SEQUENCE LISTING

<110> Maksymowych, Walter P. *et al.*

<120> METHODS AND COMPOSITIONS FOR DIAGNOSING ANKYLOSING SPONDYLITIS USING BIOMARKERS

<130> BBI-235PC

<140> PCT/US06/42564
<141> 2006-10-31

<150> 60/732444
<151> 2005-11-1

<160> 37

<170> FastSEQ for Windows Version 4.0

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<220>
<223> D2E7 light chain variable region

<400> 1
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Thr Leu Gln 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 Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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<220>
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<400> 2
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
50 55 60

Glu 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 Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<221> VARIANT
<222>)9
<223> Xaa = Thr or Ala

<400> 3
Gln Arg Tyr Asn Arg Ala Pro Tyr Xaa
1 5

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<220>
<223> D2E7 heavy chain variable region CDR3

<221> VARIANT
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<223> Xaa = Tyr or Asn

<400> 4
Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Xaa
1 5 10

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<400> 5
Ala Ala Ser Thr Leu Gln Ser
1 5

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<223> D2E7 heavy chain variable region CDR2

<400> 6
Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu
 1   5   10   15
Gly

<210> 7
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<220>
<223> D2E7 light chain variable region CDR1

<400> 7
Arg Ala Ser Gln Gly Ile Arg Asn Tyr Leu Ala
 1   5   10

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<223> D2E7 heavy chain variable region CDR1

<400> 8
Asp Tyr Ala Met His
 1   5

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<220>
<223> 2SD4 light chain variable region

<400> 9
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Thr Leu Gln 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 Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Tyr
                85   90   95
Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

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<400> 10
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20   25   30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val
        35   40   45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
    50   55   60
Glu Gly Arg Phe Ala Val Ser Arg Asp Asn Ala Lys Asn Ala Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Thr Lys Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Asn Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

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<220>
<223> 2SD4 light chain variable region CDR3

<400> 11
Gln Lys Tyr Asn Ser Ala Pro Tyr Ala
 1   5

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<400> 12
Gln Lys Tyr Asn Arg Ala Pro Tyr Ala
 1   5

<210> 13
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<220>
<223> VL10E4 light chain variable region CDR3

<400> 13
Gln Lys Tyr Gln Arg Ala Pro Tyr Thr
1 5

<210> 14
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<220>
<223> VL100A9 light chain variable region CDR3

<400> 14
Gln Lys Tyr Ser Ser Ala Pro Tyr Thr
1 5

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<212> PRT
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<220>
<223> VLL100D2 light chain variable region CDR3

<400> 15
Gln Lys Tyr Asn Ser Ala Pro Tyr Thr
1 5

<210> 16
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<220>
<223> VLL0F4 light chain variable region CDR3

<400> 16
Gln Lys Tyr Asn Arg Ala Pro Tyr Thr
1 5

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<223> LOE5 light chain variable region CDR3

<400> 17
Gln Lys Tyr Asn Ser Ala Pro Tyr Tyr
1 5

<210> 18
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<223> VLLOG7 light chain variable region CDR3

<400> 18
Gln Lys Tyr Asn Ser Ala Pro Tyr Asn
1 5

<210> 19
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<220>
<223> VLLOG9 light chain variable region CDR3

<400> 19
Gln Lys Tyr Thr Ser Ala Pro Tyr Thr
1 5

<210> 20
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<212> PRT
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<220>
<223> VLLOH1 light chain variable region CDR3

<400> 20
Gln Lys Tyr Asn Arg Ala Pro Tyr Asn
1 5

<210> 21
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<220>
<223> VLLOH10 light chain variable region CDR3

<400> 21
Gln Lys Tyr Asn Ser Ala Ala Tyr Ser
1 5

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<220>
<223> VL1B7 light chain variable region CDR3

<400> 22
Gln Gln Tyr Asn Ser Ala Pro Asp Thr
1 5

<210> 23
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<223> VL1C1 light chain variable region CDR3

<400> 23
Gln Lys Tyr Asn Ser Asp Pro Tyr Thr
1 5

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<223> VL0.1F4 light chain variable region CDR3

<400> 24
Gln Lys Tyr Ile Ser Ala Pro Tyr Thr
1 5

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<223> VL0.1H8 light chain variable region CDR3

<400> 25
Gln Lys Tyr Asn Arg Pro Pro Tyr Thr
1 5

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<220>
<223> LOE7.A light chain variable region CDR3

<400> 26
Gln Arg Tyr Asn Arg Ala Pro Tyr Ala
1 5

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<400> 27
Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Asn
1 5 10

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<220>
<223> VH1B11 heavy chain variable region CDR3

<400> 28
Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Lys
1 5 10

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<220>
<223> VH1D8 heavy chain variable region CDR3

<400> 29
Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Tyr
1 5 10

<210> 30
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<220>
<223> VH1A11 heavy chain variable region CDR3

<400> 30
Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Asp
1 5 10

<210> 31
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<223> VH1B12 heavy chain variable region CDR3

<400> 31
Ala Ser Tyr Leu Ser Thr Ser Phe Ser Leu Asp Tyr
1 5 10

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<400> 32
Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu His Tyr
 1   5   10

<210> 33
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<220>
<223> VH1F6 heavy chain variable region CDR3

<400> 33
Ala Ser Phe Leu Ser Thr Ser Ser Ser Leu Glu Tyr
 1   5   10

<210> 34
<211> 12
<212> PRT
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<220>
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<400> 34
Ala Ser Tyr Leu Ser Thr Ala Ser Ser Leu Glu Tyr
 1   5   10

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<220>
<223> VH1-D2.N heavy chain variable region CDR3

<400> 35
Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Asn
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<400> 36
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atcacttgtc gggcaagtca gggcatcaga aattacttag cctggtatca gcaaaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct 180
cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctacagcct 240

gaagatgttg caacttatta ctgtcaaagg tataaccgtg caccgtatac ttttggccag 300
gggaccaagg tggaaatcaa a 321

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<400> 37
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ccggcaggtc cctgagactc 60
tcctgtgcgg cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
ccagggaagg gcctggaatg ggtctcagct atcacttgga atagtggtca catagactat 180
gcggactctg tggagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggat acggccgtat attactgtgc gaaagtctcg 300
taccttagca ccgcgtcctc ccttgactat tggggccaag gtaccctggt caccgtctcg 360
agt 363
1

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