SEQUENCE LISTING

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JIANG, Hong
ELTORAI, Adam

<120> COMPOSITIONS AND METHODS FOR TREATING AMYLOID PLAQUE ASSOCIATED SYMPTOMS

<130> 047563-434951

<150> US 61/419,060
<151> 2010-12-02

<150> US 61/548,542
<151> 2011-10-18

<160> 39

<170> PatentIn version 3.5

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caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa cgtagaatct 240

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cctgtggagg aggatgatat tgcaatgtat ttctgtcagc aaagtaggaa ggttccgtgg 360

acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 420

atcttcccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg 480

aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 540

aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 600

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cctgagctgg tgaagcctgg ggcttcagtg aagatgtcct gcaaggcttc tggatacaca 180

ttcactgact acaacatgca ctgggtgaag cagagccatg gaaagagcct tgagtggatt 240

ggatatatta accctaacaa tggtggtact agctacaacc agaagttcaa gggcaaggcc 300

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

Val Glu Tyr Tyr Gly Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro
50 55 60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Val Glu Ser
65 70 75 80

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

Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile Ala Met Tyr Phe Cys
100 105 110

Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
115 120 125

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

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

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
                165                 170                 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
            180                 185                 190

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

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

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
        35                  40                  45

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
    50                  55                  60

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

Gly Tyr Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
                85                  90                  95

Lys Gly Lys Ala Thr Leu Thr Val Asn Lys Ser Ser Ser Thr Ala Tyr
            100                 105                 110

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
        115                 120                 125

Thr Leu Leu Ser Pro Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
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130 135 140

Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
145 150 155 160

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
165 170 175

Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
195 200 205

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Gln Thr Val
210 215 220

Thr Cys Asn Val Ala His Pro Ala Ser
225 230

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atgagctgta agtccagtca aagtgtttta tacagttcaa atcagaagaa ctacttggcc 180

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccgctagg 240

aaatctggtg tccctgatcg cttcacaggc agtggatctg ggacagattt tactcttacc 300

atcagcagtg tacaagctga agacctggca gtttattact gtcatcaata cctctcctcg 360

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tccatcttcc caccatccag tgagcagtta acatctggag gtgcctcagt cgtgtgcttc 480

ttgaacaact tctaccccaa agacatcaat gtcaagtgga agattgatgg cagtgaacga 540

caaaatggcg tcctgaacag ttggactgat caggacagca aagacagcac ctacagcatg 600

agcagcaccc tcacgttgac caaggacgag tatgaacgac ataacagcta tacctgtgag 660

gccactcaca agacatcaac ttcacccatt 690

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tgcaaggctt ctgggtatac cttcacagaa tatccaatgc actgggtgaa gcaggctcca 180

ggaaaggatt tcaagtggat gggcatgata tacaccgaca ctggagagcc aacatatgct 240

gaagagttca agggacggtt tgccttctct ttggagacct ctgccaacac tgcctatttg 300

cagatcaaca acctcaaaaa tgaggacacg gctacatatt tctgtgtggg tggttacttg 360

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Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45

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

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg
65 70 75 80

Lys Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110

Tyr Cys His Gln Tyr Leu Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
115 120 125

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

Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe
145                 150                 155                 160

Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp
                165                 170                 175

Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp
            180                 185                 190

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

Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys
    210                 215                 220

Thr Ser Thr Ser Pro Ile
225                 230
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<210> 8
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Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
            20                  25                  30

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Asp Phe
    50                  55                  60

Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Thr Tyr Ala
65                  70                  75                  80

Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn
                85                  90                  95

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr
            100                 105                 110

Tyr Phe Cys Val Gly Gly Tyr Leu Phe Ser Tyr Trp Gly Gln Gly Thr
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115 120 125

Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro
130 135 140

Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly
145 150 155 160

Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn
165 170 175

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

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

Trp Pro Ser Gln Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
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gtcactatca cttgcaaggc gagtgaggac attaatagct atttaagctg gttccagcag 180

aaaccaggga aatctcctaa gaccctgatc tatcgtgcaa acagattggt agatggggtc 240

ccatcaaggt tcagtggcag tggatctggg caagattatt ctctcaccat cagcagcctg 300

gagtatgaag atatgggaat ttattattgt ctacagtatg atgagtttcc tctcacgttc 360

ggtgctggga ccaagctgga gctgacacgg gctgatgctg caccaactgt atccatcttc 420

ccaccatcca gtgagcagtt aacatctgga ggtgcctcag tcgtgtgctt cttgaacaac 480

ttctacccca aagacatcaa tgtcaagtgg aagattgatg gcagtgaacg acaaaatggc 540

gtcctgaaca gttggactga tcaggacagc aaagacagca cctacagcat gagcagcacc 600

ctcacgttga ccaaggacga gtatgaacga cataacagct atacctgtga ggccactcac 660

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aacacccact ctggagagcc aaaatatgca gaagatttca agggacggtt tgccttctct 240

