LFA-3 signal sequence

```
1   ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG GTC TGC
1   Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val Val Cys

55  CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT
19  Leu Leu His Cys Phe Gly Phe Ile Ser Cys
```

LFA-3

```
85  TTT TCC CAA CAA ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA
29  Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro

139 AGC AAT GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA
47  Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala

193 GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG GTT TAT
65  Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg Val Tyr

247 TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA TCA TCA GAT GAA
83  Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr Ser Ser Asp Glu

301 GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT ACC ATG AAG TTC TTT CTT
101 Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp Thr Met Lys Phe Phe Leu

355 TAT GTC
119 Tyr Val
```

IgG1 (hinge, CH2, CH3)

```
361 GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG
121 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro

415 TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC
139 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr

469 CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG
157 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

523 TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG
175 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

577 GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC
193 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His

631 CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC
211 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

685 CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA
229 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

739 CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC
247 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser

793 CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG
265 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu

847 AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG TTG GAC TCC
283 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser

901 GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG
301 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

955 CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC
319 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

1009 ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
337 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys •••
```

FIG 1A

LFA-3 signal sequence

```
  1 ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG GTC TGC
  1 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val Val Cys
 55 CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT
 19 Leu Leu His Cys Phe Gly Phe Ile Ser Cys
```

LFA-3

```
 85 TTT TCC CAA CAA ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA
 29 Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro
139 AGC AAT GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA
 47 Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
193 GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG GTT TAT
 65 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg Val Tyr
247 TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA TCA TCA GAT GAA
 83 Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr Ser Ser Asp Glu
301 GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT ACC ATG AAG TTC TTT CTT
101 Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp Thr Met Lys Phe Phe Leu
355 TAT GTC
119 Tyr Val
```

IgG1 (hinge, CH2, CH3)

```
361 GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG
121 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
415 TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC
139 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
469 CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG
157 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
523 TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG
175 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
577 GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC
193 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
631 CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC
211 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
685 CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA
229 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
739 CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC
247 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
793 CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG
265 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
847 AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG TTG GAC TCC
283 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
901 GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG
301 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
955 CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC
319 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                                    *
1009 ACG CAG AAG AGC CTC TCC CTG TCT CCG GAT TCC AAC CTA TGG AAC TGA
337 Thr Gln Lys Ser Leu Ser Leu Ser Pro Asp Ser Asn Leu Trp Asn ***
```

