SEQUENCE LISTING

<110> UCB PHARMA S.A.
Adams, Ralph
Popplewell, Andrew
Rapecki, Stephen

<120> Antibody molecules which bind IL-17A and IL-17F

<130> G0035-WO01

<160> 20

<170> PatentIn version 3.3

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<213> Rattus rattus

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Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Leu Val Ser Asn Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

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

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

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

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<223> gL7

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ggcaaagccc ccaagctcct gatctatctg gtttccaatc gggagtctgg agtccccagc 180

aggttcagcg gcagtgggtc tggaactgac tttaccctga caatctcctc actccagccc 240

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser 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 Ser Pro Pro Gln Tyr Tyr Glu Gly Ser Ile Tyr Arg Leu Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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cgggattcag tgaaagggcg atttaccatc agcagggata atgcaaagaa cagtctgtac 240

ctgcagatga actctctgag agctgaggac accgctgtct actattgtgc aagcccaccc 300

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Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Glu Ser Val Thr Thr Leu

20 25 30

Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

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

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

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
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<213> Artificial

<220>
<223> Signal+gL7+constant domain

<400> 12

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1 5 10 15

Asp Ala Arg Cys Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

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

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Trp
100 105 110

Ser Asp Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

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

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

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

225 230

<210> 13
<211> 645
<212> DNA
<213> Artificial

<220>
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ggcaaagccc ccaagctcct gatctatctg gtttccaatc gggagtctgg agtccccagc 180

aggttcagcg gcagtgggtc tggaactgac tttaccctga caatctcctc actccagccc 240

gaagatttcg ccacctacta ttgccagcag acttggagcg acccttggac atttggacag 300

ggcacaaaag tggagatcaa gcgtacggta gcggccccat ctgtcttcat cttcccgcca 360

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ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

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<223> signal+gL7+constant domain

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attacctgca gggctgacga aagcgtgacc acattgatgc actggtacca acagaagcct 180

ggcaaagccc ccaagctcct gatctatctg gtttccaatc gggagtctgg agtccccagc 240

aggttcagcg gcagtgggtc tggaactgac tttaccctga caatctcctc actccagccc 300

gaagatttcg ccacctacta ttgccagcag acttggagcg acccttggac atttggacag 360

ggcacaaaag tggagatcaa gcgtacggta gcggccccat ctgtcttcat cttcccgcca 420

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 480

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gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 600

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660

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<211> 452
<212> PRT
<213> Artificial

<220>
<223> gH9+constant domain

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser 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 Ser Pro Pro Gln Tyr Tyr Glu Gly Ser Ile Tyr Arg Leu Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

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Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                  165                 170                 175

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

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

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
     210                 215                 220

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu
225                 230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                  245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
             260                 265                 270

Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
         275                 280                 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
     290                 295                 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
                  325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
             340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
         355                 360                 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
     370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400
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Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
405 410 415

Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Leu Gly Lys
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<210> 16
<211> 471
<212> PRT
<213> Artificial

<220>
<223> signal+gH9+constant domain

<400> 16

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Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

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

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

Glu Trp Val Ala Thr Ile Thr Tyr Glu Gly Arg Asn Thr Tyr Tyr Arg
65 70 75 80

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

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

Tyr Tyr Cys Ala Ser Pro Pro Gln Tyr Tyr Glu Gly Ser Ile Tyr Arg
115 120 125

Leu Trp Phe Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

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

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
165 170 175

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

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
210 215 220

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

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
340 345 350

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
370 375 380

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

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Leu Gly Lys
465 470

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<212> DNA
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<220>
<223> gH9+constant domain

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cgggattcag tgaaagggcg atttaccatc agcagggata atgcaaagaa cagtctgtac 240

ctgcagatga actctctgag agctgaggac accgctgtct actattgtgc aagcccaccc 300

cagtactatg agggctcaat ctacagattg tggtttgccc attggggcca gggaacactg 360

gtgaccgtct cgagcgcttc tacaaagggc ccatccgtct tccccctggc gccctgctcc 420

aggagcacct ccgagagcac agccgccctg ggctgcctgg tcaaggacta cttccccgaa 480

ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540

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ttgggcacga agacctacac ctgcaacgta gatcacaagc ccagcaacac caaggtggac 660

