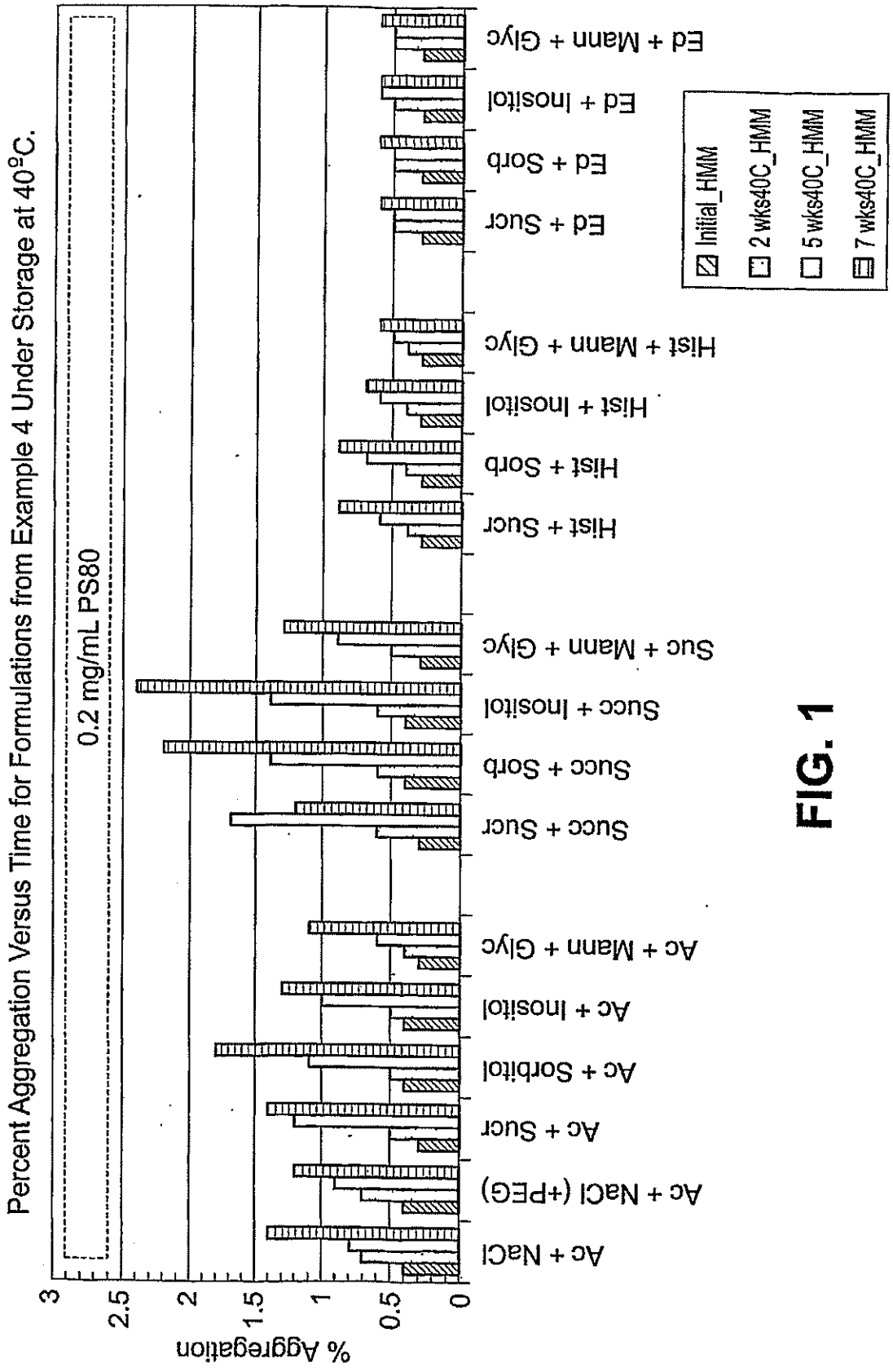

Percent Aggregation Versus Time for Formulations from Example 4 Under Storage at 40°C.
0.2 mg/mL PS80
% Aggregation
0
0.5
1
1.5
2
2.5
3
Ac + NaCl
Ac + NaCl (+PEG)
Ac + Sucr
Ac + Sorbitol
Ac + Inositol
Ac + Mann + Glyc
Succ + Sucr
Succ + Sorb
Succ + Inositol
Suc + Mann + Glyc
Hist + Sucr
Hist + Sorb
Hist + Inositol
Hist + Mann + Glyc
Ed + Sucr
Ed + Sorb
Ed + Inositol
Ed + Mann + Glyc
Initial_HMM
2 wks40C_HMM
5 wks40C_HMM
7 wks40C_HMM

