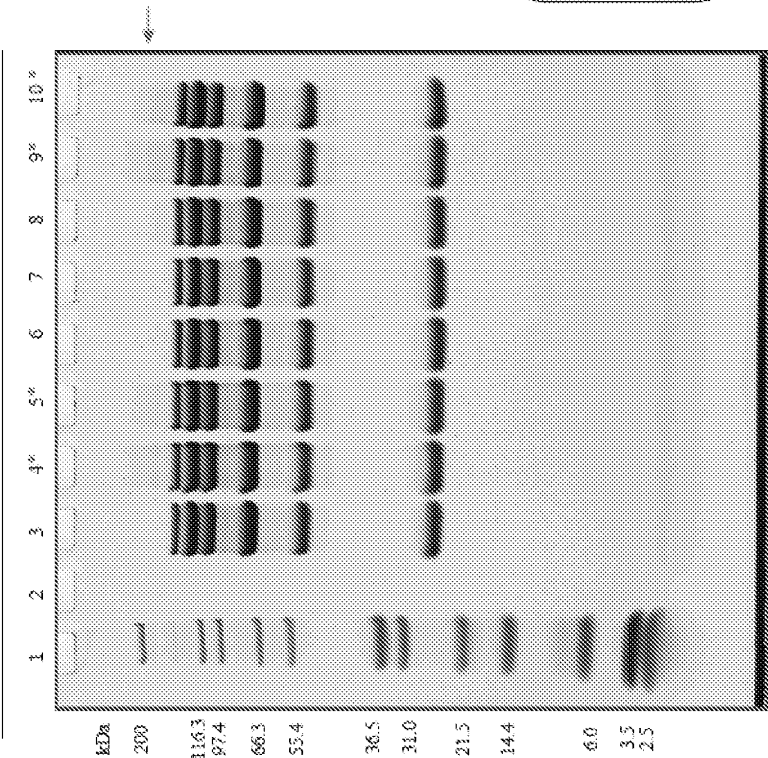


Formulations 1-7 Non Reduced



Lane	Sample Name (Sample #)
1	Mark 12 MW marker
2	Blank
3	Reference Standard
4	14 day, 40°C F1
5	14 day, 40°C F2
6	14 day, 40°C F3
7	14 day, 40°C F4
8	14 day, 40°C F5
9	14 day, 40°C F6
10	14 day, 40°C F7

Sample load	10 µg
SDS-PAGE gel and buffer	4.12% Bis-Tris
Sample heating	10' x 70°C
Electrophoresis	35' x 200V
Stain	Simply Blue
Stain/destain time	1.5 hours / Overnight
Marker	Mark 12

