

SEQUENCE LISTING

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 Guettner, Achim

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

<130> 54389

<140> Herewith

<141> Herewith

<150> 61/391388

<151> 2010-10-08

<160> 17

<170> PatentIn version 3.3

<210> 1

<211> 5

<212> PRT

<213> artificial

<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
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 <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
 <211> 9
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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
 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

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<210> 9
<211> 327
<212> DNA
<213> HOMO SAPIENS
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<220>
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<222> (1)..(327)
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- 82 -

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

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

<400> 14
 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

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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

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<400> 15
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Thr Met Glu Thr Pro Ala Glu Leu Leu Phe Leu Leu Leu Leu Trp Leu
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Pro	Asp	Thr	Thr	Gly	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu				
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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									

<210> 16
 <211> 783
 <212> DNA
 <213> homo sapiens

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

<400> 16
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 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

<210> 17
 <211> 260
 <212> PRT
 <213> homo sapiens

<400> 17

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