FIG. 1

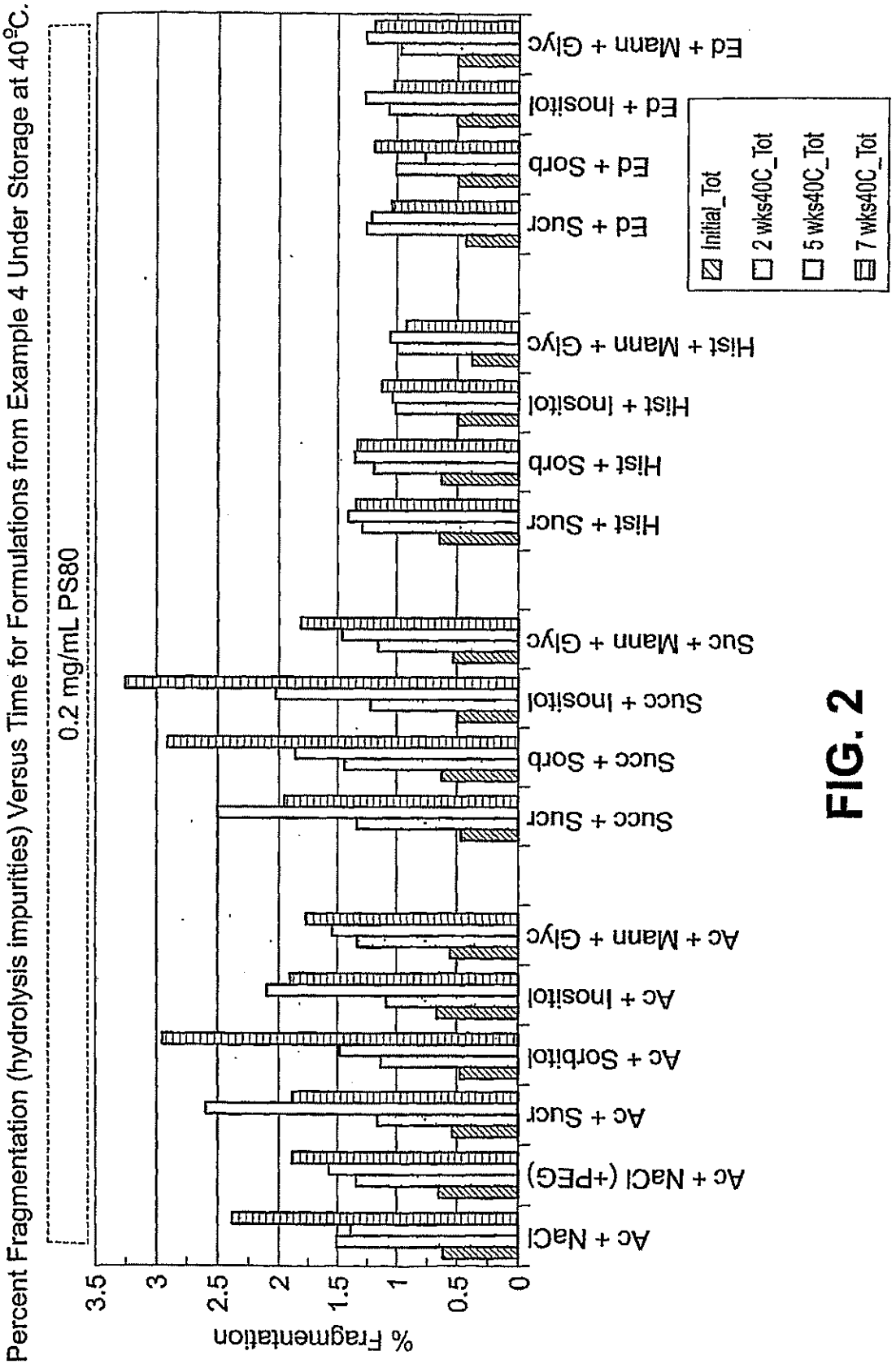

Percent Fragmentation (hydrolysis impurities) Versus Time for Formulations from Example 4 Under Storage at 40°C.
0.2 mg/mL PS80
% Fragmentation
3.5
3
2.5
2
1.5
1
0.5
0
Ac + NaCl
Ac + NaCl (+PEG)
Ac + Sucr
Ac + Sorbitol
Ac + Inositol
Ac + Mann + Glyc
Succ + Sucr
Succ + Sorb
Succ + Inositol
Suc + Mann + Glyc
Hist + Sucr
Hist + Sorb
Hist + Inositol
Hist + Mann + Glyc
Ed + Sucr
Ed + Sorb
Ed + Inositol
Ed + Mann + Glyc
Initial_Tot
2 wks40C_Tot
5 wks40C_Tot
7 wks40C_Tot