FIG. 1A

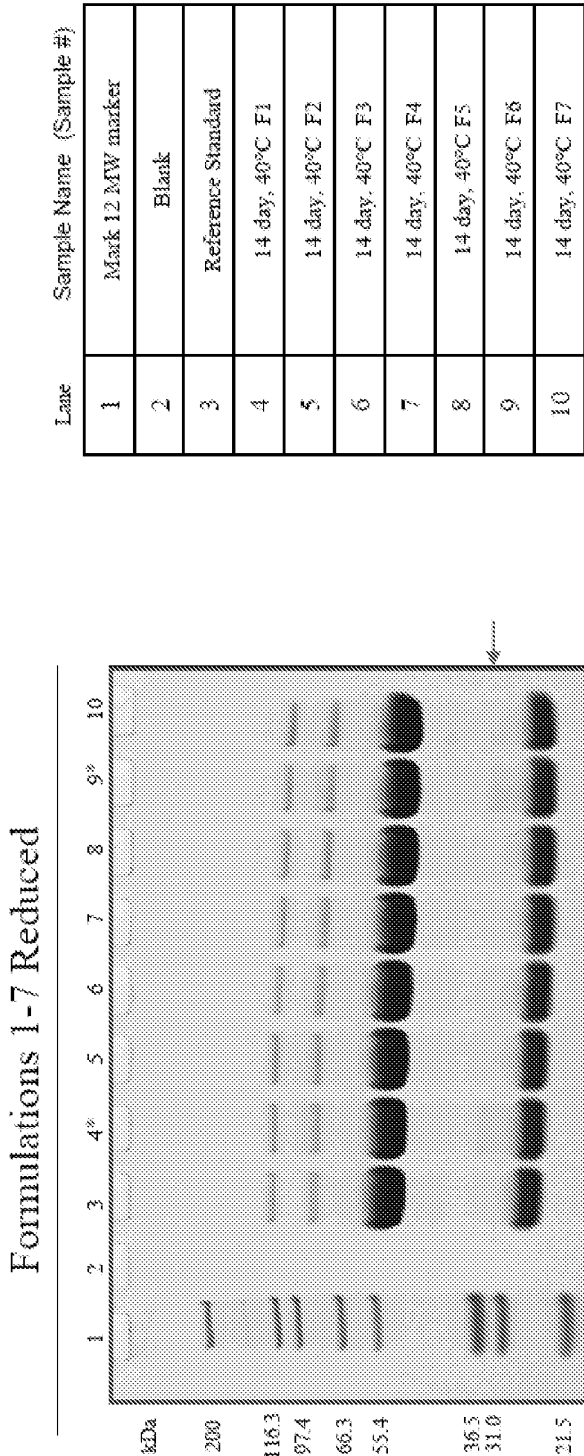


FIG. 1B

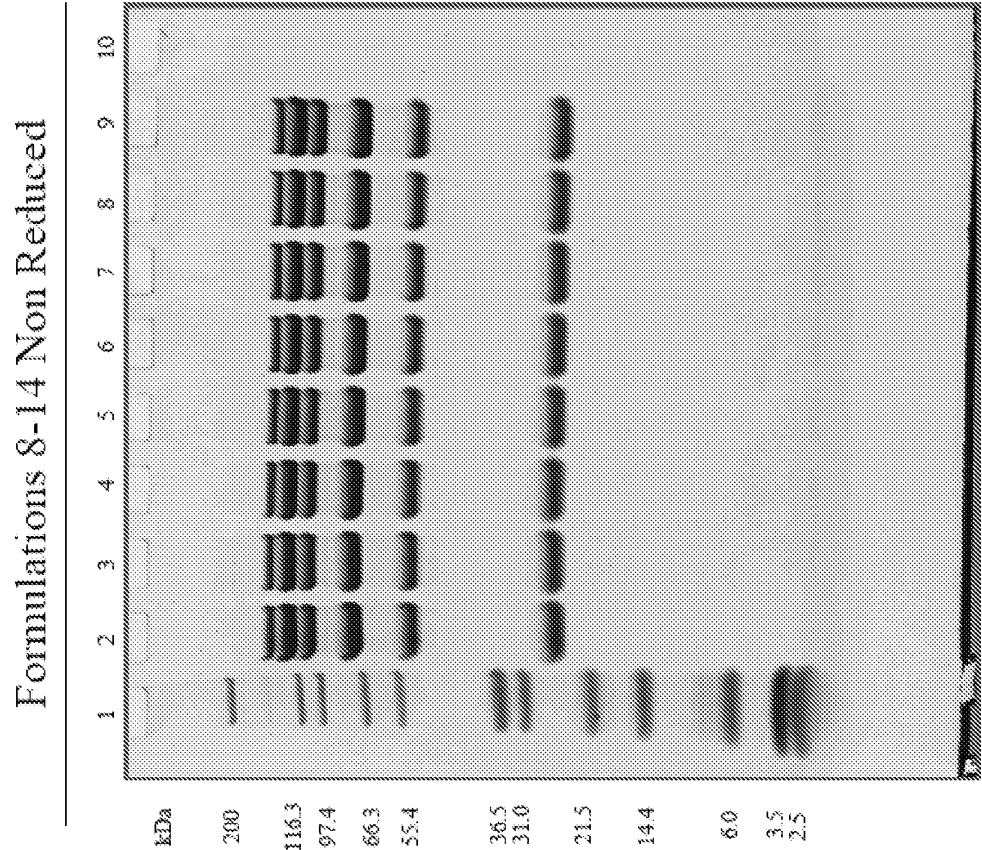


FIG. 1C

Lane	Sample Name (Sample #)
1	Mark 12 MW marker
2	Reference Standard
3	14 day, 40°C F8
4	14 day, 40°C F9
5	14 day, 40°C F10
6	14 day, 40°C F11
7	14 day, 40°C F12
8	14 day, 40°C F13
9	14 day, 40°C F14
10	Blank

