FIG. 1A

New LDP02 Heavy DNA – – contains cloning sites (lower case),Kozak sequence (upper case) and Leader (lower case)

gaattctcgagatcgatCTCACCatgggatggagctgtatcatcctcttcttggtagcaacagctacaggtgtccactcccag
gtgCAATTGGTGCAGTCTGGGGGCTGAGGTTAAGAAGCCTGGGGGCTTCAGTGAA
GGTGTCCTGCAAGGGTTCTGGCTACACCTTCACCAGCTACTGGATGCATTGGG
TGAGGCAGGCGCCTGGCCAACGTCTAGAGTGGATCGGAGAGATTGATCCTTC
TGAGAGTAATACTAACTACAATCAAAAAATTCAAGGGACGCGTCACATTGACT
GTAGACATTTCCGCTAGCACAGCCTACATGGAGCTCTCCAGCCTGAGATCTG
AGGACACTGCGGTCTACTATTGTGCAAGAGGGGGGTTACGACGGATGGGACTA
TGCTATTGACTACTGGGGTCAAGGCACCCTGGTCACCGTCAGCTCAGCCTCCA
CCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGG
GGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGC
TGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCT
CCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG
CAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCAC
ACATGCCCACCGTGCCCAGCACCTGAACTCGCGGGGGCACCGTCAGTCTTCC
TCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACT
GGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG
AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCA
GGACTGGCTGAATGGC

AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA
AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT
GCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTG
GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC
AGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTC
CTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG
AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA
GAAGAGCCTCTCCCTGTCTCCGGGTAAAtaatctagagca

New LDP02 Heavy Protein (space between VHL, VH and Human IgG1-FcRmut)
MGWSCIILFLVATATGVHS
QVQLVQSGAEVKKPGASVKVSCKGSGYTFTSYWMHWVRQAPGQRLEWIGEIDP
SESNTNYNQKFKGRVTLTVDISASTAYMELSSLRSEDTAVYYCARGGYDGWDY
AIDYWGQGTLVTVSS
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

FIG. 1B

SUBSTITUTE SHEET (RULE 26)

FIG. 2

New LDP02 Light DNA – contains cloning sites (lower case),Kozak sequence (upper case) and Leader (lower case)

gaattctcgagatcgatCTCACCatgggatggagctgtatcatcctcttcttggtagcaacagctacaggtgtccactcgat
GTAGTGATGACTCAAAGTCCACTCTCCCTGCCTGTCACCCCTGGAGAACCAGC
TTCTATCTCTTGCAGGTCTAGTCAGAGTCTTGCAAAGAGTTATGGGAACACCT
ATTTGTCTTGGTACCTGCAGAAGCCTGGCCAGTCTCCACAGCTCCTCATCTAT
GGGATTTCCAACACAGATTTTCTGGGGTGCCAGACAGGTTCAGTGGCAGTGGTT
CAGGGACAGATTTCACACTCAAGATCTCGCGAGTAGAGGCTGAGGACGTGGG
AGTGTATTACTGCTTACAAGGTACACATCAGCCGTACACGTTCGGACAGGGG
ACCAAGGTGGAGATCAAGCGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
GCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA
ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
CCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGGCAGGACAGCAAGGACAG
CACCTACAGCCTCAGCAGCACCCTGACCCTGAGCAAAGCAGACTACGAGAAA
CACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCA
CAAAGAGCTTCAACAGGGGAGAGTGTTagtctagagcagc

New LDP02 Light Protein (space between VKL, VK and Human C Kappa)

MGWSCIILFLVATATGVHS
DVVMTQSPLSLPVTPGEPASISCRSSQSLAKSYGNTYLSWYLQKPGQSPQLLIYGI
SNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGTHQPYTFGQGTKVEI
K
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE
SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIG. 3

PAIRWISE newMLN02-no sig LDP-02-no sig.txt

```
A   1 DVVMTQSPLSLPVTPGEPASISCRSSQSLAKSYGNTYLSWYLQKPGQSPQ  50
      |||||||||||||||||||||||||||||||||||||||||||||||||||
B   1 DVVMTQSPLSLPVTPGEPASISCRSSQSLAKSYGNTYLSWYLQKPGQSPQ  50

     51 LLIYGISNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGTHQP 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||
     51 LLIYGISNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGTHQP 100

    101 YTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK 150
        |||||||||||||||||||||||||||||||||||||||||||||||||||
    101 YTFGQGTKVEIKRADAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK 150

    151 VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE 200
        |||||||||||||||||||||||||||||||||||||||||||||||||||
    151 VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE 200

    201 VTHQGLSSPVTKSFNRGEC 219
        |||||||||||||||||||
    201 VTHQGLSSPVTKSFNRGEC 219
```