FIG. 2

FIG. 3

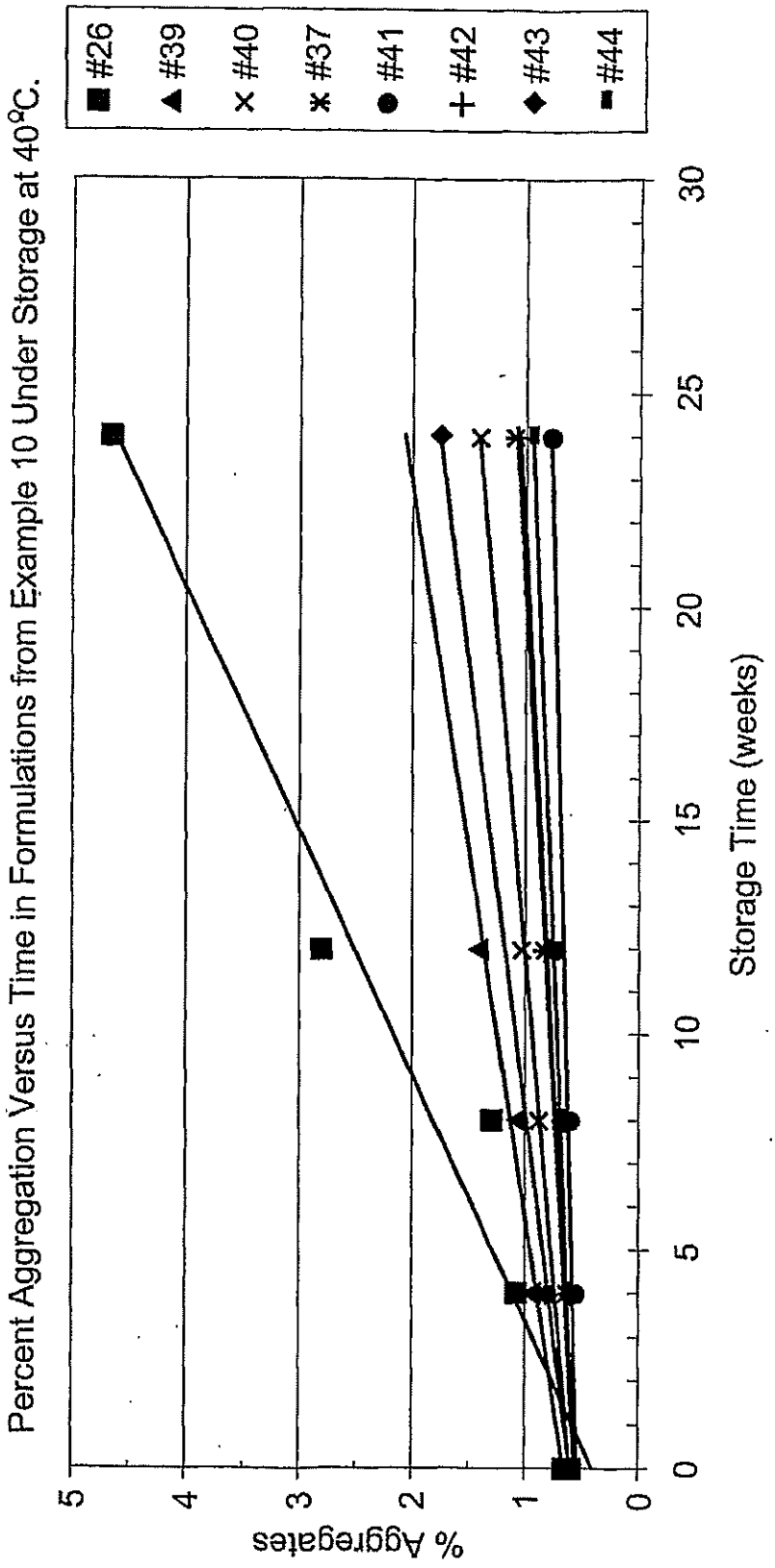

Percent Aggregation Versus Time in Formulations from Example 10 Under Storage at 40°C.
#26
#39
#40
#37
#41
#42
#43
#44
% Aggregates
0
1
2
3
4
5
Storage Time (weeks)
0
5
10
15
20
25
30

FIG. 4

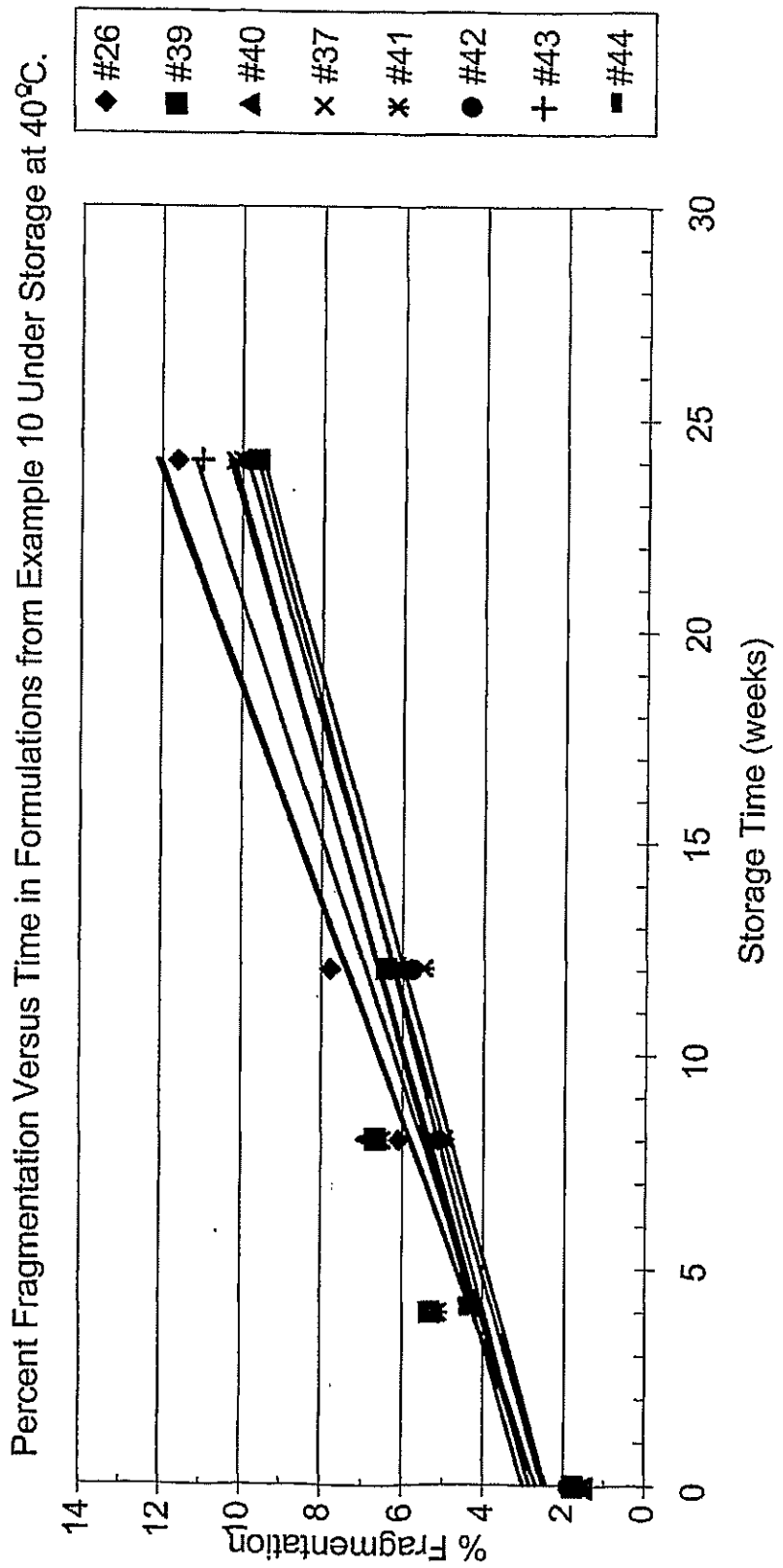

Percent Fragmentation Versus Time in Formulations from Example 10 Under Storage at 40°C.
#26
#39
#40
#37
#41
#42
#43
#44
% Fragmentation
0
2
4
6
8
10
12
14
Storage Time (weeks)
0
5
10
15
20
25
30