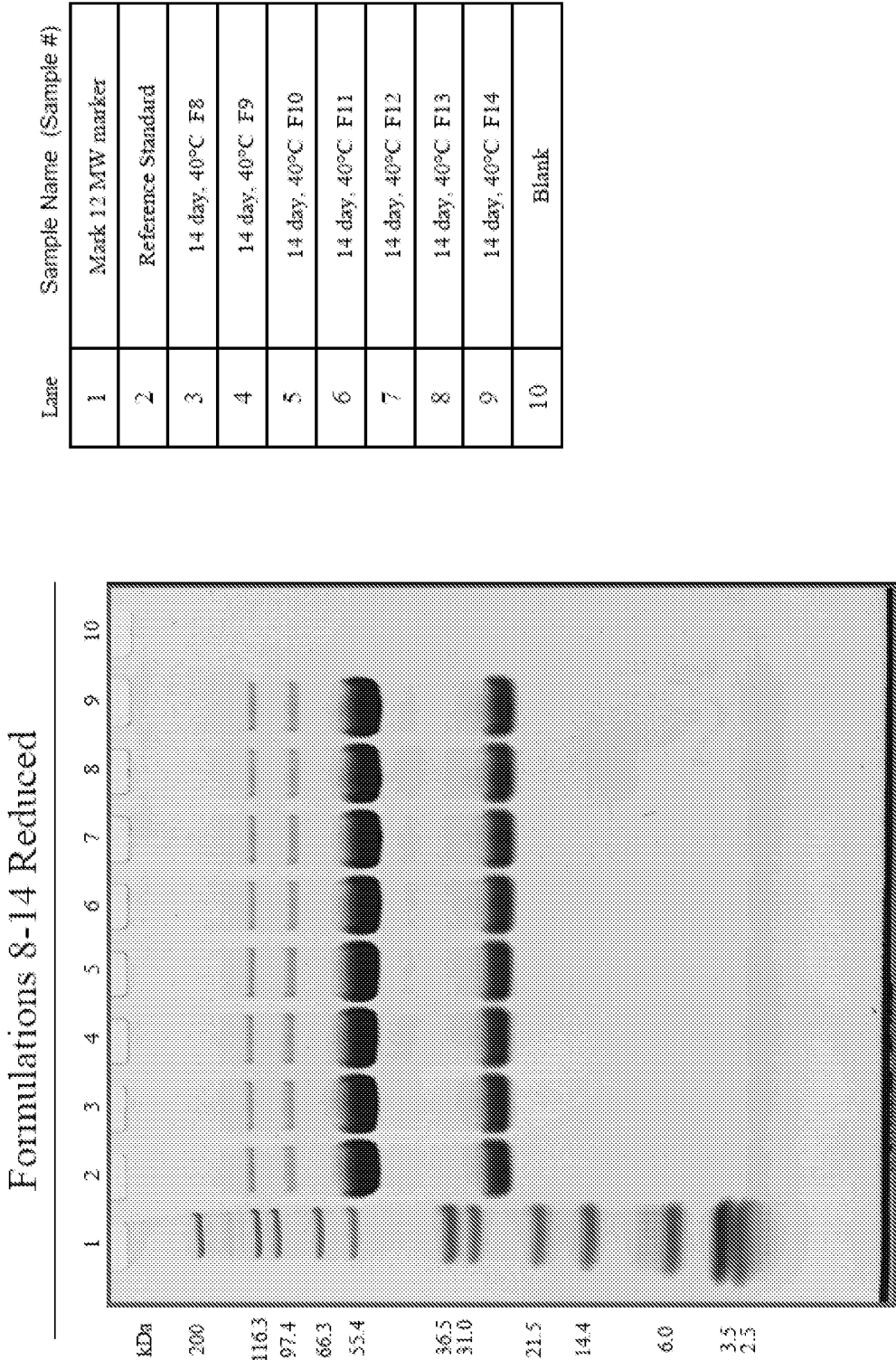


FIG. 1D

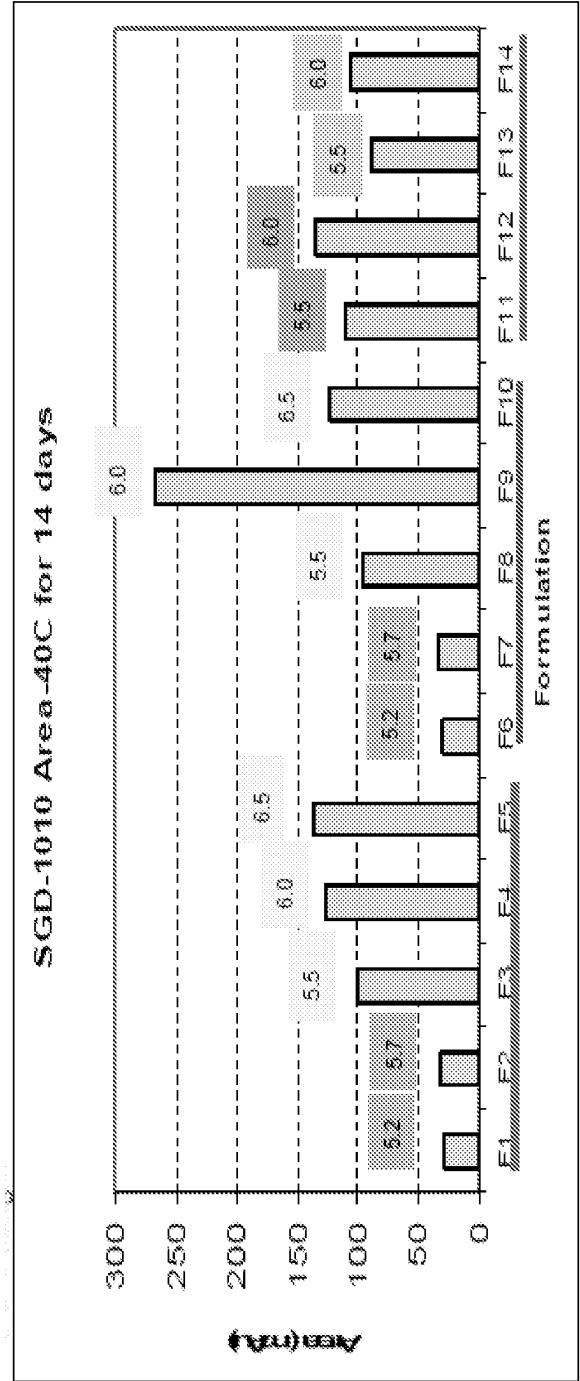


FIG. 1E