ttggaaacct ctgccagcac tgcctattta cagataagca acctcaaaaa tgaggacacg 300

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Met Asp Met Arg Thr Pro Ala Gln Phe Leu Gly Ile Leu Leu Leu Trp
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Phe Pro Gly Ile Lys Cys Asp Ile Lys Leu Thr Gln Ser Pro Ser Ser
20 25 30

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

Glu Asp Ile Asn Ser Tyr Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys
50 55 60

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

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

Ile Ser Ser Leu Glu Tyr Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln
100 105 110

Tyr Asp Glu Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
115 120 125

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

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

Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu

165 170 175

Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp
180 185 190

Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr
195 200 205

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

Ala Ser Gly Tyr Thr Phe Thr Thr Ala Gly Met Gln Trp Val Gln Lys
35 40 45

Met Pro Gly Lys Gly Phe Lys Trp Ile Gly Trp Ile Asn Thr His Ser
50 55 60

Gly Glu Pro Lys Tyr Ala Glu Asp Phe Lys Gly Arg Phe Ala Phe Ser
65 70 75 80

Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Ser Asn Leu Lys
85 90 95

Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Met Gly Gly Tyr Ala
100 105 110

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys
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Thr Thr Pro Pro Ser
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tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 240

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atcaccaatg tacaagctga agacctggca gtttattact gtcatcaata cctctcctcg 360

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caaaatggcg tcctgaacag ttggactgat caggacagca aagacagcac ctacagcatg 600

agcagcaccc tcacgttgac caaggacgag tatgaacgac ataacagcta tacctgtgag 660

gccactcaca agacatcaac ttcacccatt 690

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gaagagttca agggacggtt tgccttctct ttggagacct ctgccagcac tgcctatttg 300

cagatcaaca acctcaaaaa tgaggacacg gctacatatt tctgtgtagg tggttacttg 360

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            20                  25                  30

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
        35                  40                  45

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

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

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

Phe Thr Leu Thr Ile Thr Asn Val Gln Ala Glu Asp Leu Ala Val Tyr
            100                 105                 110

Tyr Cys His Gln Tyr Leu Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
        115                 120                 125

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

Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe
145                 150                 155                 160

Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp
                165                 170                 175

Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp
            180                 185                 190

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

Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys
    210                 215                 220

Thr Ser Thr Ser Pro Ile
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<400> 16

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

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe
    50                  55                  60

Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Thr Tyr Val
65                  70                  75                  80

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

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr
            100                 105                 110

Tyr Phe Cys Val Gly Gly Tyr Leu Phe Ser Tyr Trp Gly Gln Gly Thr
        115                 120                 125

Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro
    130                 135                 140

Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly
145                 150                 155                 160

Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn
                165                 170                 175

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

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

Trp Pro Ser Gln Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
    210                 215                 220
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Gly Tyr Thr Phe Thr Asp Tyr Asn Met His
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<400> 18

Tyr Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 19
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<400> 19

Arg Ala Ser Glu Ser Val Glu Tyr Tyr Gly Thr Ser Leu Met Gln
1 5 10 15

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Ala Ala Ser Asn Val Glu Ser
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Gln Gln Ser Arg Lys Val Pro Trp Thr

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Gly Tyr Thr Phe Thr Glu Tyr Pro Met His
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<220>
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<400> 23

Met Ile Tyr Thr Asp Thr Gly Glu Pro Thr Tyr Ala Glu Glu Phe Lys
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Gly

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<400> 24

Gly Tyr Leu Phe Ser Tyr
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Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
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Ala

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<400> 26

Trp Ala Ser Ala Arg Lys Ser
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His Gln Tyr Leu Ser Ser Tyr Thr
1 5

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Gly Tyr Thr Phe Thr Thr Ala Gly Met Gln
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<210> 29
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<212> PRT
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<220>
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<400> 29

Trp Ile Asn Thr His Ser Gly Glu Pro Lys Tyr Ala Glu Asp Phe Lys
1 5 10 15

Gly

<210> 30
<211> 8
<212> PRT
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Met Gly Gly Tyr Ala Met Asp Tyr
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<210> 31
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<220>
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His Gln Tyr Leu Ser Ser Tyr Thr

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