FIG. 5

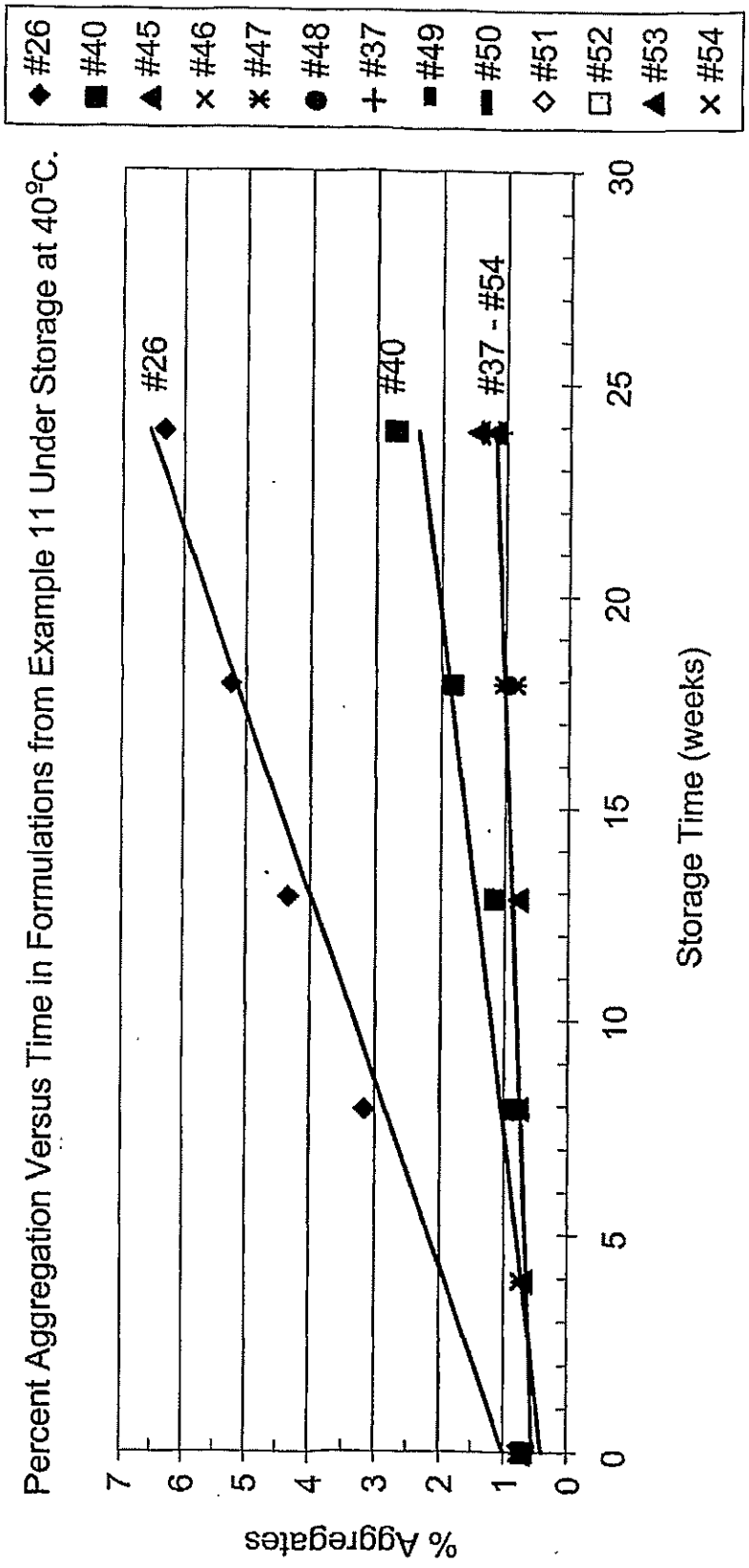

Percent Aggregation Versus Time in Formulations from Example 11 Under Storage at 40°C.
#26
#40
#45
#46
#47
#48
#37
#49
#50
#51
#52
#53
#54
#26
#40
#37 - #54
% Aggregates
Storage Time (weeks)
0
1
2
3
4
5
6
7
0
5
10
15
20
25
30