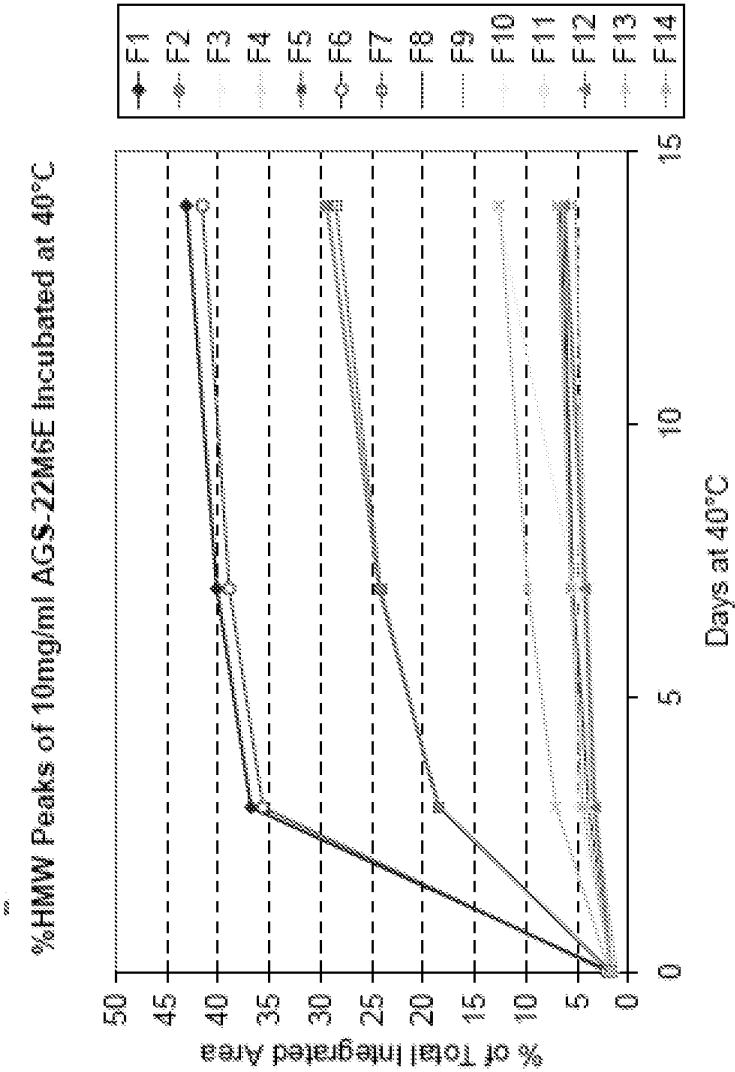


FIG. 1F

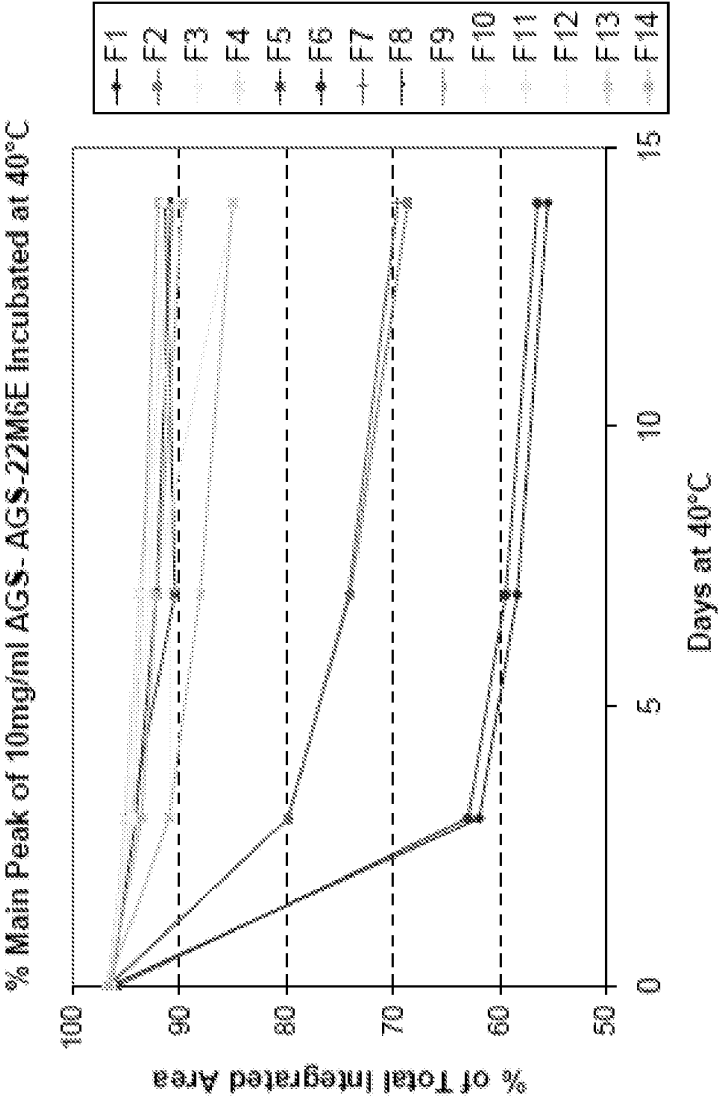


FIG. 1G

