EPO - DG 2
07. 06. 2012
59

SEQUENCE LISTING

<110> Bayer Schering Pharma Aktiengesellschaft

<120> Neutralizing prolactin receptor antibody Mat3 and its therapeutic use

<130> BHC113039

<160> 17

<170> PatentIn version 3.5

<210> 1
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> 005-C04-mat3-VH

<400> 1

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

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

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

Ser Asp Ile Ala Arg Leu Ser Ser Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Gly Leu Asp Ala Arg Arg Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 2
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<212> PRT
<213> Artificial Sequence

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<223> 005-C04-mat3-VL

<400> 2

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

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

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65                  70                  75                  80

Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser
                85                  90                  95

Leu Asn Gly Trp Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

Gln
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<210> 3
<211> 354
<212> DNA
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<223> 005-C04-mat3-VH

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gaggtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60

tcctgcgccg cctccggctt caccttctcc agctactgga tgcactgggt ccgacaggcc 120

cctggcaagg gcctggaatg ggtgtccgat atcgcccggc tgtcctccta caccaactac 180

gccgactccg tgaagggccg gttcaccatc tcccgggaca actccaagaa caccctgtac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtgc cagaggcctg 300

gacgccagac ggatggacta ttggggccag ggcaccctgg tcaccgtcag ctca 354

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<211> 339
<212> DNA
<213> Artificial Sequence

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<223> 005-C04-mat3-VL

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cagtccgtgc tgacccagcc tccttccgcc tctggcaccc ctggccagag agtgaccatc 60

tcctgcaccg gctcctccag caacatcggc gctggctacg tggtgcactg gtatcagcag 120

ctgcccggca ccgcccccaa gctgctgatc taccggaaca accagcggcc ctccggcgtg 180

cccgacagat tctccggctc caagtccggc acctccgcct ccctggccat ctccggcctg 240

agatctgagg acgaggccga ctactactgc gccgcctggg acgactccct gaacggctgg 300

ctgttcggcg gaggcaccaa gttaaccgtg ctgggccag 339

<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 005-C04-mat3-HCDR1

<400> 5

Phe Ser Ser Tyr Trp Met His Trp
1 5

<210> 6
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> 005-C04-mat3-HCDR2

<400> 6

Ser Asp Ile Ala Arg Leu Ser Ser Tyr Thr Asn Tyr Ala Asp Ser Val
1 5 10 15

Lys Gly Arg

<210> 7
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 005-C04-mat3-HCDR3

<400> 7

Ala Arg Gly Leu Asp Ala Arg Arg Met Asp Tyr
1 5 10

<210> 8
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 005-C04-mat3-LCDR1

<400> 8

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Val Val His
1 5 10

<210> 9
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> 005-C04-mat3-LCDR2

<400> 9

Arg Asn Asn Gln Arg Pro Ser
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<210> 10
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 005-C04-mat3-LCDR3

<400> 10

Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly Trp
1 5 10

<210> 11
<211> 453
<212> PRT
<213> Macaca fascicularis

<400> 11

Gln Leu Pro Pro Gly Lys Pro Glu Ile Phe Lys Cys Arg Ser Pro Asn
1 5 10 15

Lys Glu Thr Phe Thr Cys Trp Trp Arg Pro Gly Thr Asp Gly Gly Leu
20 25 30

Pro Thr Asn Tyr Ser Leu Thr Tyr His Arg Glu Gly Glu Thr Leu Met
35 40 45

His Glu Cys Pro Asp Tyr Ile Thr Gly Gly Pro Asn Ser Cys His Phe
50 55 60

Gly Lys Gln Tyr Thr Ser Met Trp Arg Thr Tyr Val Met Met Val Asn
65 70 75 80

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

Val Thr Tyr Ile Val Gln Pro Asp Pro Pro Leu Glu Leu Thr Val Glu
100 105 110

Val Lys Gln Pro Glu Asp Arg Lys Pro Tyr Leu Trp Met Lys Trp Ser
115 120 125

Pro Pro Thr Leu Ile Asp Leu Lys Thr Gly Trp Phe Thr Leu Leu Tyr
130 135 140

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Glu Ile Arg Leu Lys Pro Glu Lys Ala Ala Glu Trp Glu Thr His Phe
145                 150                 155                 160

Ala Gly Gln Gln Thr Glu Phe Lys Ile Leu Ser Leu His Pro Gly Gln
                165                 170                 175

Lys Tyr Leu Val Gln Val Arg Cys Lys Pro Asp His Gly Tyr Trp Ser
            180                 185                 190

Ala Trp Ser Pro Ala Thr Phe Ile Gln Ile Pro Ser Asp Phe Ile Met
        195                 200                 205

Asn Asp Ile Glu Gly Arg Met Asp Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415
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Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys His
435 440 445

