SEQUENCE LISTING

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<120> METHODS OF TREATING PSORIASIS USING IL-17 BINDING MOLECULES

<130> 54389

<140> Herewith
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<151> 2010-10-08

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<170> PatentIn version 3.3

<210> 1
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<220>
<223> CDR1 = hypervariable region 1 of heavy chain of AIN457

<400> 1

Asn Tyr Trp Met Asn
1 5

<210> 2
<211> 17
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDR2 = hypervariable region 2 of heavy chain of AIN457

<400> 2

Ala Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Gly Ser Val Lys
1 5 10 15

Gly

<210> 3
<211> 18

<212> PRT
<213> ARTIFICIAL

<220>
<223> CDR3 = hypervariable region 3 of heavy chain of AIN457

<400> 3

Asp Tyr Tyr Asp Ile Leu Thr Asp Tyr Tyr Ile His Tyr Trp Tyr Phe
1 5 10 15

Asp Leu

<210> 4
<211> 12
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDR1' = hypervariable region 1 of light chain of AIN457

<400> 4

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 5
<211> 7
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDR2' = hypervariable region 2 of light chain AIN457

<400> 5

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 6
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<213> ARTIFICIAL

<220>
<223> CDR3' = hypervariable region 3 of light chain AIN457

<400> 6

Gln Gln Tyr Gly Ser Ser Pro Cys Thr
1 5

<210> 7
<211> 381
<212> DNA
<213> HOMO SAPIENS

<220>
<221> CDS
<222> (1)..(381)

<400> 7

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gag gtg cag ttg gtg gag tct ggg gga ggc ttg gtc cag cct ggg ggg       48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agt aac tat       96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30

tgg atg aac tgg gtc cgc cag gct cca ggg aaa ggg ctg gag tgg gtg      144
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

gcc gcc ata aac caa gat gga agt gag aaa tac tat gtg ggc tct gtg      192
Ala Ala Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Gly Ser Val
    50                  55                  60

aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat      240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

ctg caa atg aac agc ctg aga gtc gag gac acg gct gtg tat tac tgt      288
Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gtg agg gac tat tac gat att ttg acc gat tat tac atc cac tat tgg      336
Val Arg Asp Tyr Tyr Asp Ile Leu Thr Asp Tyr Tyr Ile His Tyr Trp
            100                 105                 110

tac ttc gat ctc tgg ggc cgt ggc acc ctg gtc act gtc tcc tca          381
Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 8
<211> 127
<212> PRT
<213> HOMO SAPIENS

<400> 8

```
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 Ala Ser Gly Phe Thr Phe Ser Asn Tyr
```

```
            20                  25                  30

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

Ala Ala Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Gly 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 Val Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Val Arg Asp Tyr Tyr Asp Ile Leu Thr Asp Tyr Tyr Ile His Tyr Trp
            100                 105                 110

Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 9
<211> 327
<212> DNA
<213> HOMO SAPIENS

<220>
<221> CDS
<222> (1)..(327)

<400> 9

```
gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg       48
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc       96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc      144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt      192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag      240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80
```

```
cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca ccg      288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

tgc acc ttc ggc caa ggg aca cga ctg gag att aaa cga                  327
Cys Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
            100                 105
```

<210> 10
<211> 109
<212> PRT
<213> HOMO SAPIENS

<400> 10

```
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

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

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

Cys Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
            100                 105
```

<210> 11
<211> 10
<212> PRT
<213> artificial

<220>
<223> CDR1-x = hypervariable domain x of heavy chain of AIN457

<400> 11