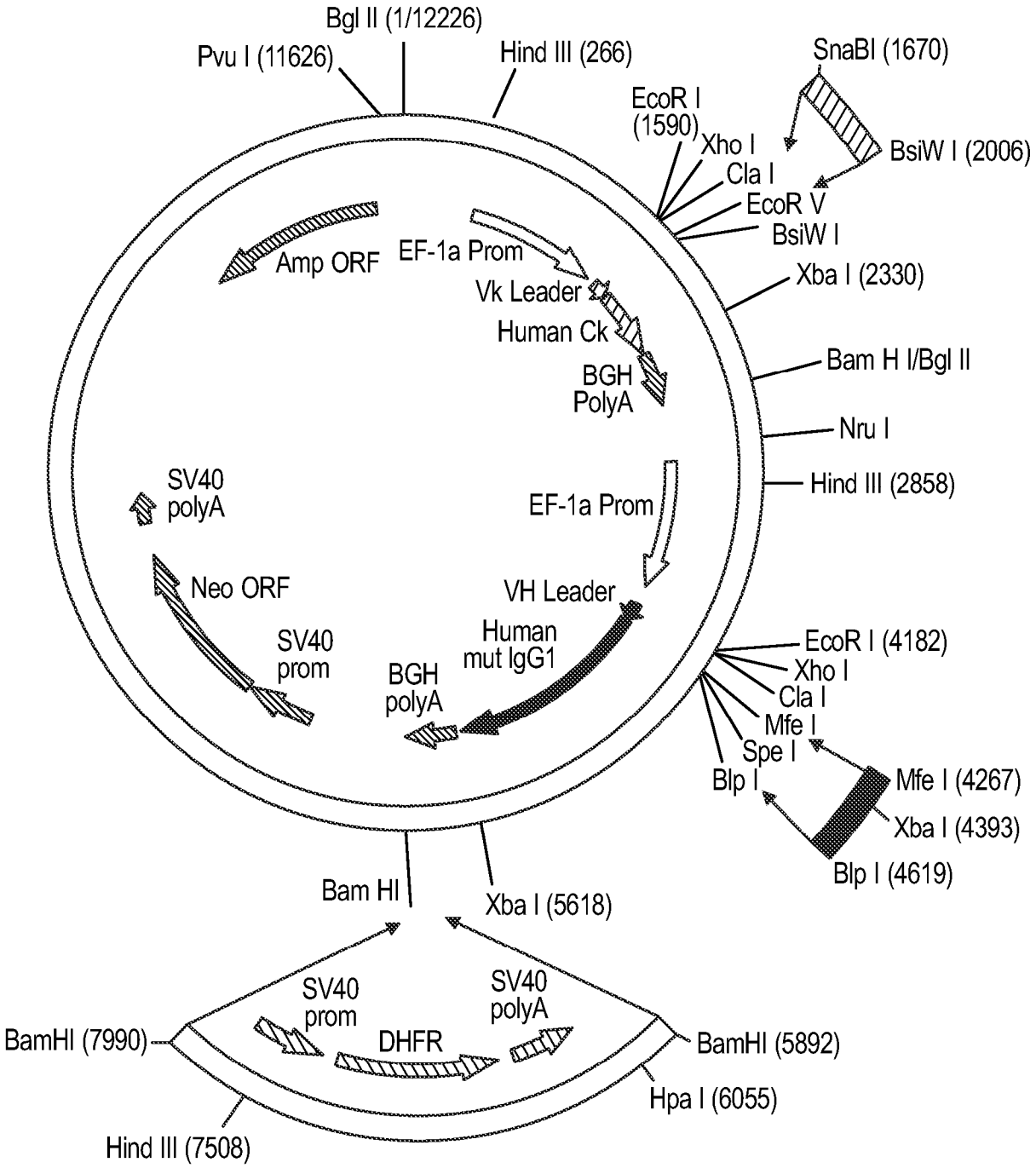
FIG. 4

Pairwise Hum kappa-const MI:Mur kappa-const.txt

```
A   1 rtvaapsvfifppsdeqlksgtasvvcllnnfypreakvqwkvdnalqsg  50
      |   |||.|  |||||  |||  ||  ||||||||::  |.||:|  . .
B   1 radaaptvsifppsseqltsggasvvcflnnfypkdinvkwkidgserqn  50

     51 nsqesvteqdskdstyslsstltlskadyekhkvyacevthqglsspvtk 100
          |  |:|||||||||||:|||||||.| :|||:|   | ||  ||. .||:| |
     51 gvlnswtdqdskdstysmsstltltkdeyerhnsytceathktstspivk 100

    101 sfnrgec 107
          |||||  ||
    101 sfnrnec 107
```