His His His His His
450

<210> 12
<211> 222
<212> PRT
<213> Homo sapiens

<400> 12

Gln Leu Pro Pro Gly Lys Pro Glu Ile Phe Lys Cys Arg Ser Pro Asn
1 5 10 15

Lys Glu Thr Phe Thr Cys Trp Trp Arg Pro Gly Thr Asp Gly Gly Leu
20 25 30

Pro Thr Asn Tyr Ser Leu Thr Tyr His Arg Glu Gly Glu Thr Leu Met
35 40 45

His Glu Cys Pro Asp Tyr Ile Thr Gly Gly Pro Asn Ser Cys His Phe
50 55 60

Gly Lys Gln Tyr Thr Ser Met Trp Arg Thr Tyr Ile Met Met Val Asn
65 70 75 80

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

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

Val Lys Gln Pro Glu Asp Arg Lys Pro Tyr Leu Trp Ile Lys Trp Ser
115 120 125

Pro Pro Thr Leu Ile Asp Leu Lys Thr Gly Trp Phe Thr Leu Leu Tyr
130 135 140

Glu Ile Arg Leu Lys Pro Glu Lys Ala Ala Glu Trp Glu Ile His Phe
145 150 155 160

Ala Gly Gln Gln Thr Glu Phe Lys Ile Leu Ser Leu His Pro Gly Gln
165 170 175

Lys Tyr Leu Val Gln Val Arg Cys Lys Pro Asp His Gly Tyr Trp Ser
180 185 190

Ala Trp Ser Pro Ala Thr Phe Ile Gln Ile Pro Ser Asp Phe Thr Met

195 200 205

Asn Asp Ile Glu Gly Arg Met Asp His His His His His His
210 215 220

<210> 13
<211> 222
<212> PRT
<213> Mus musculus

<400> 13

Gln Ser Pro Pro Gly Lys Pro Glu Ile His Lys Cys Arg Ser Pro Asp
1 5 10 15

Lys Glu Thr Phe Thr Cys Trp Trp Asn Pro Gly Ser Asp Gly Gly Leu
20 25 30

Pro Thr Asn Tyr Ser Leu Thr Tyr Ser Lys Glu Gly Glu Lys Asn Thr
35 40 45

Tyr Glu Cys Pro Asp Tyr Lys Thr Ser Gly Pro Asn Ser Cys Phe Phe
50 55 60

Ser Lys Gln Tyr Thr Ser Ile Trp Lys Ile Tyr Ile Ile Thr Val Asn
65 70 75 80

Ala Thr Asn Glu Met Gly Ser Ser Thr Ser Asp Pro Leu Tyr Val Asp
85 90 95

Val Thr Tyr Ile Val Glu Pro Glu Pro Pro Arg Asn Leu Thr Leu Glu
100 105 110

Val Lys Gln Leu Lys Asp Lys Lys Thr Tyr Leu Trp Val Lys Trp Leu
115 120 125

Pro Pro Thr Ile Thr Asp Val Lys Thr Gly Trp Phe Thr Met Glu Tyr
130 135 140

Glu Ile Arg Leu Lys Ser Glu Glu Ala Asp Glu Trp Glu Ile His Phe
145 150 155 160

Thr Gly His Gln Thr Gln Phe Lys Val Phe Asp Leu Tyr Pro Gly Gln
165 170 175

Lys Tyr Leu Val Gln Thr Arg Cys Lys Pro Asp His Gly Tyr Trp Ser
180 185 190

Arg Trp Gly Gln Glu Lys Ser Ile Glu Ile Pro Asn Asp Phe Thr Leu
195 200 205

Lys Asp Ile Glu Gly Arg Met Asp His His His His His His
210 215 220

<210> 14
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> VH protein

<400> 14

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

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

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

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

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

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

Ala Arg His Arg Gly Asn Tyr Tyr Ala Thr Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 15
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> VL protein

<400> 15

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

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Gly Tyr Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Arg Glu Ser Gly Val Pro Asp
50 55 60

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

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

Glu Leu Pro Pro Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

Ala

<210> 16
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> VH DNA

<400> 16
gaggtgcagc tcgtggagtc tggcggcgga ctggtgcagc ctggcggcag cctgagactg 60

agctgcgccg tgagcggctt caccttcagc agctacggca tgagctgggt gcgccaggct 120

cctggcaagg gactggaatg ggtggccacc gtgtccagcg gcggcaccta cacctactac 180

cccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc cagacaccgg 300

ggcaactact acgccaccta ctactatgcc atggactact ggggccaggg caccctggtg 360

accgtgagct ca 372

<210> 17
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> VL DNA

<400> 17
gatatcgtgc tgacccagag ccccgacagc ctggccgtga gcctgggcga gcgggccacc 60

atcaactgca aggccagcaa gtccgtgagc accagcggct acacctacat gcactggtat 120

cagcagaagc ccggccagcc ccccaagctg ctgatctacc tggccagcaa ccgggagagc 180

ggcgtgcccg accggtttag cggcagcggc tccggcaccg acttcaccct gaccatcagc 240

cccgtgcagg ccgaggacgt ggccacctac tactgccagc acagcggcga gctgcccccc 300

agcttcggcc agggcaccaa gctggaaatc aagcgggcc 339