FIG. 1A

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

gaattctcgagatcgatCTCACCatgggatggagctgtatcatcctcttcttggtagcaacagctacaggtgtccactcccag
gtgCAATTGGTGCAGTCTGGGGCTGAGGTTAAGAAGCCTGGGGCTTCAGTGAA
GGTGTCCTGCAAGGGTTCTGGCTACACCTTCACCAGCTACTGGATGCATTGGG
TGAGGCAGGCGCCTGGCCAACGTCTAGAGTGGATCGGAGAGATTGATCCTTC
TGAGAGTAATACTAACTACAATCAAAAATTCAAGGGACGCGTCACATTGACT
GTAGACATTTCCGCTAGCACAGCCTACATGGAGCTCTCCAGCCTGAGATCTG
AGGACACTGCGGTCTACTATTGTGCAAGAGGGGGTTACGACGGATGGGACTA
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

FIG. 2

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

gaattctcgagatcgatCTCACCatgggatggagctgtatcatcctcttcttggtagcaacagctacaggtgtccactccgat
GTAGTGATGACTCAAAGTCCACTCTCCCTGCCTGTCACCCCTGGAGAACCAGC
TTCTATCTCTTGCAGGTCTAGTCAGAGTCTTGCAAAGAGTTATGGGAACACCT
ATTTGTCTTGGTACCTGCAGAAGCCTGGCCAGTCTCCACAGCTCCTCATCTAT
GGGATTTCCAACAGATTTTCTGGGGTGCCAGACAGGTTCAGTGGCAGTGGTT
CAGGGACAGATTTCACACTCAAGATCTCGCGAGTAGAGGCTGAGGACGTGGG
AGTGTATTACTGCTTACAAGGTACACATCAGCCGTACACGTTCGGACAGGGG
ACCAAGGTGGAGATCAAGCGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC
GCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA
ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
CCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAG
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