pLKTOK38D

FIG. 5

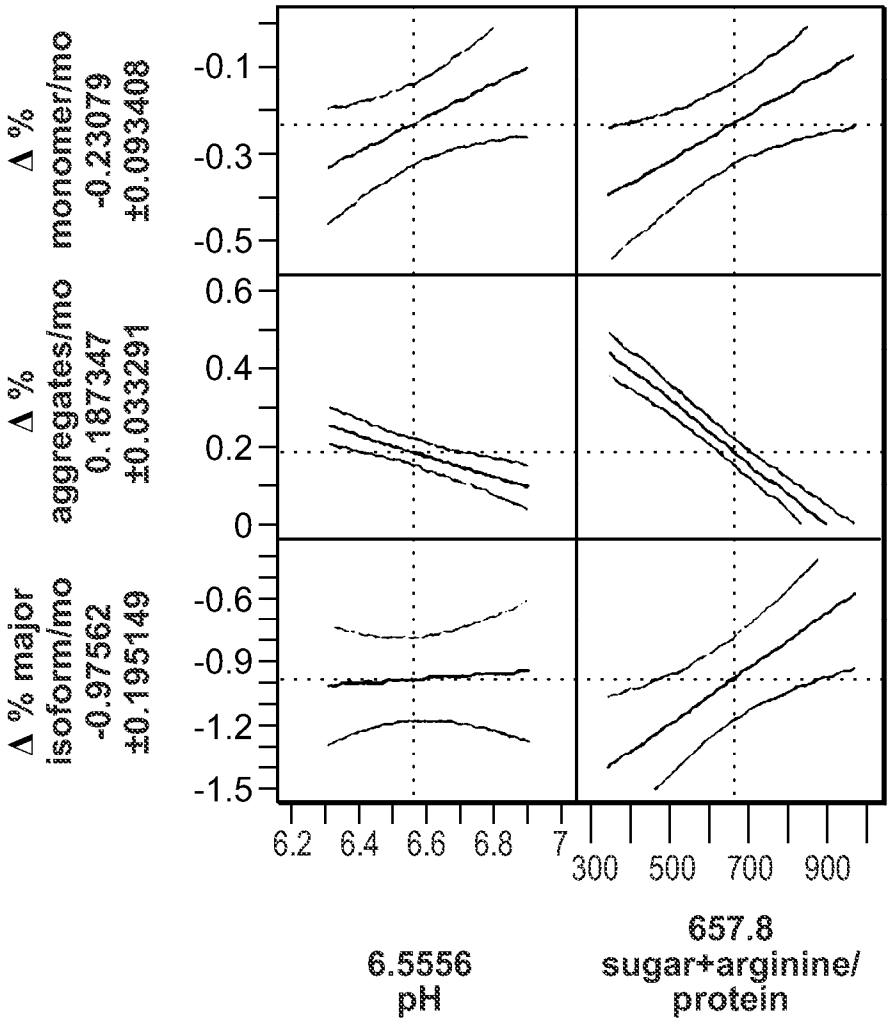
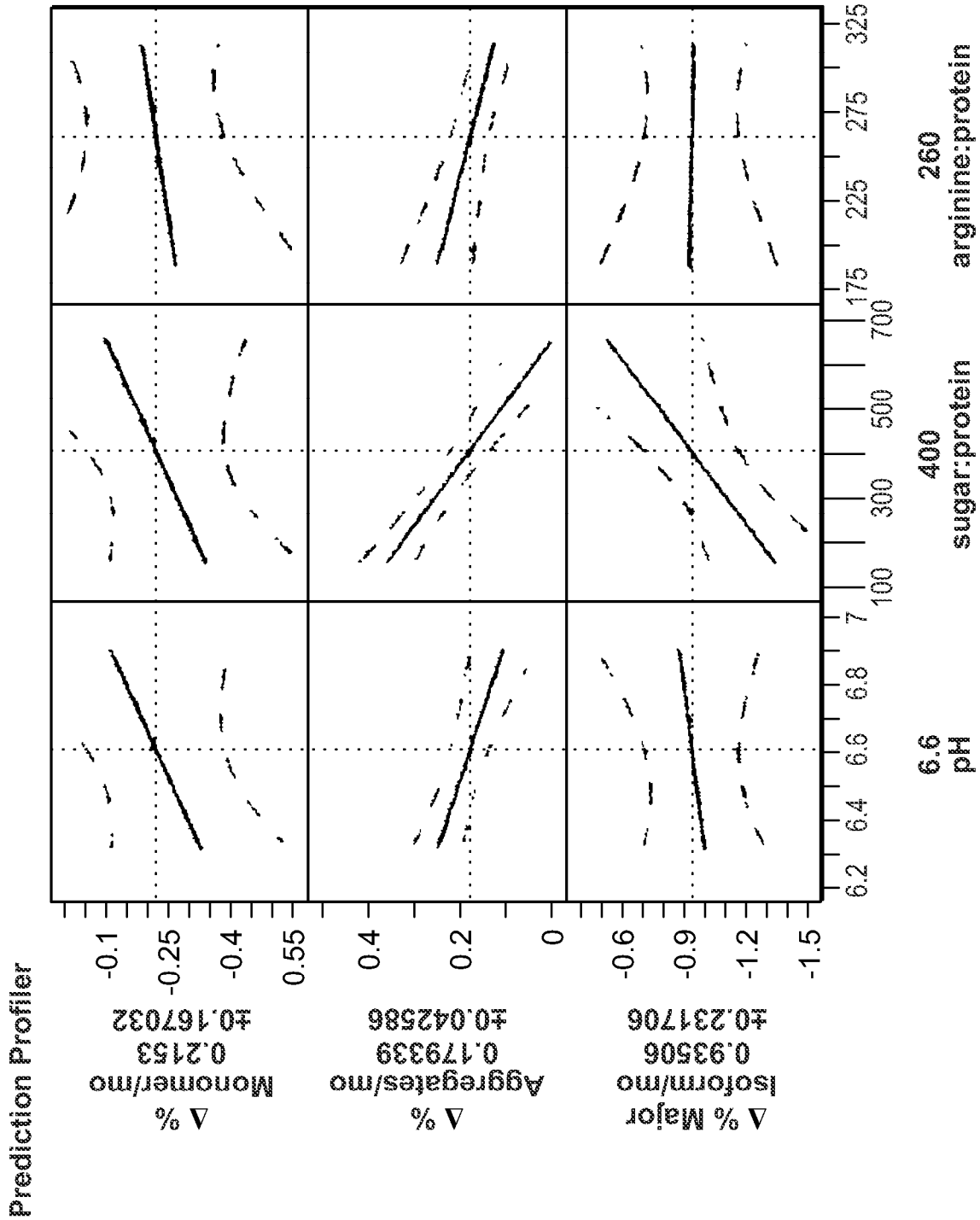