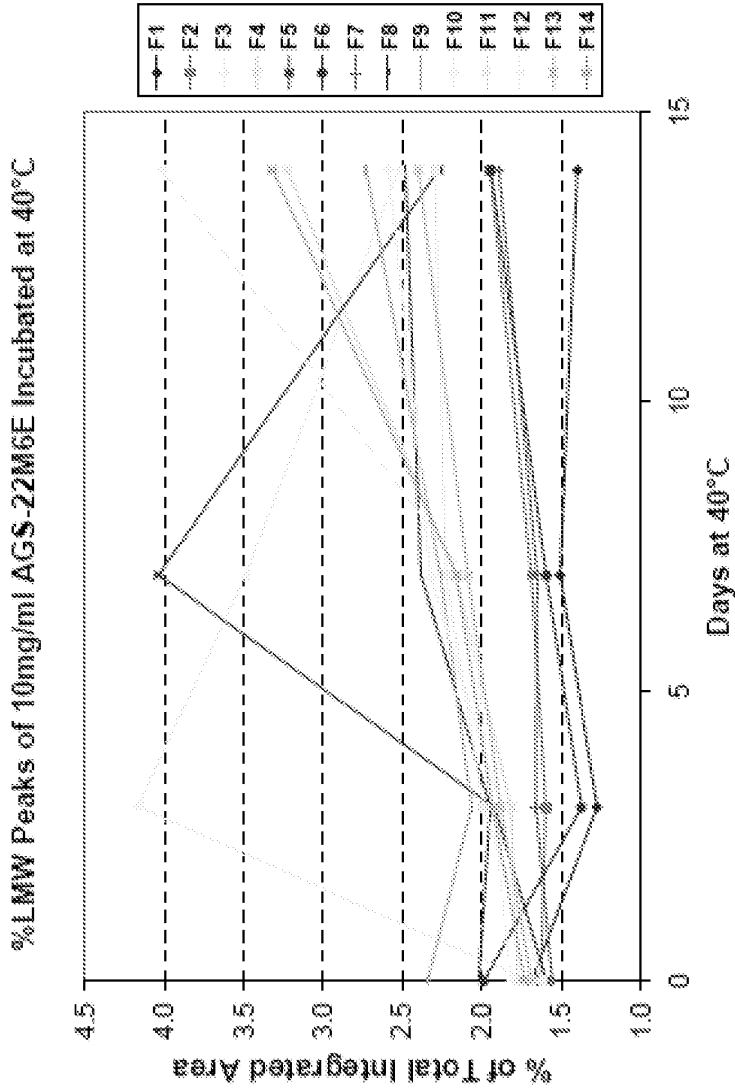


FIG. 1H

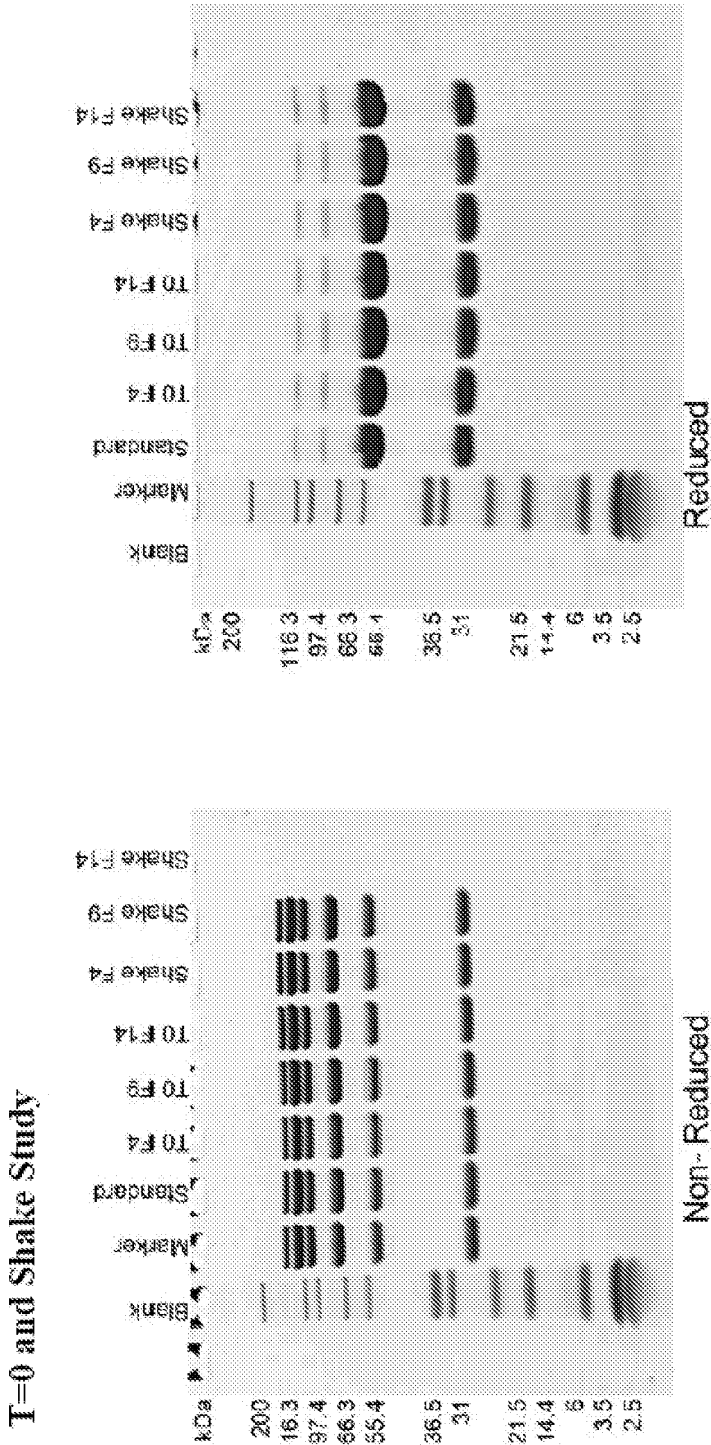


FIG. 2A