FIG. 1B

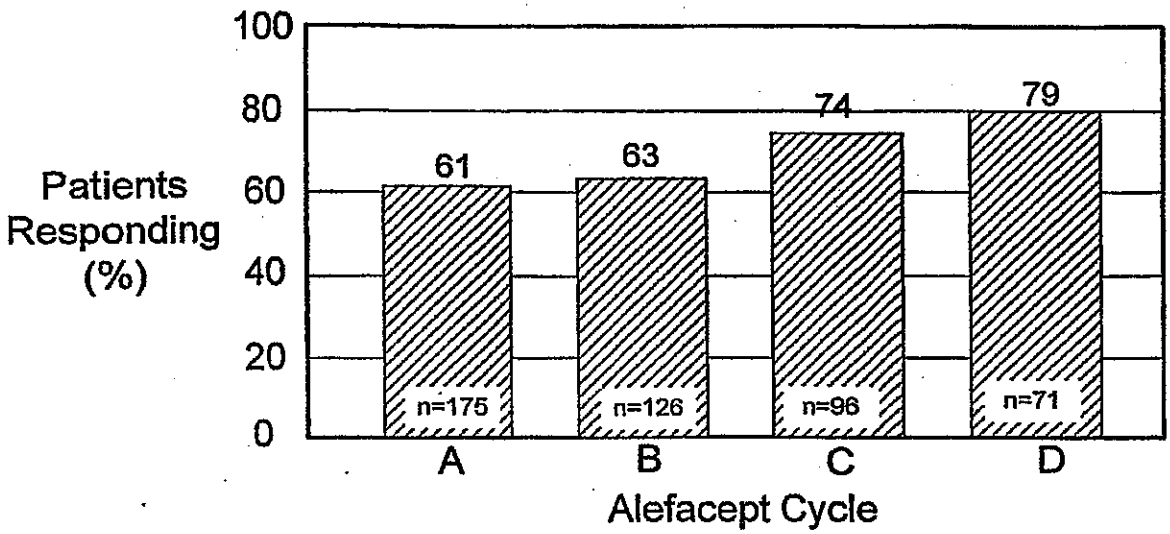

100
80
60
40
20
0
Patients Responding (%)
61
63
74
79
n=175
n=126
n=96
n=71
A
B
C
D
Alefacept Cycle

FIG. 2

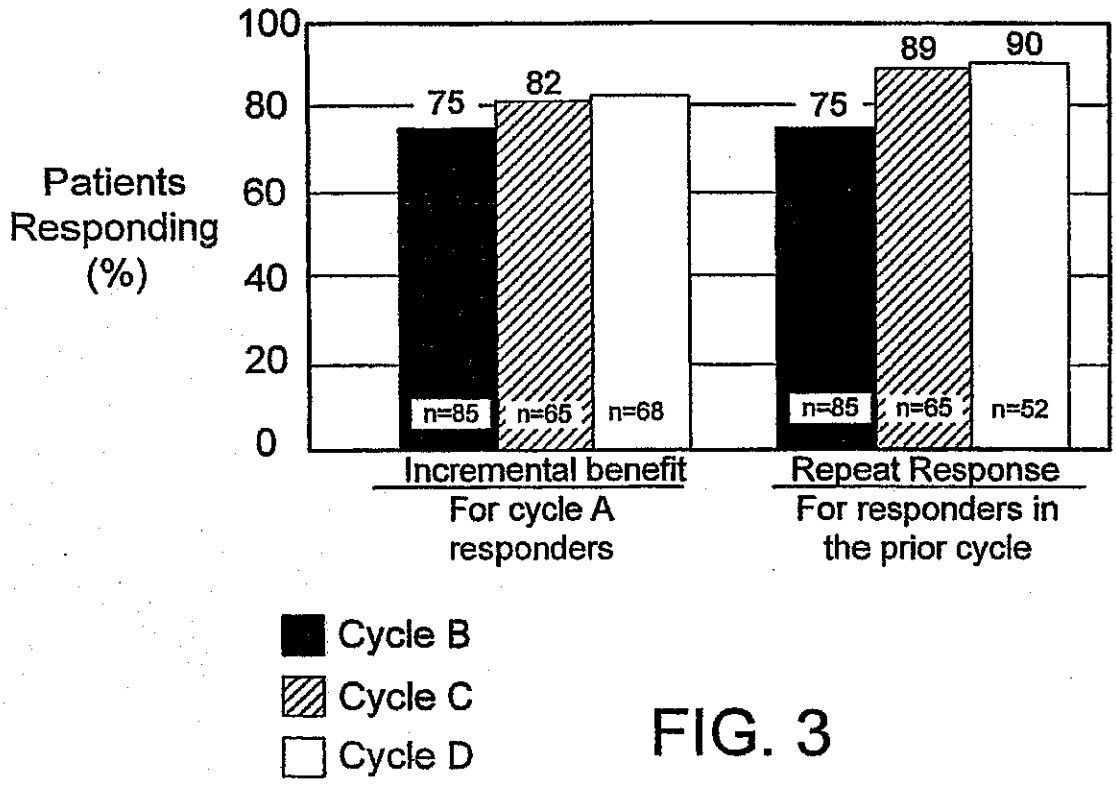

100
80
60
40
20
0
Patients Responding (%)
75
82
75
89
90
n=85
n=65
n=68
n=85
n=65
n=52
Incremental benefit
For cycle A responders
Repeat Response
For responders in the prior cycle
Cycle B
Cycle C
Cycle D