FIG. 6

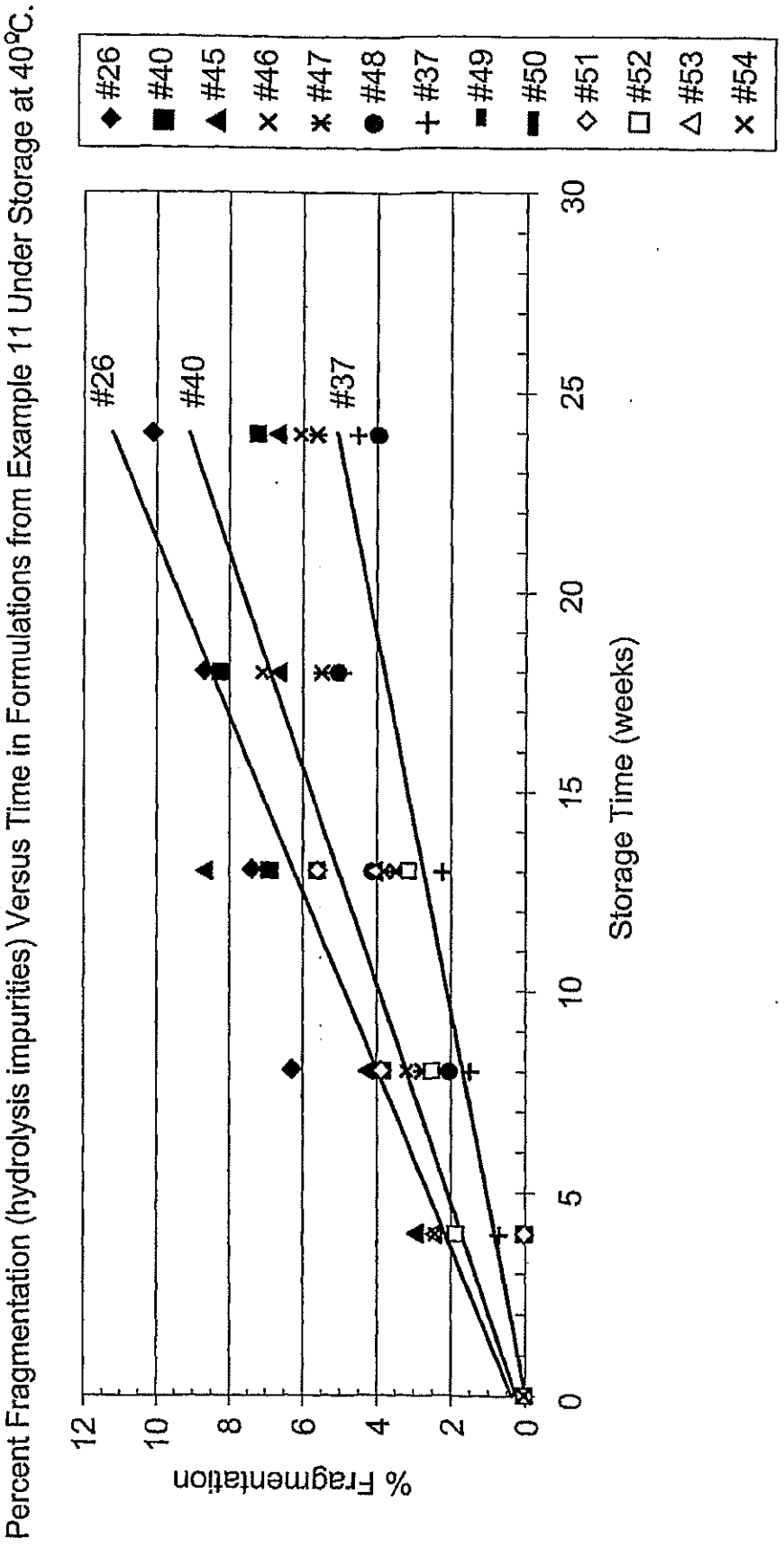

Percent Fragmentation (hydrolysis impurities) Versus Time in Formulations from Example 11 Under Storage at 40°C.
% Fragmentation
Storage Time (weeks)
0
2
4
6
8
10
12
0
5
10
15
20
25
30
#26
#40
#37
#26
#40
#45
#46
#47
#48
#37
#49
#50
#51
#52
#53
#54

FIG. 7

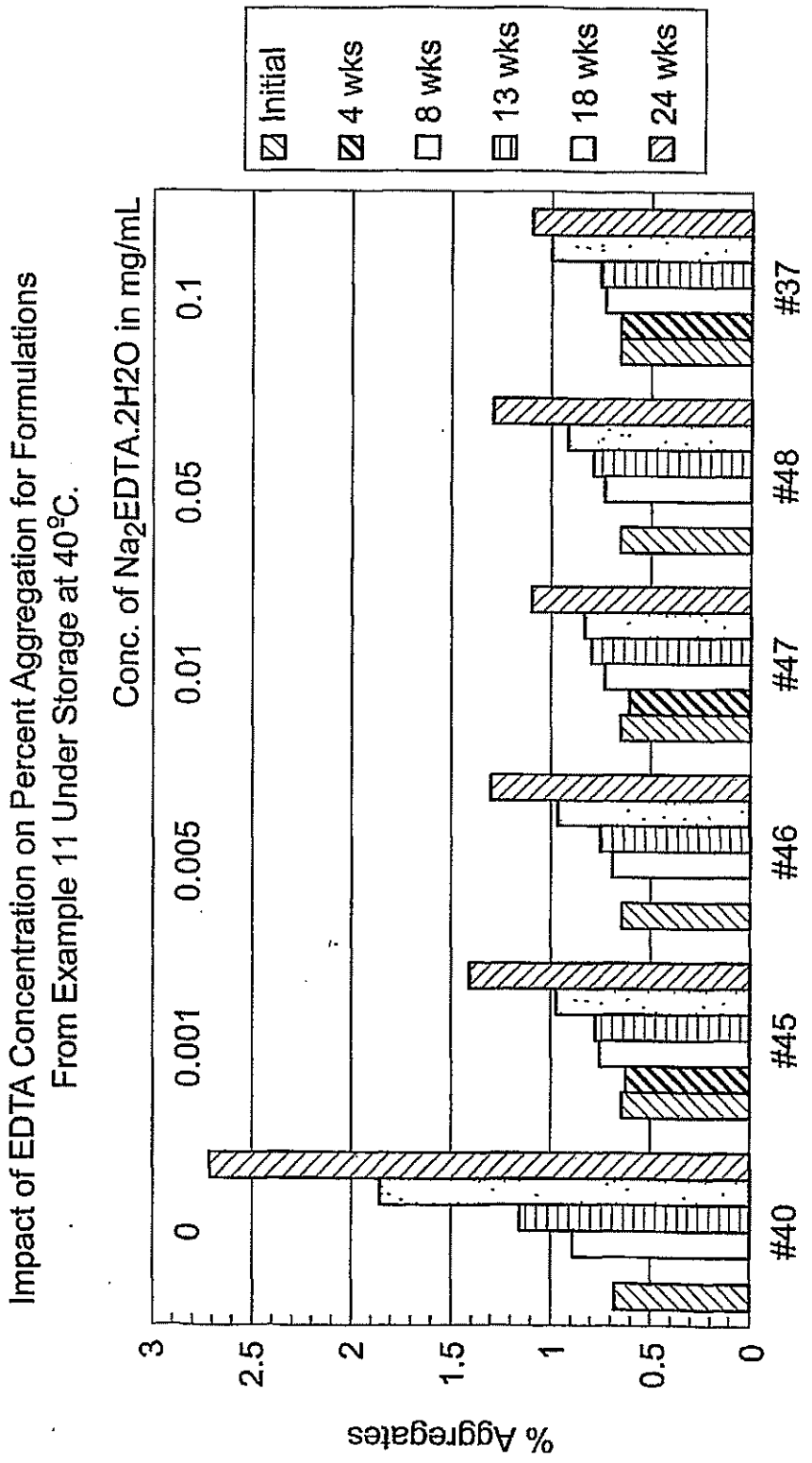

Impact of EDTA Concentration on Percent Aggregation for Formulations From Example 11 Under Storage at 40°C.
Initial
4 wks
8 wks
13 wks
18 wks
24 wks
Conc. of Na2EDTA.2H2O in mg/mL
0
0.001
0.005
0.01
0.05
0.1
#40
#45
#46
#47
#48
#37
% Aggregates
3
2.5
2
1.5
1
0.5
0