Ten Cycle Fz/Th Study

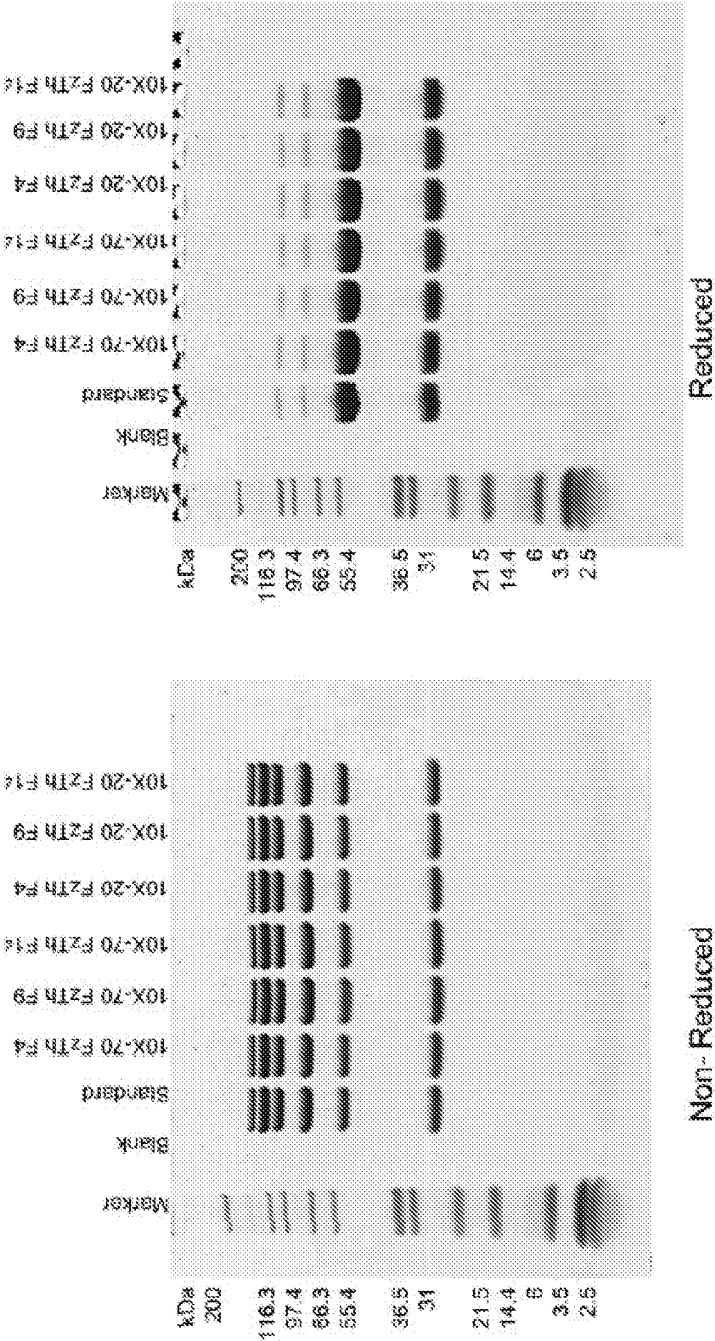


FIG. 2B

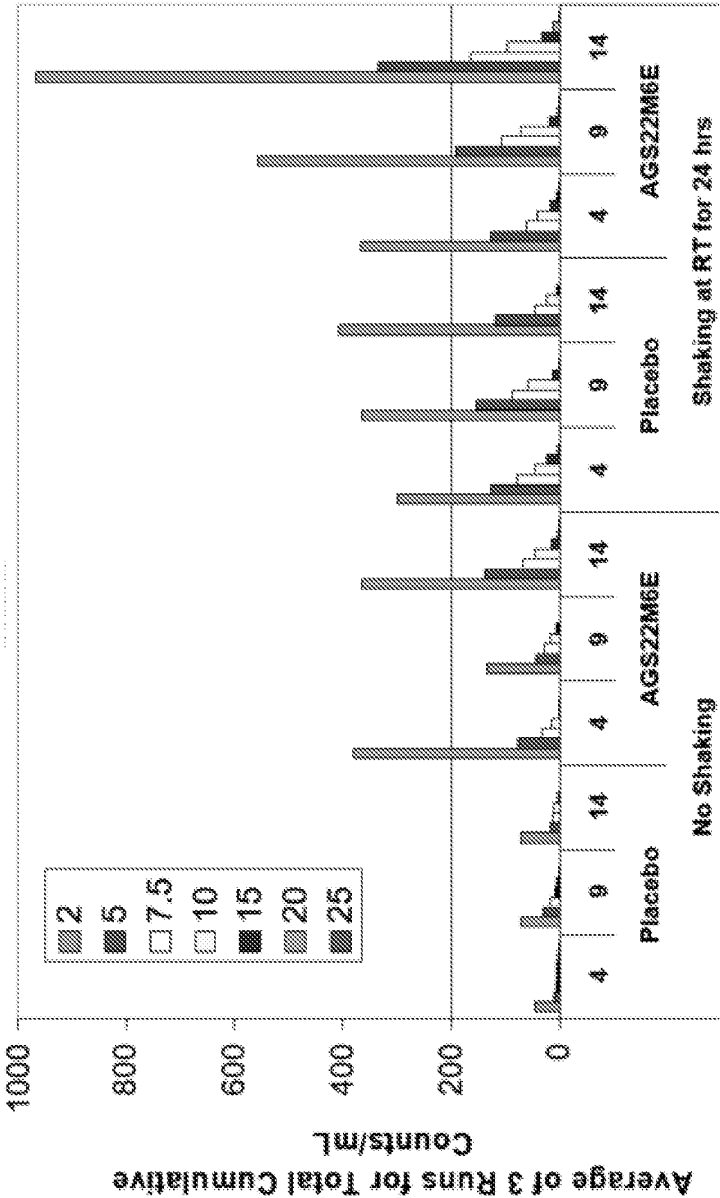