Δ % monomer/mo
-0.23079
±0.093408
Δ % aggregates/mo
0.187347
±0.033291
Δ % major isoform/mo
-0.97562
±0.195149
-0.1
-0.3
-0.5
0.6
0.4
0.2
0
-0.6
-0.9
-1.2
-1.5
6.2
6.4
6.6
6.8
7
300
500
700
900
6.5556
pH
657.8
sugar+arginine/
protein

FIG. 6A

FIG. 6B


Prediction Profiler
Δ % Major isoform/mo
0.93506
±0.231706
Δ % Aggregates/mo
0.179339
±0.042586
Δ % Monomer/mo
0.2153
±0.167032
-1.5
-1.2
-0.9
-0.6
0
0.2
0.4
0.55
-0.4
-0.25
-0.1
6.2
6.4
6.6
6.8
7
100
300
500
700
175
225
275
325
6.6
pH
400
sugar:protein
260
arginine:protein

GM607'Cl antibody kappa light chain variable region

SEQ ID NO: 14

FIG. 7

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20                  25                  30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
    50                  55                  60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85                  90                  95

Leu Gln Thr Pro Gln Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
```

21/28'CL antibody heavy chain variable region

SEQ ID NO: 15

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

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

Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Gly Tyr Tyr Gly Ser Gly Ser Asn Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
```