FIG. 3

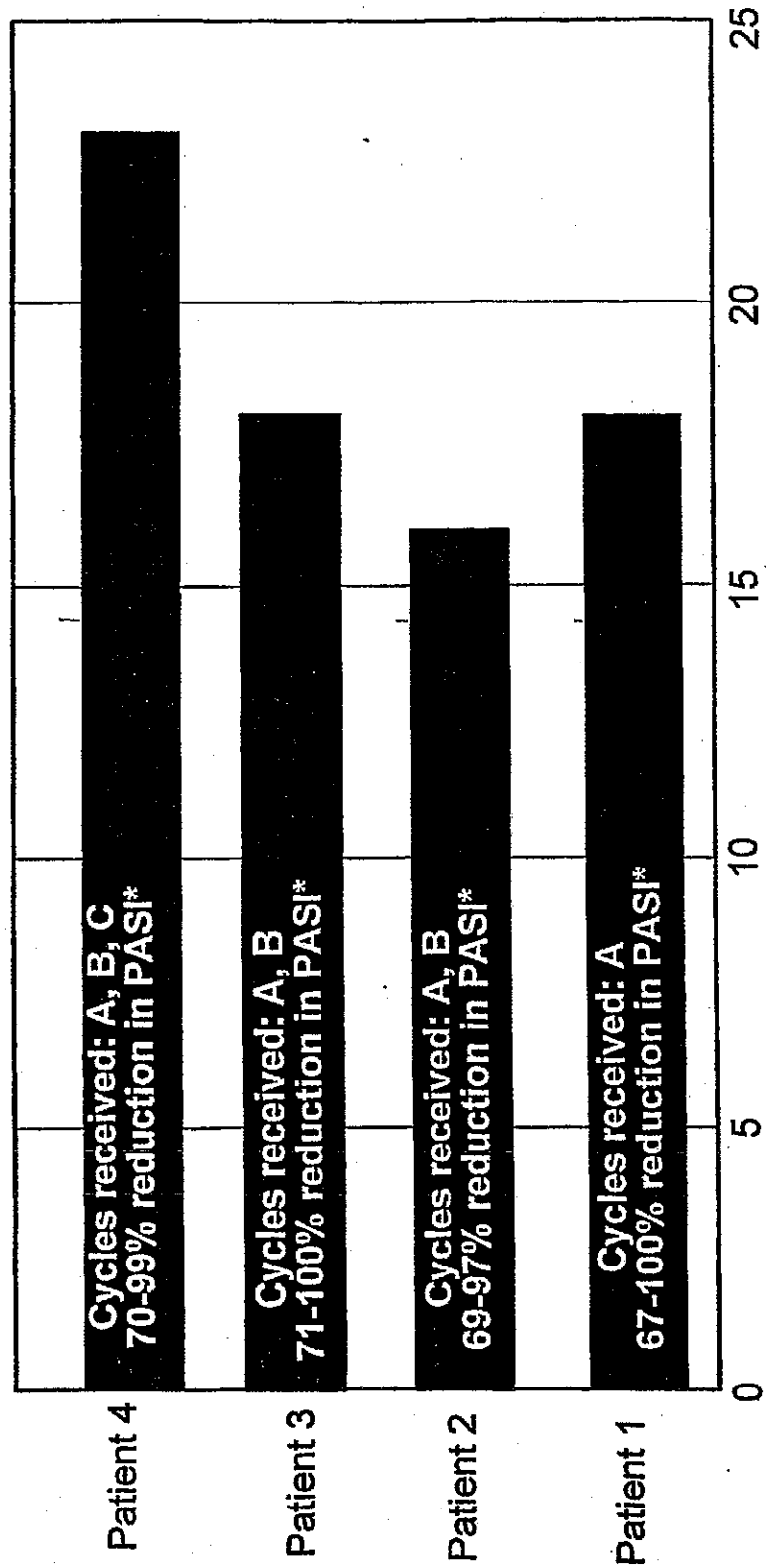

Cycles received: A, B, C
70-99% reduction in PASI*
Cycles received: A, B
71-100% reduction in PASI*
Cycles received: A, B
69-97% reduction in PASI*
Cycles received: A
67-100% reduction in PASI*
Patient 4
Patient 3
Patient 2
Patient 1
0
5
10
15
20
25
Months of treatment-free response
* Range of percentage reduction in PASI over treatment-free period.