FIG. 2C

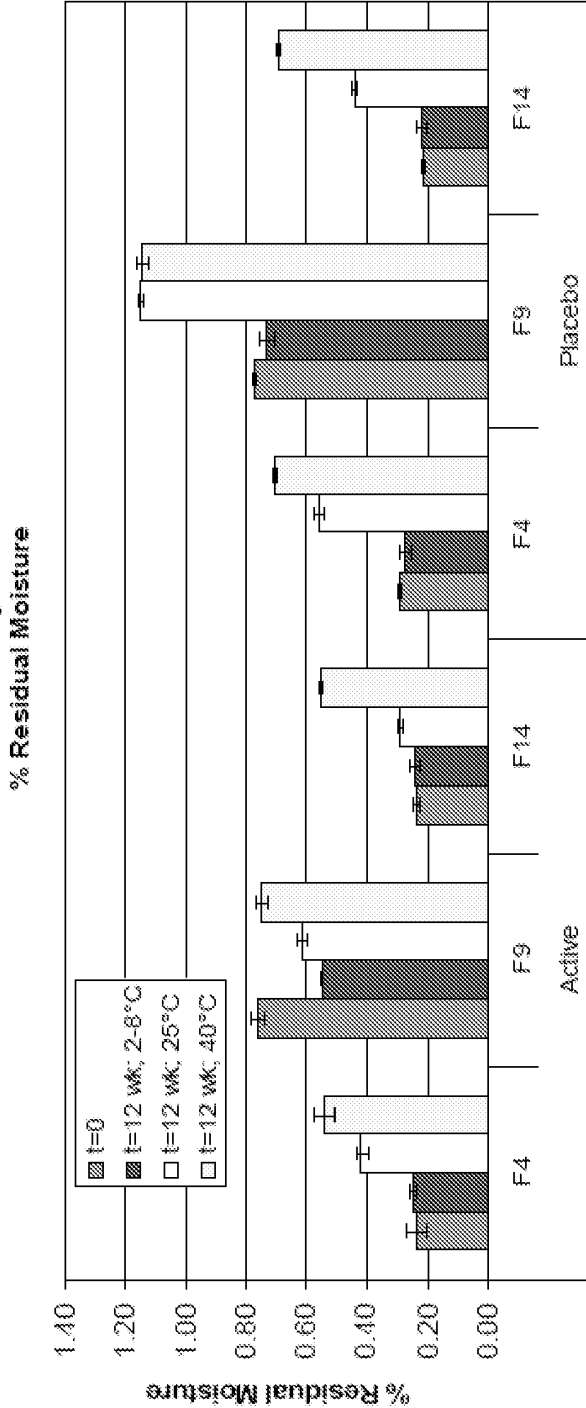


FIG. 3A

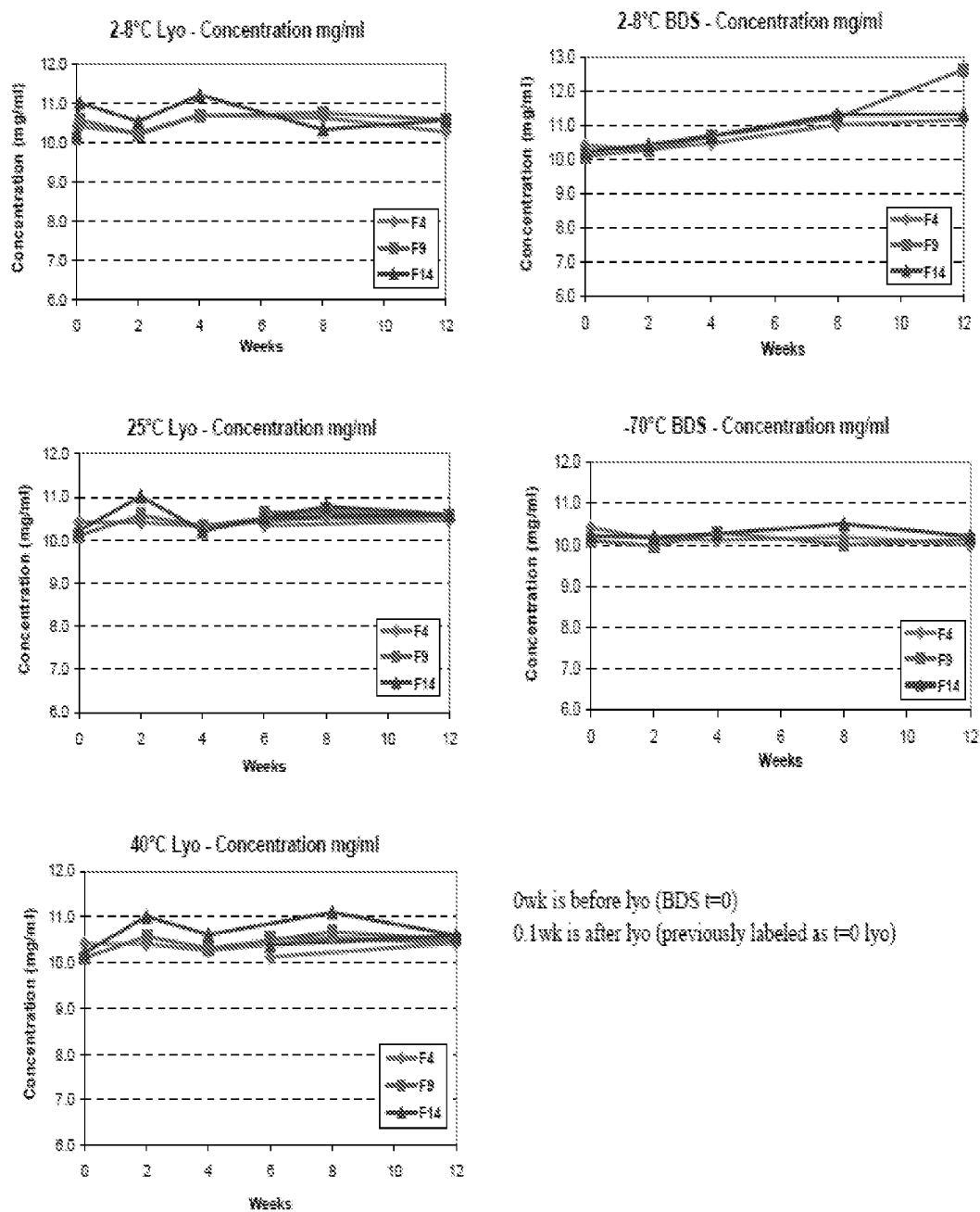


FIG. 3B