FIG. 8

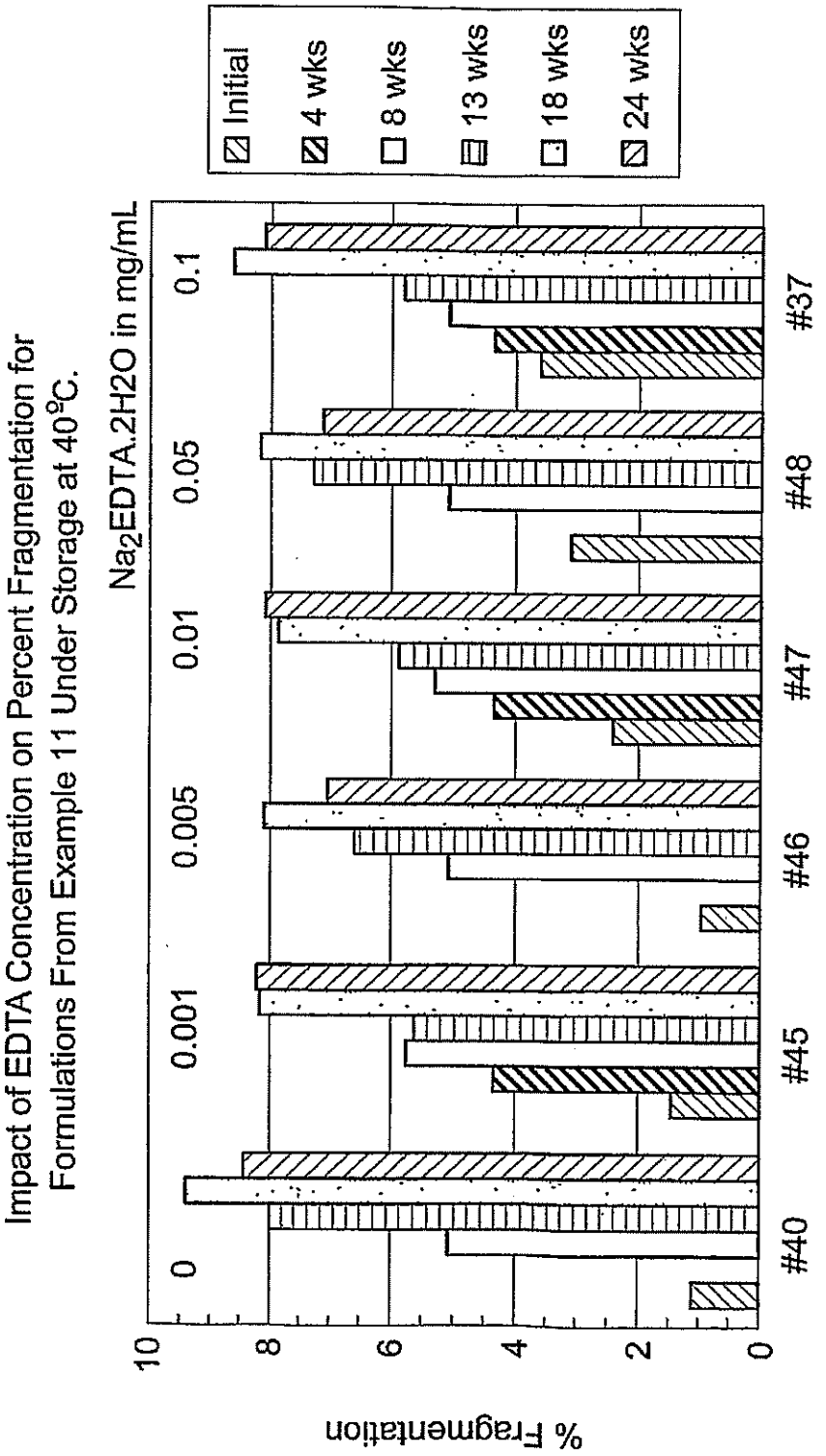

Impact of EDTA Concentration on Percent Fragmentation for Formulations From Example 11 Under Storage at 40°C.
Initial
4 wks
8 wks
13 wks
18 wks
24 wks
Na2EDTA.2H2O in mg/mL
0
0.001
0.005
0.01
0.05
0.1
#40
#45
#46
#47
#48
#37
% Fragmentation
10
8
6
4
2
0