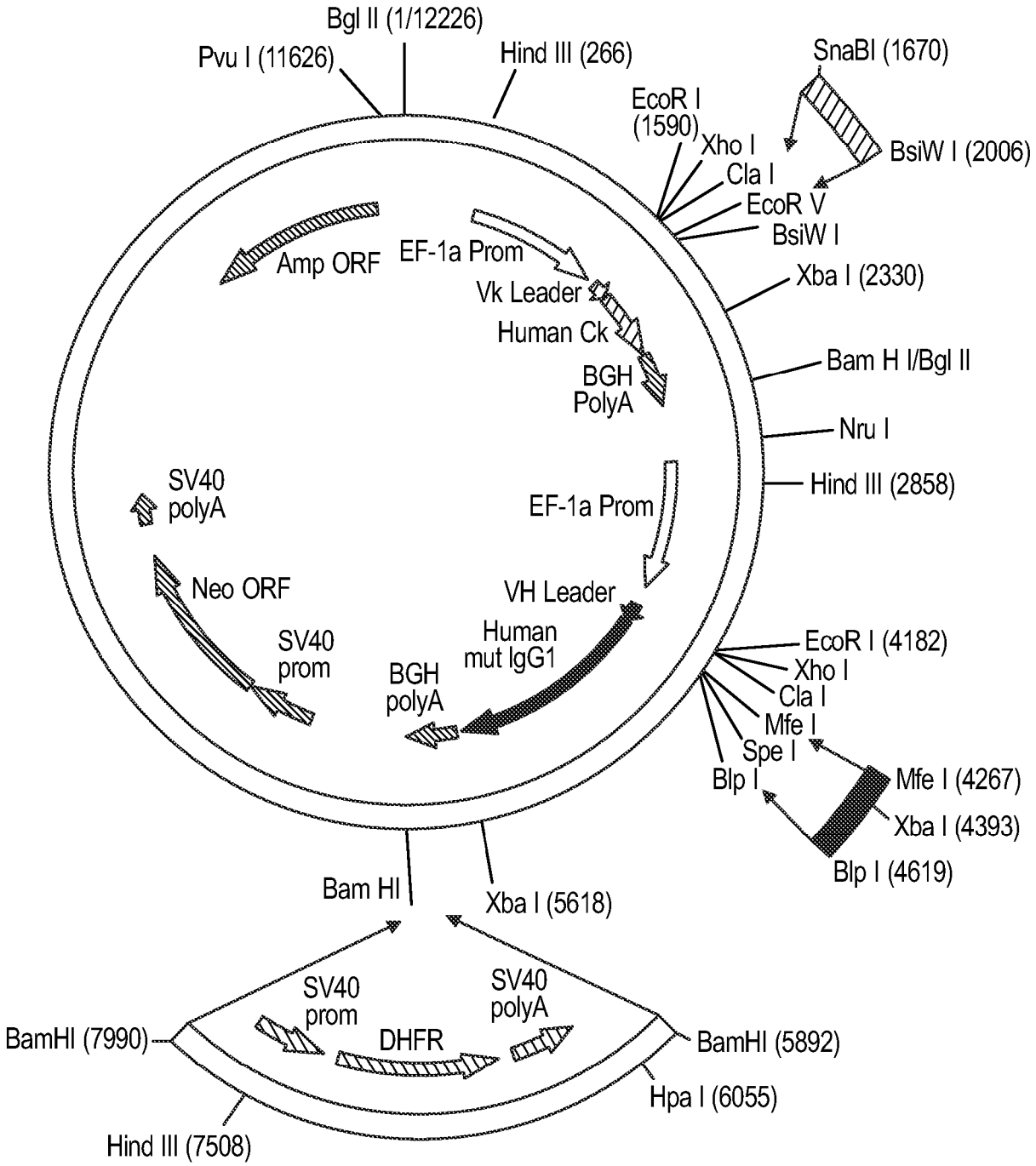
```
A   1 DVVMTQSPLSLPVTPGEPASISCRSSQSLAKSYGNTYLSWYLQKPGQSPQ  50
      ||||||||||||||||||||||||||||||||||||||||||||||||||
B   1 DVVMTQSPLSLPVTPGEPASISCRSSQSLAKSYGNTYLSWYLQKPGQSPQ  50
                .         .         .         .         .
 51   LLIYGISNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGTHQP 100
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 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

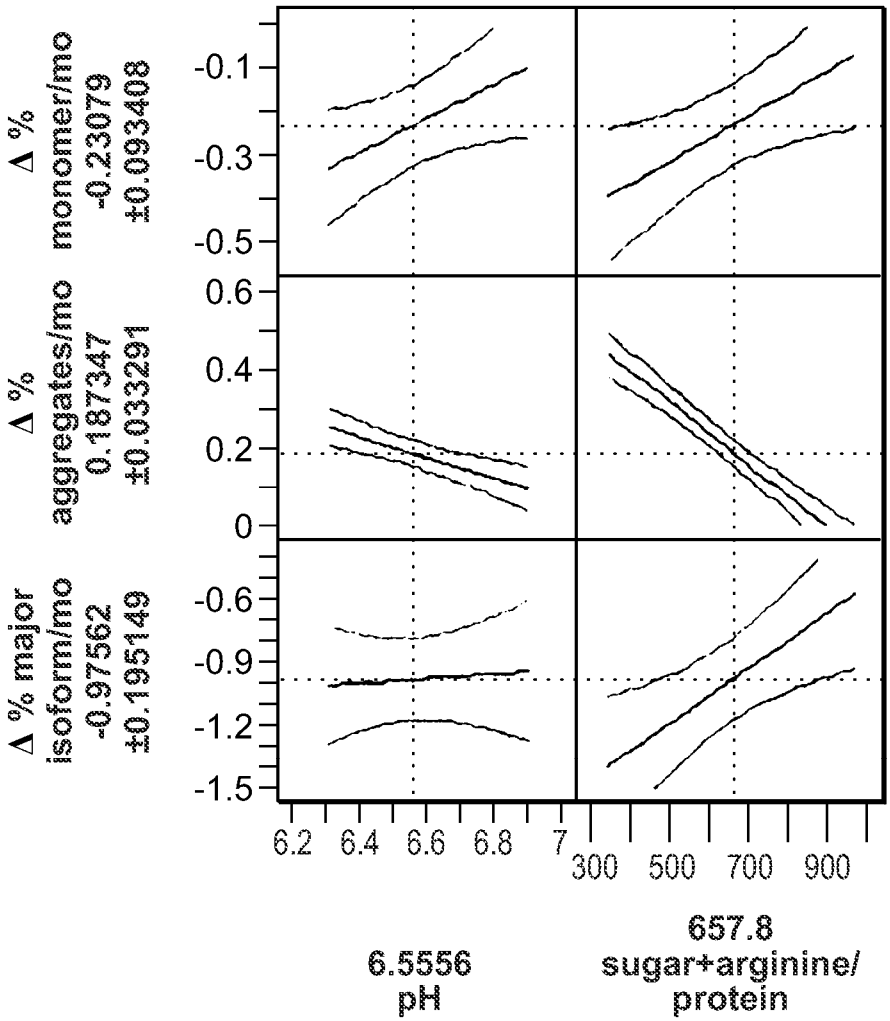

Δ % monomer/mo
-0.23079
±0.093408
Δ % aggregates/mo
0.187347