```
Gly Phe Thr Phe Ser Asn Tyr Trp Met Asn
1               5                   10
```

<210> 12
<211> 11
<212> PRT
<213> artificial

<220>
<223> CDR2-x = hypervariable domain of heavy chain x of AIN457

<400> 12

Ala Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr
1 5 10

<210> 13
<211> 23
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDR3-x = hypervariable domain x of heavy chain AIN457

<400> 13

Cys Val Arg Asp Tyr Tyr Asp Ile Leu Thr Asp Tyr Tyr Ile His Tyr
1 5 10 15

Trp Tyr Phe Asp Leu Trp Gly
20

<210> 14
<211> 711
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (1)..(708)

<400> 14

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acc atg gaa acc cca gcg gag ctt ctc ttc ctc ctg cta ctc tgg ctc       48
Thr Met Glu Thr Pro Ala Glu Leu Leu Phe Leu Leu Leu Leu Trp Leu
1               5                  10                  15

cca gat acc acc gga gaa att gtg ttg acg cag tct cca ggc acc ctg       96
Pro Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
            20                  25                  30

tct ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag      144
Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
        35                  40                  45
```

```
agt gtt agc agc agc tac tta gcc tgg tac cag cag aaa cct ggc cag      192
Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
    50                  55                  60

gct ccc agg ctc ctc atc tat ggt gca tcc agc agg gcc act ggc atc      240
Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
65                  70                  75                  80

cca gac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc      288
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
                85                  90                  95

atc agc aga ctg gag cct gaa gat ttt gca gtg tat tac tgt cag cag      336
Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
            100                 105                 110

tat ggt agc tca ccg tgc acc ttc ggc caa ggg aca cga ctg gag att      384
Tyr Gly Ser Ser Pro Cys Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
        115                 120                 125

aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat      432
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac      480
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145                 150                 155                 160

ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc      528
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac      576
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac      624
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc      672
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210                 215                 220

tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag                  711
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
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<210> 15
<211> 236
<212> PRT
<213> homo sapiens

<400> 15

Thr Met Glu Thr Pro Ala Glu Leu Leu Phe Leu Leu Leu Leu Trp Leu

```
1               5                   10                  15

Pro Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
            20                  25                  30

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

Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
    50                  55                  60

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

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

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
            100                 105                 110

Tyr Gly Ser Ser Pro Cys Thr Phe Gly Gln Gly Thr Arg 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
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<210> 16
<211> 783
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (1)..(780)

<400> 16

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acc atg gaa ttg ggg ctg agc tgg gtt ttc ctt gtt gct att tta gaa       48
Thr Met Glu Leu Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Glu
1               5                   10                  15

ggt gtc cac tgt gag gtg cag ttg gtg gag tct ggg gga ggc ttg gtc       96
Gly Val His Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
            20                  25                  30

cag cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc      144
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
        35                  40                  45

ttt agt aac tat tgg atg aac tgg gtc cgc cag gct cca ggg aaa ggg      192
Phe Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

ctg gag tgg gtg gcc gcc ata aac caa gat gga agt gag aaa tac tat      240
Leu Glu Trp Val Ala Ala Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr
65                  70                  75                  80

gtg ggc tct gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag      288
Val Gly Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
                85                  90                  95

aac tca ctg tat ctg caa atg aac agc ctg aga gtc gag gac acg gct      336
Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala
            100                 105                 110

gtg tat tac tgt gtg agg gac tat tac gat att ttg acc gat tat tac      384
Val Tyr Tyr Cys Val Arg Asp Tyr Tyr Asp Ile Leu Thr Asp Tyr Tyr
        115                 120                 125

atc cac tat tgg tac ttc gat ctc tgg ggc cgt ggc acc ctg gtc act      432
Ile His Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
    130                 135                 140

gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc      480
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
145                 150                 155                 160

tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc      528
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
                165                 170                 175
```

```
aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc      576
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
            180                 185                 190

ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga      624
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
        195                 200                 205

ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc      672
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
    210                 215                 220

acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag      720
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
225                 230                 235                 240

gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa act cac aca tgc      768
Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
                245                 250                 255

cca ccg tgc cca taa                                                 783
Pro Pro Cys Pro
            260
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<210> 17
<211> 260
<212> PRT
<213> homo sapiens

<400> 17

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Thr Met Glu Leu Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Glu
1               5                   10                  15

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

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

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

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

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

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala
```

```
            100                 105                 110

Val Tyr Tyr Cys Val Arg Asp Tyr Tyr Asp Ile Leu Thr Asp Tyr Tyr
        115                 120                 125

Ile His Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
    130                 135                 140

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
                165                 170                 175

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
            180                 185                 190

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

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

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

Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
                245                 250                 255

Pro Pro Cys Pro
            260
```