FIG. 9

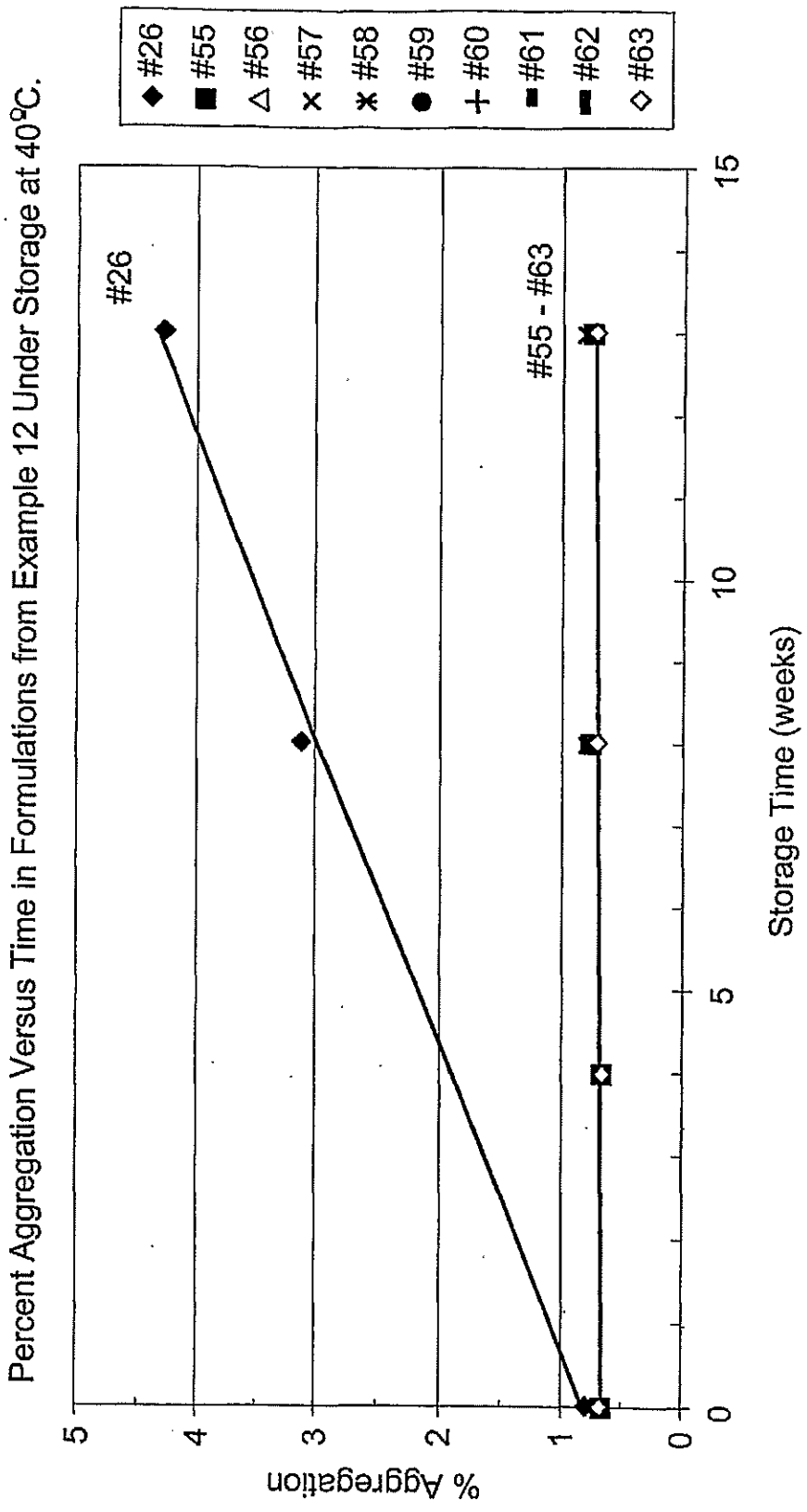

Percent Aggregation Versus Time in Formulations from Example 12 Under Storage at 40°C.
#26
#55
#56
#57
#58
#59
#60
#61
#62
#63
#26
#55 - #63
% Aggregation
Storage Time (weeks)
0
1
2
3
4
5
0
5
10
15