FIG. 4

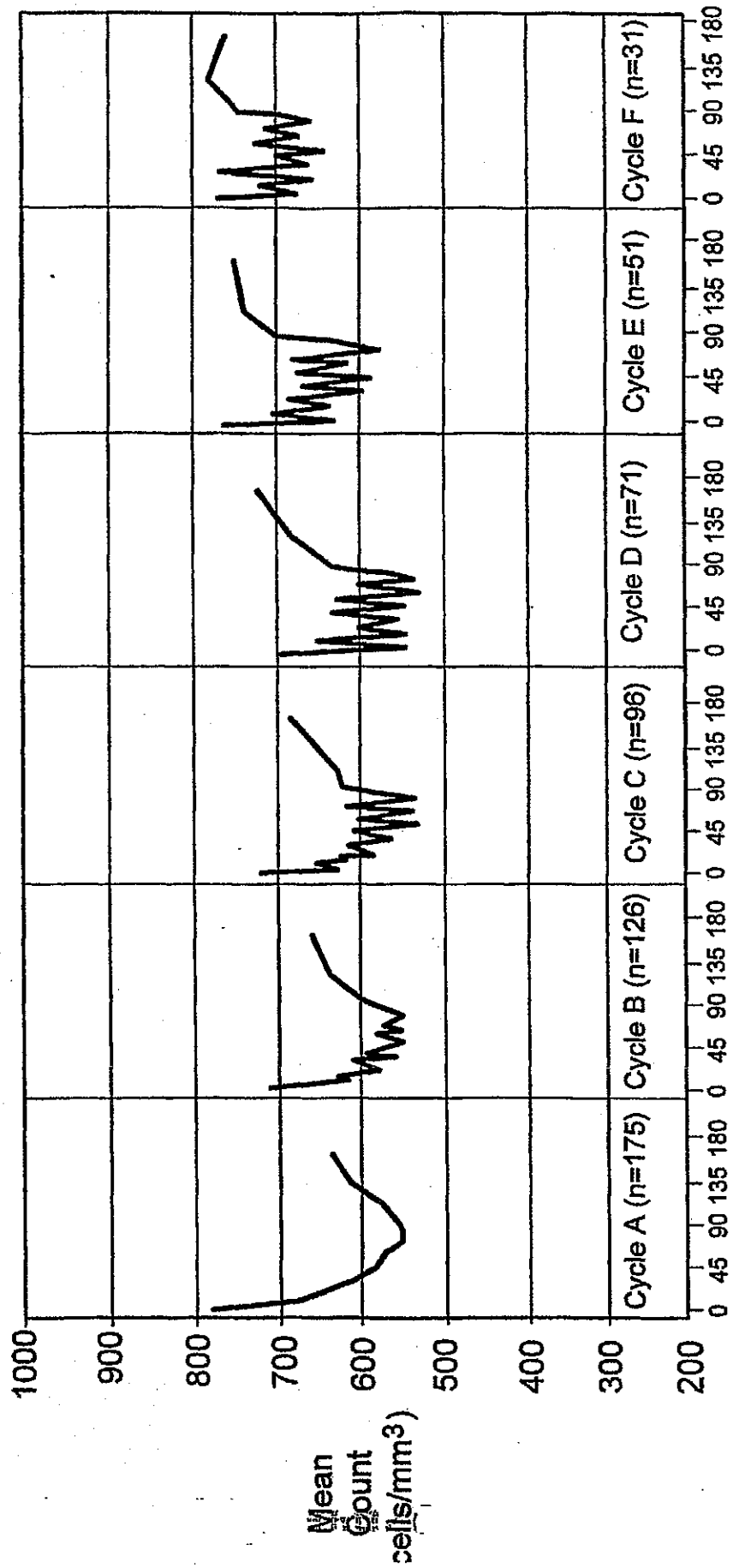

Mean Count (cells/mm3)
1000
900
800
700
600
500
400
300
200
Cycle A (n=175)
Cycle B (n=126)
Cycle C (n=96)
Cycle D (n=71)
Cycle E (n=51)
Cycle F (n=31)
