcccctaagc 540

tcctgatcta ttctgcatcc cgattgcaaa gtggggtccc atcaaggttc agtggcagtg 600

gatctgggac agatttcact ctcaccatca gcagtgtgca acctgaagat tttgcaactt 660

actactgtca acagctgcag aggaagctac gacgttcggc caagggacca ggtggaaatc 720

aaacgggcgg ccgctgcaca tctgtcttca tcttt 755

<210> 20
<211> 251
<212> PRT
<213> Artificial sequence

<220>
<223> An earlier version of the C1-3 amino acid sequence

<400> 20

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

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45

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

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

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

Tyr Cys Ala Lys Thr Thr Ala Lys Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Arg Leu Gln Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Val Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Leu Gln Arg Lys Leu Arg Arg Ser Ala Lys Gly Pro Gly Gly Asn Gln
225 230 235 240

Thr Gly Gly Arg Cys Thr Ser Val Phe Ile Phe
245 250

<210> 21
<211> 5
<212> PRT
<213> Homo sapiens

<400> 21

Ser Tyr Ala Met Ser
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<210> 22
<211> 17
<212> PRT
<213> Homo sapiens

<400> 22

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Gly

<210> 23
<211> 7
<212> PRT
<213> Homo sapiens

<400> 23

Thr Thr Ala Lys Phe Asp Tyr
1 5

<210> 24
<211> 11
<212> PRT
<213> Homo sapiens

<400> 24

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 25
<211> 7
<212> PRT
<213> Homo sapiens

<400> 25

Ser Ala Ser Arg Leu Gln Ser
1 5

<210> 26
<211> 9
<212> PRT
<213> Homo sapiens

<400> 26

Gln Gln Leu Gln Arg Lys Pro Thr Thr
1 5

<210> 27
<211> 14
<212> PRT
<213> Homo sapiens

<400> 27

Ala Thr Asp Pro Glu Asn Ile Ile Lys Glu Met Pro Met Cys
1 5 10