FIG. 10

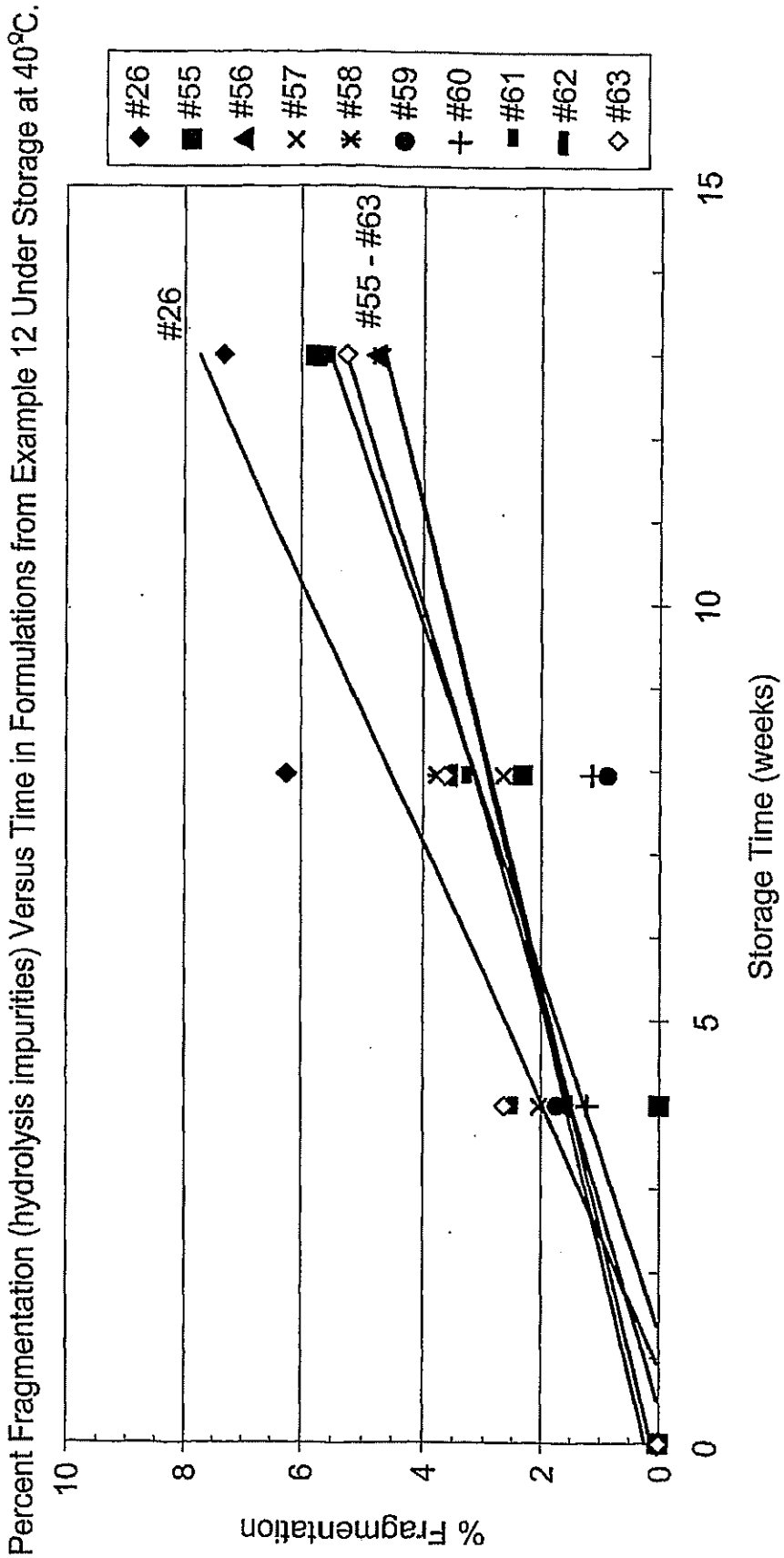

Percent Fragmentation (hydrolysis impurities) Versus Time in Formulations from Example 12 Under Storage at 40°C.
#26
#55 - #63
#26
#55
#56
#57
#58
#59
#60
#61
#62
#63
% Fragmentation
0
2
4
6
8
10
0
5
10
15
Storage Time (weeks)

FIG. 11A

Ticilimumab (11.2.1) Heavy Chain DNA (SEQ ID NO: 1)

```
atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag   60
gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc  120
tgtgcagcgt ctggattcac cttcagtagc tatggcatgc actgggtccg ccaggctcca  180
ggcaaggggc tggagtgggt ggcagttata tggtatgatg gaagtaataa atactatgca  240
gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctg  300
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatccgagg  360
ggagctaccc tttactacta ctactacggt atggacgtct ggggccaagg gaccacggtc  420
accgtctcct cagcctccac caagggccca tcggtcttcc ccctggcgcc ctgctccagg  480
agcacctccg agagcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg  540
gtgacggtgt cgtggaactc aggcgctctg accagcggcg tgcacacctt cccagctgtc  600
ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcaacttc  660
ggcacccaga cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag  720
acagttgagc gcaaatgttg tgtcgagtgc ccaccgtgcc cagcaccacc tgtggcagga  780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct  840
gaggtcacgt gcgtggtggt ggacgtgagc cacgaagacc ccgaggtcca gttcaactgg  900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cacgggagga gcagttcaac  960
agcacgttcc gtgtggtcag cgtcctcacc gttgtgcacc aggactggct gaacggcaag 1020
gagtacaagt gcaaggtctc caacaaaggc ctcccagccc ccatcgagaa aaccatctcc 1080
aaaaccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctaccc cagcgacatc 1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac acctcccatg 1260
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380
cagaagagcc tctccctgtc tccgggtaaa tga                               1413
```

FIG. 11B

Ticilimumab (11.2.1) Heavy Chain Protein (SEQ ID NO: 2)

```
[QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV IWYDGSNKYY   60
ADSVKGRFTI  SRDNSKNTLY LQMNSLRAED TAVYYCARDP RGATLYYYYY GMDVWGQGTT  120
VTVSS]ASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA  180
VLQSSGLYSL  SSVVTVPSSN FGTQTYTCNV DHKPSNTKVD KTVERKCCVE CPPCPAPPVA  240
GPSVFLFPPK  PKDTLMISRT PEVTCVVVDV SHEDPEVQFN WYVDGVEVHN AKTKPREEQF  300
NSTFRVVSVL  TVVHQDWLNG KEYKCKVSNK GLPAPIEKTI SKTKGQPREP QVYTLPPSRE  360
EMTKNQVSLT  CLVKGFYPSD IAVEWESNGQ PENNYKTTPP MLDSDGSFFL YSKLTVDKSR  420
WQQGNVFSCS  VMHEALHNHY TQKSLSLSPG K                                  451
```

The variable region (SEQ ID NO:5) is depicted [between brackets] and the CDRs are underlined. CDR1 is indicated by SEQ ID NO:7, CDR2 by SEQ ID NO:8, and CDR3 by SEQ ID NO:9.

FIG. 11C

Ticilimumab (11.2.1) Light Chain DNA (SEQ ID NO: 3)

```
atggacatga gggtccccgc tcagctcctg gggctcctgc tactctggct ccgaggtgcc   60
agatgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga   120
gtcaccatca cttgccgggc aagtcagagc attaacagct atttagattg gtatcagcag   180
aaaccaggga aagcccctaa actcctgatc tatgctgcat ccagtttgca aagtggggtc   240
ccatcaaggt tcagtggcag tggatctggg acagatttca ctctcaccat cagcagtctg   300
caacctgaag attttgcaac ttactactgt caacagtatt acagtactcc attcactttc   360
ggccctggga ccaaagtgga aatcaaacga actgtggctg caccatctgt cttcatcttc   420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac   480
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac   540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc   600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat   660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta gtga          714
```

FIG. 11D

Ticilimumab (11.2.1) Light Chain Protein SEQ ID NO: 4

```
[DIQMTQSPSS LSASVGDRVT ITCRASQSIN SYLDWYQQKP GKAPKLLIYA ASSLQSGVPS    60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYSTPFTFGP GTKVEIK]RTV AAPSVFIFPP   120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT   180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                               214
```

The variable region (SEQ ID NO:6) is depicted [between brackets] and the CDRs are underlined. CDR1 is indicated by SEQ ID NO:10, CDR2 by SEQ ID NO:11, and CDR3 by SEQ ID NO:12.