0 45 90 135 180
Time (days)

FIG. 5

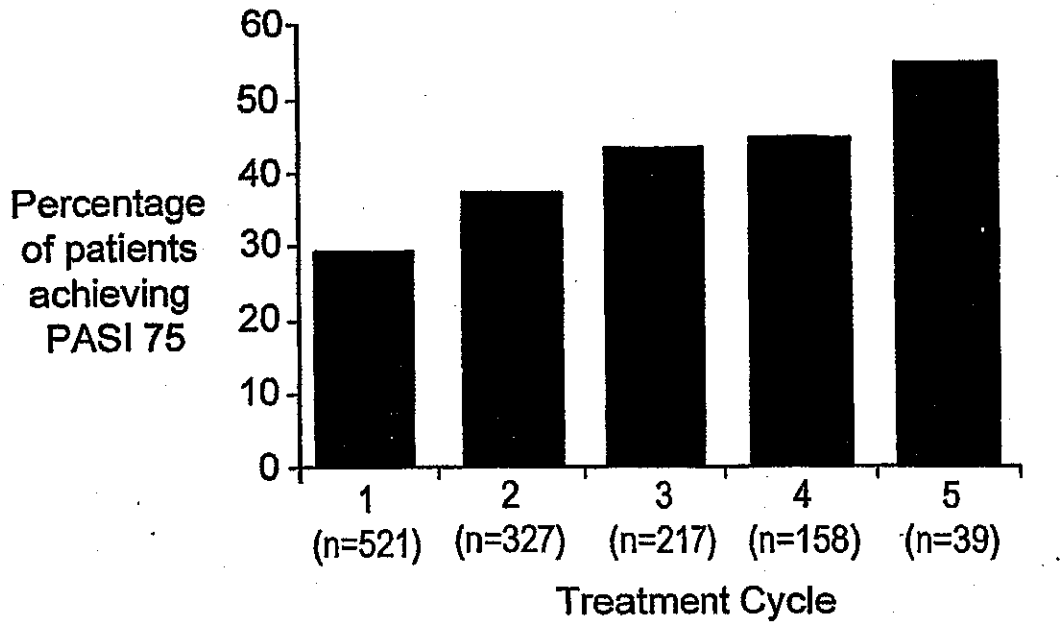

Percentage of patients achieving PASI 75
60
50
40
30
20
10
0
1 (n=521)
2 (n=327)
3 (n=217)
4 (n=158)
5 (n=39)
Treatment Cycle