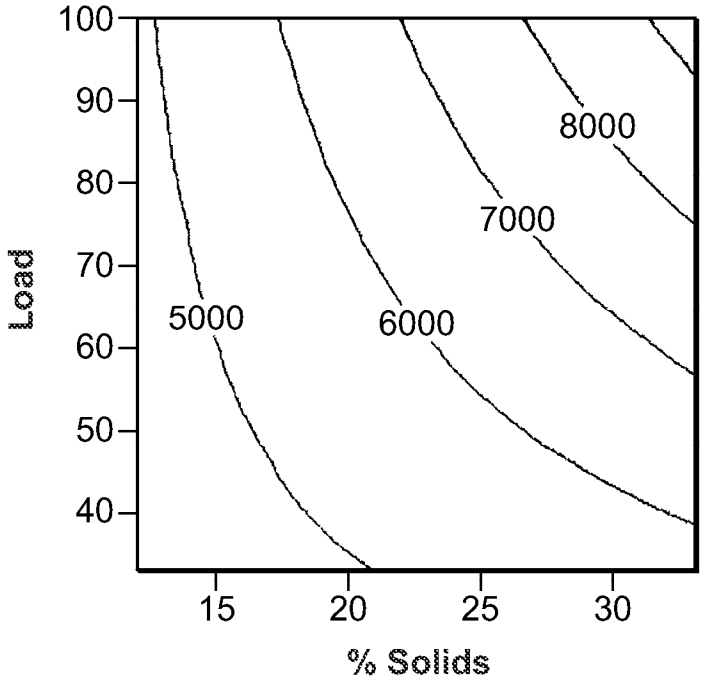

100
90
80
70
60
50
40
Load
8000
7000
6000
5000
15
20
25
30
% Solids

FIG. 8

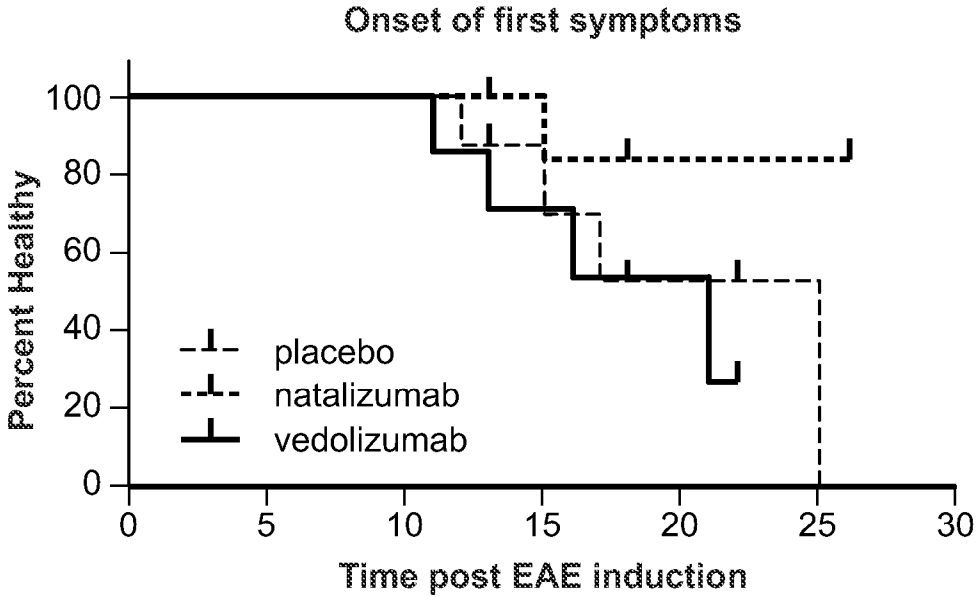

Onset of first symptoms
100
80
60
40
20
0
Percent Healthy
placebo
natalizumab
vedolizumab
0
5
10
15
20
25
30
Time post EAE induction

FIG. 9

SEQUENCE LISTING

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<120> FORMULATION FOR ANTI-ALPHA-4-BETA-7 ANTIBODY

<130> 079259-0615

<140>

<141>

<150> 61/585,859

<151> 2012-01-12

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<151> 2011-10-24

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<151> 2011-05-02

<160> 15

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<210> 1

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ctggggcttc agtgaaggtg tcctgcaagg gttctggcta caccttcacc agctactgga 180

tgcattgggt gaggcaggcg cctggccaac gtctagagtg gatcggagag attgatcctt 240

ctgagagtaa tactaactac aatcaaaaat tcaagggacg cgtcacattg actgtagaca 300

tttccgctag cacagcctac atggagctct ccagcctgag atctgaggac actgcggtct 360

actattgtgc aagagggggt tacgacggat gggactatgc tattgactac tggggtcaag 420

gcaccctggt caccgtcagc tcagcctcca ccaagggccc atcggtcttc cccctggcac 480

cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc aaggactact 540

tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc gtgcacacct 600

tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg accgtgccct 660

ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc agcaacacca 720

aggtggacaa gaaagttgag cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc 780