±0.033291
Δ % major isoform/mo
-0.97562
±0.195149
-0.1
-0.3
-0.5
0.6
0.4
0.2
0
-0.6
-0.9
-1.2
-1.5
6.2
6.4
6.6
6.8
7
300
500
700
900
6.5556
pH
657.8
sugar+arginine/
protein

FIG. 6A

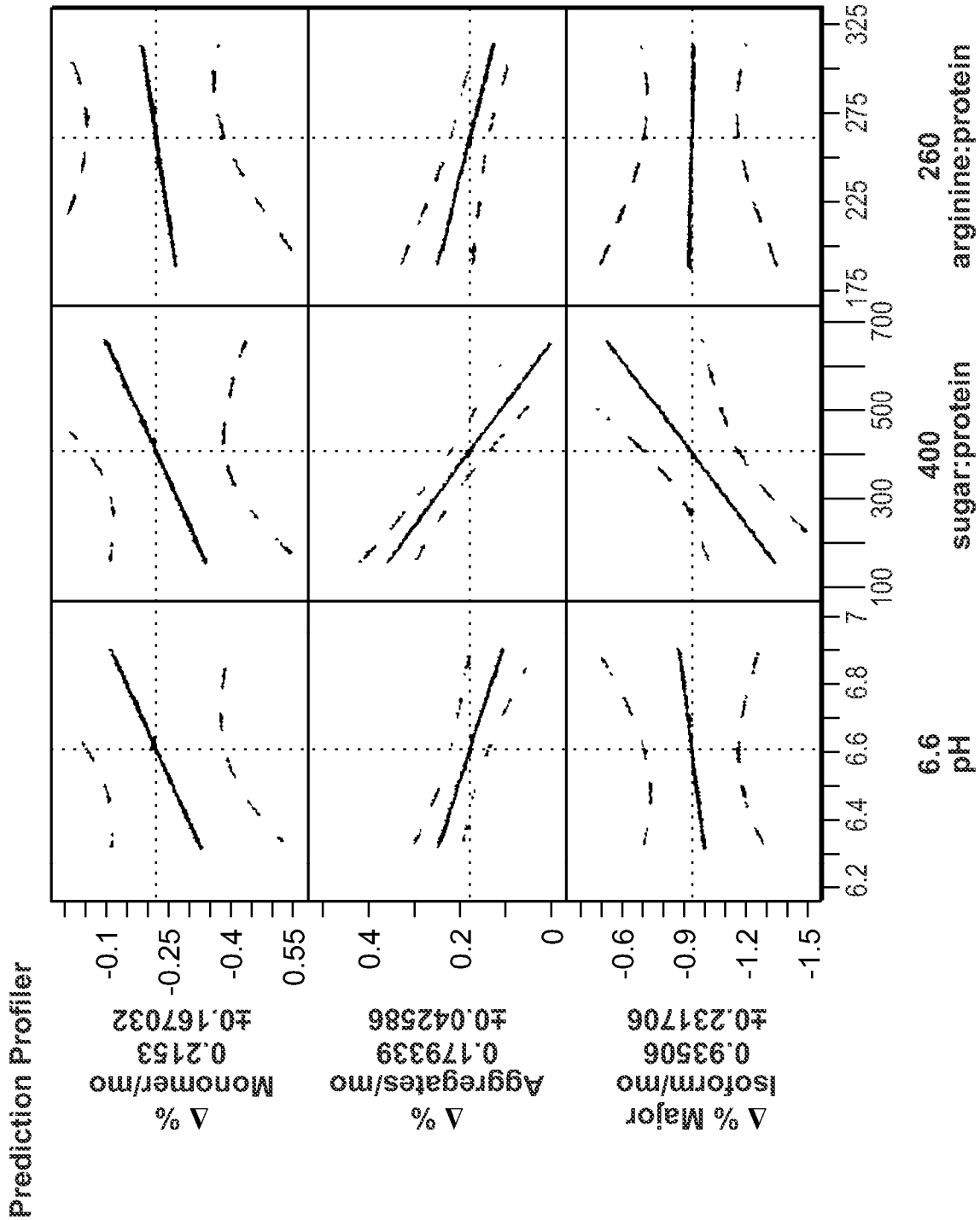

Prediction Profiler
Δ % Major isotorm/mo
0.93506
±0.231706
Δ % Aggregates/mo
0.179339
±0.042586
Δ % Monomer/mo
0.2153
±0.167032
-1.5
-1.2
-0.9
-0.6
0
0.2
0.4
0.55
-0.4
-0.25
-0.1
6.2
6.4
6.6
6.8
7
100
300
500
700
175
225
275
325
6.6
pH
400
sugar:protein
260
arginine:protein

FIG. 6B

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
```