FIG. 6A

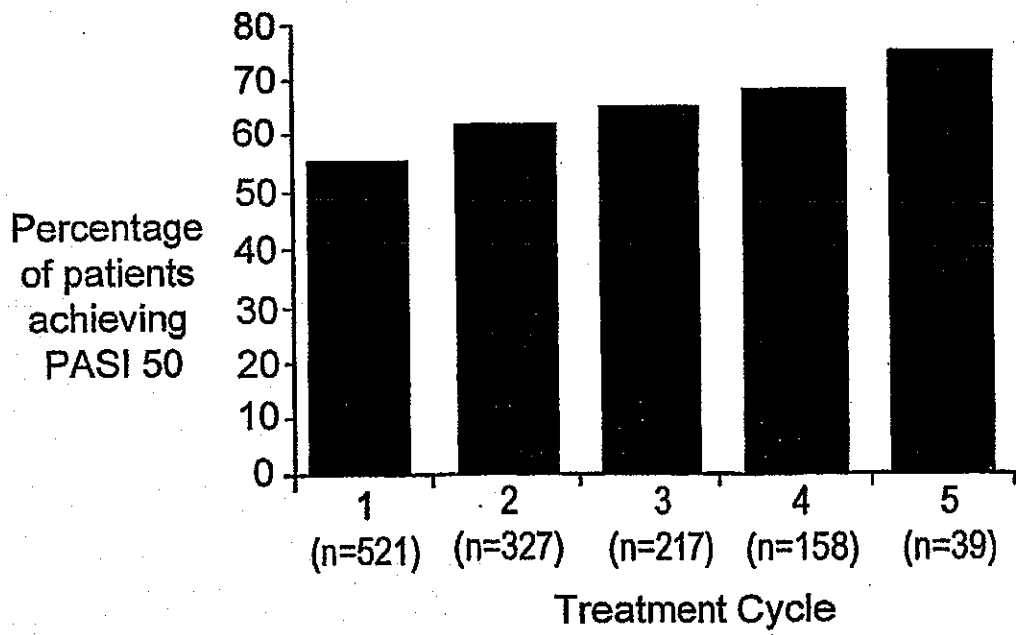

Percentage of patients achieving PASI 50
80
70
60
50
40
30
20
10
0
1 (n=521)
2 (n=327)
3 (n=217)
4 (n=158)
5 (n=39)
Treatment Cycle