aagagagttg gtgagaggcc agcacaggga gggagggtgt ctgctggaag ccaggctcag 720

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cgcatacagg ggcaggtgct gcgctcagac ctgccaagag ccatatccgg gaggaccctg 960

cccctgacct aagcccaccc caaaggccaa actctccact ccctcagctc agacaccttc 1020

tctcctccca gatctgagta actcccaatc ttctctctgc agagtccaaa tatggtcccc 1080

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ggtgccctag agtagcctgc atccagggac aggccccagc cgggtgctga cgcatccacc 1200

tccatctctt cctcagcacc tgagttcctg gggggaccat cagtcttcct gttcccccca 1260

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gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 1380

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tgtgccaacc tctgtcccta cagggcagcc ccgagagcca caggtgtaca ccctgccccc 1680

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cacgcctccc gtgctggact ccgacggctc cttcttcctc tacagcaggc taaccgtgga 1860

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ggcaagggtc tggagtgggt ggccacaatt acctatgagg gcagaaacac ttattaccgg 240

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cagatgaact ctctgagagc tgaggacacc gctgtctact attgtgcaag cccaccccag 360

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accgtctcga gcgcttctac aaagggccca tccgtcttcc ccctggcgcc ctgctccagg 480

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gccaacctct gtccctacag ggcagccccg agagccacag gtgtacaccc tgcccccatc 1740

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gcctcccgtg ctggactccg acggctcctt cttcctctac agcaggctaa ccgtggacaa 1920

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<223> IL-17A/F heterodimer

<400> 19

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Lys Asn Phe Pro Arg Thr Val Met Val Asn Leu Asn Ile His Asn Arg
20 25 30

Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser Asp Tyr Tyr Asn Arg Ser
35 40 45

Thr Ser Pro Trp Asn Leu His Arg Asn Glu Asp Pro Glu Arg Tyr Pro
50 55 60

Ser Val Ile Trp Glu Ala Lys Cys Arg His Leu Gly Cys Ile Asn Ala
65 70 75 80

Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln Gln Glu
85 90 95

Ile Leu Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser Phe Arg
100 105 110

Leu Glu Lys Ile Leu Val Ser Val Gly Cys Thr Cys Val Thr Pro Ile
115 120 125

Val His His Val Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Lys Ile Pro Lys Val Gly
145 150 155 160

His Thr Phe Phe Gln Lys Pro Glu Ser Cys Pro Pro Val Pro Gly Gly
165 170 175

Ser Met Lys Leu Asp Ile Gly Ile Ile Asn Glu Asn Gln Arg Val Ser
180 185 190

Met Ser Arg Asn Ile Glu Ser Arg Ser Thr Ser Pro Trp Asn Tyr Thr
195 200 205

Val Thr Trp Asp Pro Asn Arg Tyr Pro Ser Glu Val Val Gln Ala Gln
210 215 220

Cys Arg Asn Leu Gly Cys Ile Asn Ala Gln Gly Lys Glu Asp Ile Ser
225 230 235 240

Met Asn Ser Val Pro Ile Gln Gln Glu Thr Leu Val Val Arg Arg Lys
245 250 255

His Gln Gly Cys Ser Val Ser Phe Gln Leu Glu Lys Val Leu Val Thr
260 265 270

Val Gly Cys Thr Cys Val Thr Pro Val Ile His His Val Gln
275 280 285

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<220>
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<400> 20

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Ser Cys Pro Pro Val Pro Glu Gly Ser Met Lys Leu Asp Thr Gly Ile
20 25 30

Ile Asn Glu Asn Gln Arg Val Ser Met Ser Arg Asn Ile Glu Ser Arg
35 40 45

Ser Thr Ser Pro Trp Asn Tyr Thr Val Thr Trp Asp Pro Asn Arg Tyr
50 55 60

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

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Ala Gln Gly Lys Glu Asp Ile Ser Met Asn Ser Val Pro Ile Gln Gln
                85                  90                  95

Glu Thr Leu Val Leu Arg Arg Lys His Gln Gly Cys Ser Val Ser Phe
            100                 105                 110

Gln Leu Glu Lys Val Leu Val Thr Val Gly Cys Thr Cys Val Thr Pro
        115                 120                 125

Val Ile His His Val Gln
    130
```