cagcacctga actcgcgggg gcaccgtcag tcttcctctt cccccccaaaa cccaaggaca 840

ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg agccacgaag 900

accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat gccaagacaa 960

agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc accgtcctgc 1020

accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa gccctcccag 1080

cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca caggtgtaca 1140

ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc tgcctggtca 1200

aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag ccggagaaca 1260

actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc tacagcaagc 1320

tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg 1380

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gagca 1445

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<211> 470

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe

35 40 45

Thr Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu

50 55 60

Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn

65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Ile Ser Ala Ser

85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val

100 105 110

Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp

115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys

130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly

145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro

165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr

180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val

195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn

210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro

225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu

245 250 255

Leu Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

275 280 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly

290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn

305 310 315 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp

325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro

340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu

355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn

370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr

405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys

435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu

450 455 460

Ser Leu Ser Pro Gly Lys

465 470

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<221> source

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cagctacagg tgtccactcc gatgtagtga tgactcaaag tccactctcc ctgcctgtca 120

cccctggaga accagcttct atctcttgca ggtctagtca gagtcttgca aagagttatg 180

ggaacaccta tttgtcttgg tacctgcaga agcctggcca gtctccacag ctcctcatct 240

atgggatttc caacagattt tctggggtgc cagacaggtt cagtggcagt ggttcaggga 300

cagatttcac actcaagatc tcgcgagtag aggctgagga cgtgggagtg tattactgct 360

tacaaggtac acatcagccg tacacgttcg gacaggggac caaggtggag atcaagcgta 420

cggtggctgc accatctgtc ttcatcttcc cgccatctga tgagcagttg aaatctggaa 480

ctgcctctgt tgtgtgcctg ctgaataact tctatcccag agaggccaaa gtacagtgga 540

aggtggataa cgccctccaa tcgggtaact cccaggagag tgtcacagag caggacagca 600

aggacagcac ctacagcctc agcagcaccc tgaccctgag caaagcagac tacgagaaac 660

acaaagtcta cgcctgcgaa gtcacccatc agggcctgag ctcgcccgtc acaaagagct 720

tcaacagggg agagtgttag tctagagcag c 751

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20 25 30

Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu

35 40 45

Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro

50 55 60

Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe Ser

65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys

100 105 110

Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val

115 120 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro

130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu

145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn

165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser

180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala

195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly

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Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

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polypeptide"

<400> 5

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly

1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Ala Lys Ser

20 25 30

Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Gly

85 90 95

Thr His Gln Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105 110

Arg Ala Asp Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln

145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser

165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu

180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser

195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 6

<211> 107

<212> PRT

<213> Homo sapiens

<400> 6

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln

35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser

50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu

65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser

85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

100 105

<210> 7

<211> 107

<212> PRT

<213> Mus sp.

<400> 7

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu

1 5 10 15

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe

20 25 30

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

50 55 60

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu

65 70 75 80

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

100 105

<210> 8

<211> 5

<212> PRT

<213> Mus sp.

<400> 8

Ser Tyr Trp Met His

1 5

<210> 9

<211> 17

<212> PRT

<213> Mus sp.

<400> 9

Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn Gln Lys Phe Lys

1 5 10 15

Gly

<210> 10

<211> 12

<212> PRT

<213> Mus sp.

<400> 10

Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp Tyr

1 5 10

<210> 11

<211> 16

<212> PRT

<213> Mus sp.

<400> 11

Arg Ser Ser Gln Ser Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser

1 5 10 15

<210> 12

<211> 7

<212> PRT

<213> Mus sp.

<400> 12

Gly Ile Ser Asn Arg Phe Ser

1 5

<210> 13

<211> 9

<212> PRT

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Leu Gln Gly Thr His Gln Pro Tyr Thr

1 5

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<211> 111

<212> PRT

<213> Homo sapiens

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Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly

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Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser

20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala

85 90 95

Leu Gln Thr Pro Gln Thr Phe Gly Gln Gly Lys Val Glu Ile Lys

100 105 110

<210> 15

<211> 119

<212> PRT

<213> Homo sapiens

<400> 15

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met

35 40 45

Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe

50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Gly Tyr Tyr Gly Ser Gly Ser Asn Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115