FIG. 6B

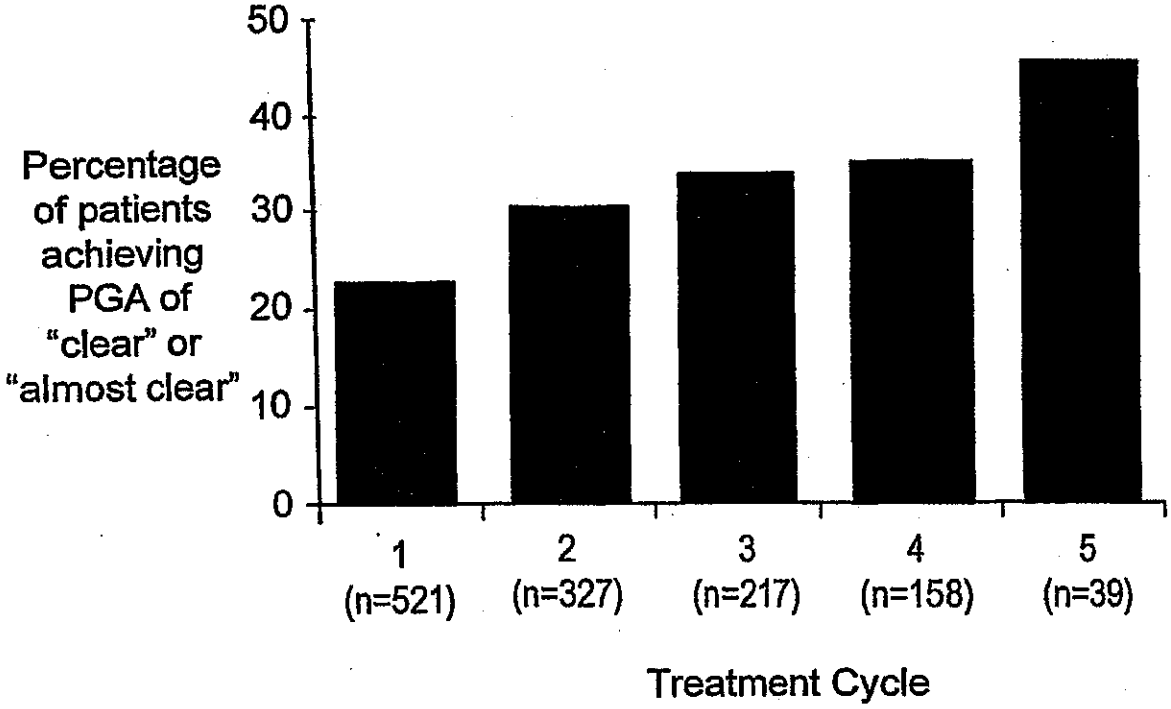

Percentage of patients achieving PGA of "clear" or "almost clear"
50
40
30
20
10
0
1 (n=521)
2 (n=327)
3 (n=217)
4 (n=158)
5 (n=39)
Treatment Cycle

FIG. 7A

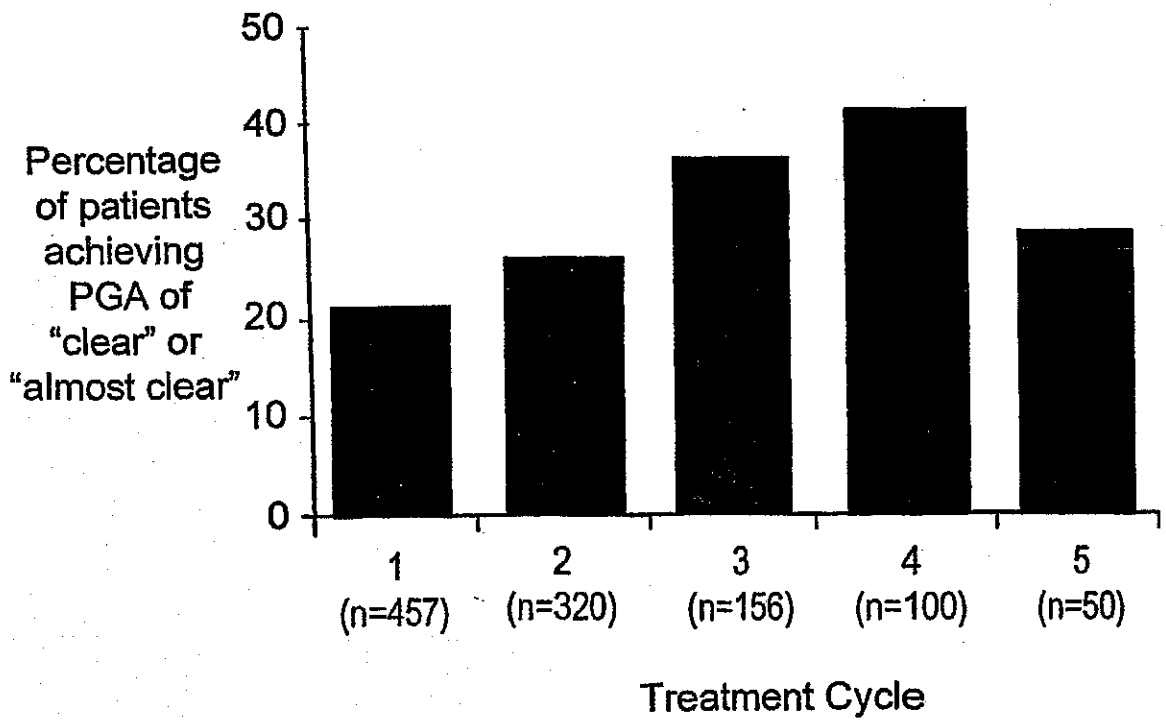

Percentage of patients achieving PGA of "clear" or "almost clear"
50
40
30
20
10
0
1 (n=457)
2 (n=320)
3 (n=156)
4 (n=100)
5 (n=50)
Treatment Cycle

FIG. 7B