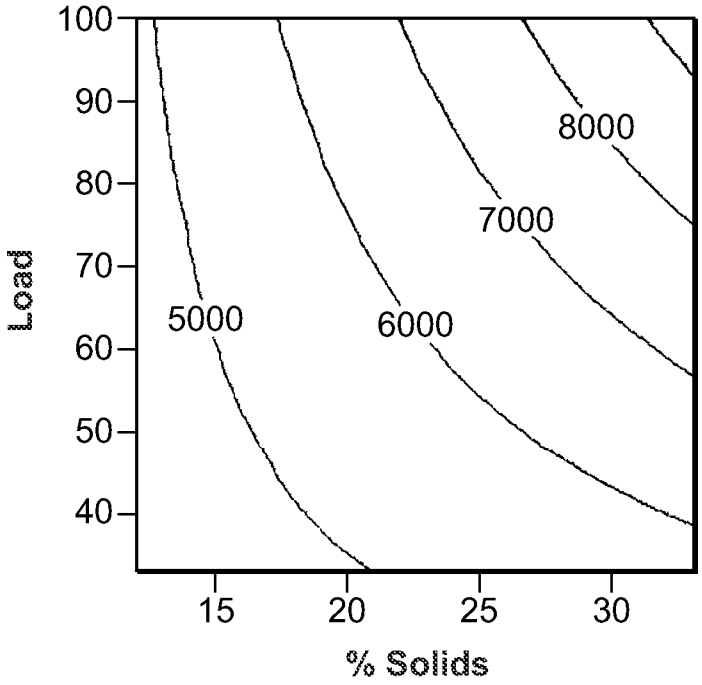

100
90
80
70
60
50
40
Load
5000
6000
7000
8000
15
20
25
30
% Solids

FIG. 8

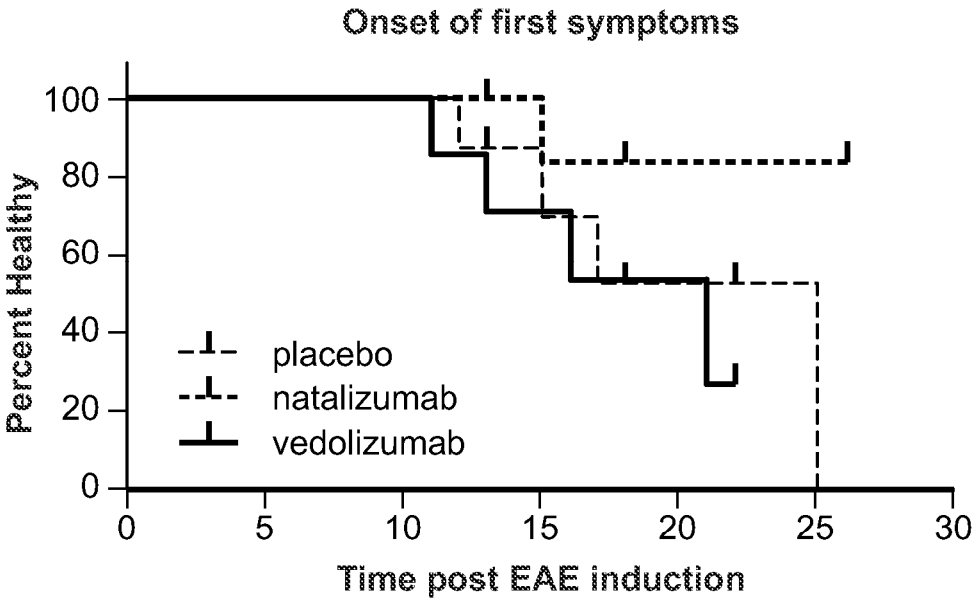

Onset of first symptoms
100
80
60
40
20
0
Percent Healthy
placebo
natalizumab
vedolizumab
0
5
10
15
20
25
30
Time post EAE induction

FIG. 9