

037 WO_ST25
SEQUENCE LISTING

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<120> Anti-Inflammatory Agents

<130> 037WO

<150> EP 09155484

<151> 2009-03-18

<150> EP 08171920

<151> 2008-12-17

<150> EP 08157547

<151> 2008-06-04

<160> 46

<170> Patent In version 3.5

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Ser Ser Ile Ser Trp Thr Gly Asp Asp Ile Tyr Glu Ala Asp Ser Leu
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Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
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Leu Gln Leu Ser Ser Leu Thr Pro Asp Asp Thr Ala Val Tyr Tyr Cys
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 Tyr Ile Cys Asn 85 Val Asn His Lys Pro Ser 90 Asn Thr Lys Val Asp 95 Lys
 Lys Val Glu 100 Pro Lys Ser Cys Asp Lys 105 Thr His Thr Cys Pro 110 Pro Cys
 Pro Ala Pro 115 Glu Leu Leu Gly Gly 120 Pro Ser Val Phe Leu 125 Phe Pro Pro
 Lys Pro 130 Lys Asp Thr Leu Met 135 Ile Ser Arg Thr Pro 140 Glu Val Thr Cys
 Val 145 Val Val Asp Val Ser 150 His Glu Asp Pro Glu 155 Val Lys Phe Asn Trp 160
 Tyr Val Asp Gly 165 Val Glu Val His Asn Ala 170 Lys Thr Lys Pro Arg 175 Glu
 Glu Gln Tyr Asn 180 Ser Thr Tyr Arg Val 185 Val Ser Val Leu Thr 190 Val Leu
 His Gln Asp 195 Trp Leu Asn Gly Lys 200 Glu Tyr Lys Cys Lys 205 Val Ser Asn
 Lys Ala 210 Leu Pro Ala Pro Ile 215 Glu Lys Thr Ile Ser 220 Lys Ala Lys Gly
 Gln 225 Pro Arg Glu Pro Gln 230 Val Tyr Thr Leu Pro 235 Pro Ser Arg Asp Glu 240
 Leu Thr Lys Asn Gln 245 Val Ser Leu Thr Cys 250 Leu Val Lys Gly Phe 255 Tyr
 Pro Ser Asp Ile 260 Ala Val Glu Trp Glu 265 Ser Asn Gly Gln Pro 270 Glu Asn
 Asn Tyr Lys 275 Thr Thr Pro Pro Val 280 Leu Asp Ser Asp Gly 285 Ser Phe Phe

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Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
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Ile Tyr Asp Asp Asn Lys Arg Pro Ser Gly Ile Pro Gly Arg Phe Ser
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Gly Ser Lys Ser Ala Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
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35 40 45

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
50 55 60

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

Ile Tyr Asp Asp Asn Lys Arg Pro Ser Gly Ile Pro Gly Arg Phe Ser
50 55 60

Gly Ser Lys Ser Ala Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
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Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
35 40 45

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
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55

60

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
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Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
85 90 95

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
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20 25 30

Phe Met Asn Trp Val Arg Gln Ser Arg Gly Lys Gly Leu Glu Trp Ile
35 40 45

Ser Ser Ile Ser Trp Thr Gly Asp Asp Ile Tyr Glu Ala Asp Ser Leu
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Pro Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Arg Gln Tyr Arg Asp Gly Arg Gly Tyr Val Val Asn Asp
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 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
 50 55 60
 Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile
 65 70 75 80
 Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
 85 90 95
 Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
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 Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
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 Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
 130 135 140
 Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
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 Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
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 His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
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 Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly
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 Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
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 Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
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 Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
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 Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe
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1 5 10 15

Thr Leu Ser Leu Thr Cys His Val Ser Gly Tyr Ser Ile Ser Asp Gly
20 25 30

Tyr Tyr Trp Gly Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp
35 40 45

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

His Lys Ser Arg Val Ser Leu Leu Ile Asp Thr Ser Lys Asn Gln Leu
65 70 75 80

Ser Leu Lys Met His Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr
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Cys Ala Arg Gly Leu His Ile Asp Gly Trp Asn Asp Ala Phe Glu Ile
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Trp Gly Arg Gly Thr Met Val Thr Val Ser Ser
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Gln Ser Val Leu Thr Gln Pro Ser Ser Val Ser Gly Thr Pro Gly Gln
1 5 10 15

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

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

Met Tyr Glu Asp Asp Glu Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Met Ser Asp Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Gly Glu Tyr Tyr Cys Ser Ala Trp Asp Asp Ser Phe
85 90 95

Arg Gly Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 43
<211> 369

<212> DNA
 <213> homo sapi ens

<400> 43
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 t ccccaggga agggact gga gt ggat t ggg agt aggcac c at ggggggaa cgccacct t c 180
 t acaat ccgt cacacaagag t cgagt cagc ct ct t aat t g acacct ccaa gaaccagt t g 240
 t ccct gaaga t gcact ct gt gaccgccgca gacacggcca t t t act act g t gcgagaggg 300
 ct t cat at cg at ggt t ggaa cgat gct t t t gagat ct ggg gccgagggac cacggt cacc 360
 gt gt cgt ca 369

<210> 44
 <211> 330
 <212> DNA
 <213> homo sapi ens

<400> 44
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 ccaggacagg ct cccaaact cct cat gt ct t gggat agt g t gct gt cct c aggggt ct ct 180
 gaccgat t ct caggct ccaa at ct ggcacc t cagcct ccc t ggccat cag t gggct ccag 240
 gct gaggat g aggcct gat t a t t act gt gca gt t t gggat g act cagt gga t ggt t gggg t 300
 t t cggcggag ggaccaagct gaccgt cct a 330

<210> 45
 <211> 369
 <212> DNA
 <213> homo sapi ens

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 t ccccaggga agggact gga gt ggat t ggg agt aggcac c at ggggggaa cgccacct t c 180
 t acaat ccgt cacacaagag t cgagt cagc ct ct t aat t g acacct ccaa gaaccagt t g 240
 t ccct gaaga t gcact ct gt gaccgccgca gacacggcca t t t act act g t gcgagaggg 300
 ct t cat at cg at ggt t ggaa cgat gct t t t gagat ct ggg gccgagggac aat ggt cacc 360
 gt gt cgt ca 369

<210> 46
 <211> 330
 <212> DNA
 <213> homo sapi ens

<400> 46
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gcaggaacgg cccccaaact gct cat gt ac gaagat gat g agcggccct c aggggt t cct	180
gaccgat t ct ct ggct ccat gt ct gacacc t cggcct cac t ggccat cag t ggact ccag	240
t ct gaggat g aggggt gaat a t t act gt t ca gcct gggat g acagt t t cag aggggt gggcg	300
t t cggcggag ggaccaagct gaccgt cct a	330