SEQUENCE LISTING

<110> SHANGHAI YILE BIOTECHNOLOGY CO., LTD.

<120> Use of Binding Molecule which Specifically Binds to Precursor of Brain-Derived Neurotrophic Factor

<130> 149071PCWO

<160> 37

<170> PatentIn version 3.3

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<223> Heavy chain CDR1

<400> 1

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Phe Ile Arg Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser Ser Ser
1 5 10 15

Val Lys Gly

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<400> 3

Thr Met Asp Tyr
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Gln His Phe Trp Ser Thr Pro Phe Thr
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<400> 7

Glu Val Lys Val Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

```
Gly Phe Ile Arg Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser Ser
    50                  55                  60

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

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

Tyr Cys Ala Ile Thr Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
            100                 105                 110

Val Ser Ser
        115
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Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Lys Lys Gln Gly Lys Ser Pro His Leu Leu Val
        35                  40                  45

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

Ser Ala Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Phe
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
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<400> 9

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Leu Ser Glu Val Lys Val Val Glu Ser Gly Gly Gly Leu Val Gln Pro
            20                  25                  30

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

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

Trp Leu Gly Phe Ile Arg Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr
65                  70                  75                  80

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

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

Thr Tyr Tyr Cys Ala Ile Thr Met Asp Tyr Trp Gly Gln Gly Thr Ser
        115                 120                 125

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
    130                 135                 140

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
145                 150                 155                 160

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
                165                 170                 175

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
            180                 185                 190

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
        195                 200                 205

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
    210                 215                 220

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
225                 230                 235                 240

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
                245                 250                 255
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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        275                 280                 285

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
305                 310                 315                 320

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335

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

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        355                 360                 365

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    370                 375                 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385                 390                 395                 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                405                 410                 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            420                 425                 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        435                 440                 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455                 460


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<223>  Light chain

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Met Asp Met Met Val Leu Ala Gln Phe Leu Ala Phe Leu Leu Leu Trp
1               5                   10                  15
```

```
Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser
            20                  25                  30

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

Gly Asn Ile His Asn Tyr Leu Ala Trp Tyr Gln Lys Lys Gln Gly Lys
    50                  55                  60

Ser Pro His Leu Leu Val Tyr Asn Ala Gln Thr Leu Ala Asp Gly Val
65                  70                  75                  80

Pro Ser Arg Phe Ser Gly Ser Ala Ser Gly Thr Gln Tyr Ser Leu Lys
                85                  90                  95

Ile Asp Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His
            100                 105                 110

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

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145                 150                 155                 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210                 215                 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210>  11
<211>  345
<212>  DNA
<213>  Artificial Sequence


<220>
<221>  misc_feature
<223>  Nucleotide sequence of heavy chain variable region

<400>  11
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gaggtgaagg tggtggagtc tggaggaggc ttggtacagc ctgggggctc tctgagactc 60

tcctgtgcaa cttctgggtt caccttcact gattactaca tgagttgggt ccgccagcct 120

ccaggaaagg cacttgagtg gttgggtttt attagaaaca aagctaatgg ttacacaaca 180

gagtacagtt catctgtgaa gggtcgattc accatctcca gagataattc ccaaagcatc 240

ctctatcttc aaatgaacac cctgagagct gaggacagtg ccacttatta ctgtgcaatc 300

actatggact actggggtca aggaacctca gtcaccgtct cctca 345

<210> 12
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Nucleotide sequence of light chain variable region

<400> 12
gacatccaga tgactcagtc tccagcctcc ctatctgcat ctgtgggaga aactgtcacc 60

atcacatgtc gagcaagtgg gaatattcac aattatttag catggtatca gaagaaacag 120

ggaaaatctc ctcacctcct ggtctataat gcacaaacct tagcagatgg tgtgccatca 180

aggttcagtg gcagtgcatc aggaacacaa tattctctca agatcgacag cctgcagcct 240

gaagattttg ggagttacta ctgtcaacat ttttggagta ctccattcac gttcggctcg 300

gggacaaagt tggaaataaa acgt 324

<210> 13
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
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<223> Nucleotide sequence of heavy chain

<400> 13
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aaggtggtgg agtctggagg aggcttggta cagcctgggg gctctctgag actctcctgt 120

gcaacttctg ggttcacctt cactgattac tacatgagtt gggtccgcca gcctccagga 180

aaggcacttg agtggttggg ttttattaga aacaaagcta atggttacac aacagagtac 240

agttcatctg tgaagggtcg attcaccatc tccagagata attcccaaag catcctctat 300

cttcaaatga acaccctgag agctgaggac agtgccactt attactgtgc aatcactatg 360

gactactggg gtcaaggaac ctcagtcacc gtctcctcag cctccaccaa gggcccatcg 420

gtcttccccc tggcaccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 480

ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 540

agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 600

gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 660

aagcccagca acaccaaggt ggacaagaaa gttgagccca aatcttgtga caaaactcac 720

acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtctt cctcttcccc 780

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 840

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 900

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 960

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1020

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gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1140

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gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1260

ttcctctata gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1320

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ccgggtaaa 1389

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<211> 708
<212> DNA
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<223> Nucleotide sequence of light chain

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agatgtgaca tccagatgac tcagtctcca gcctccctat ctgcatctgt gggagaaact 120

gtcaccatca catgtcgagc aagtgggaat attcacaatt atttagcatg gtatcagaag 180

aaacagggaa aatctcctca cctcctggtc tataatgcac aaaccttagc agatggtgtg 240

ccatcaaggt tcagtggcag tgcatcagga acacaatatt ctctcaagat cgacagcctg 300

cagcctgaag attttgggag ttactactgt caacattttt ggagtactcc attcacgttc 360

ggctcgggga caaagttgga aataaaacgt acggtggctg caccatctgt cttcatcttc 420

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 15
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<400> 15
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<210> 16
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<400> 16
ccgctcgagt tatcttcccc ttttaatggt caatg 35

<210> 17
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<400> 17
gctggctagc acccatgaaa gaagcaaaca tccgag 36

<210> 18
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<400> 18
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<400> 19
gctggctagc gcgcccatga aagaagcaaa c 31

<210> 20

<211> 31
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<400> 20
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<400> 21
catggctaca tgctgacagc cta 23

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<400> 29

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

Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu His Val
35 40 45

Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn Glu Glu
50 55 60

Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu Ser Ser
65 70 75 80

Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu Tyr Lys
85 90 95

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