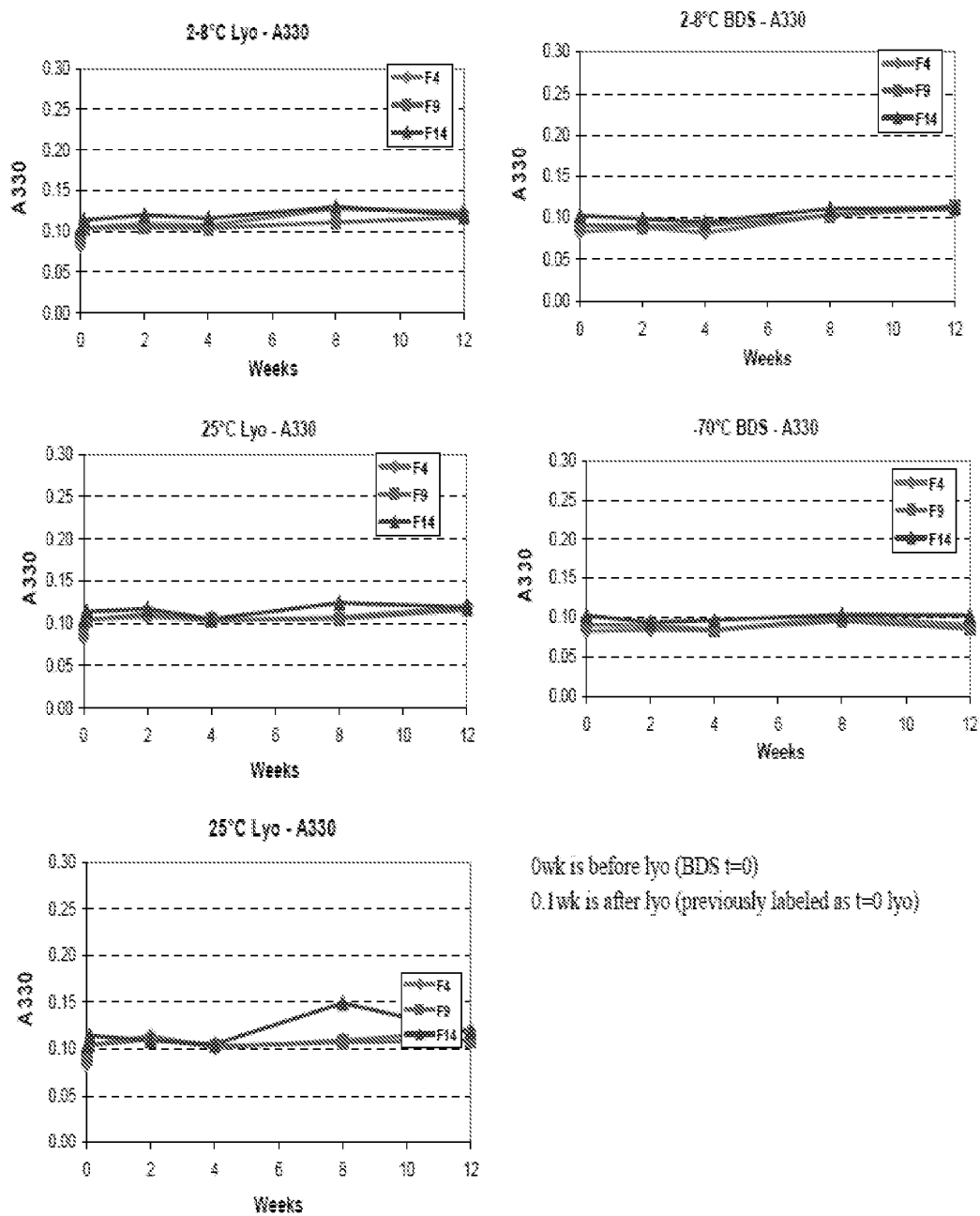


FIG. 3C

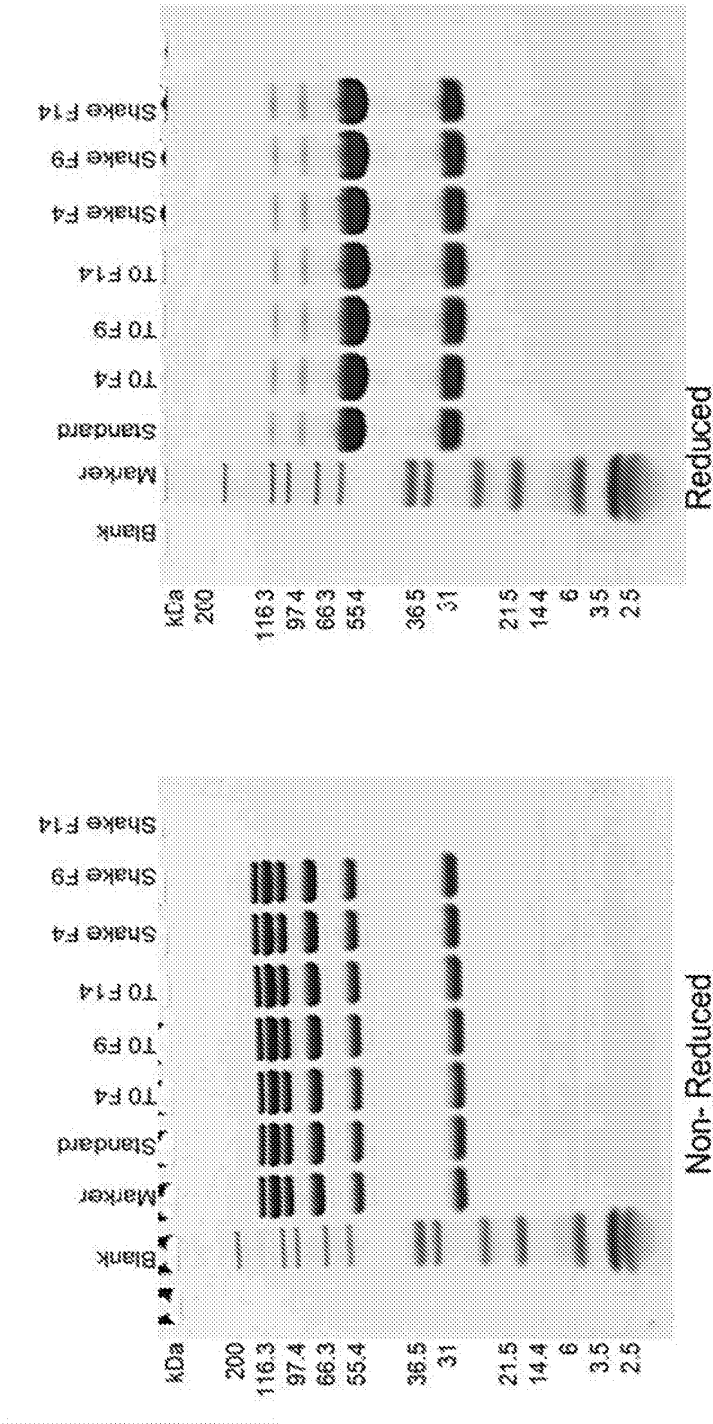


FIG. 3D

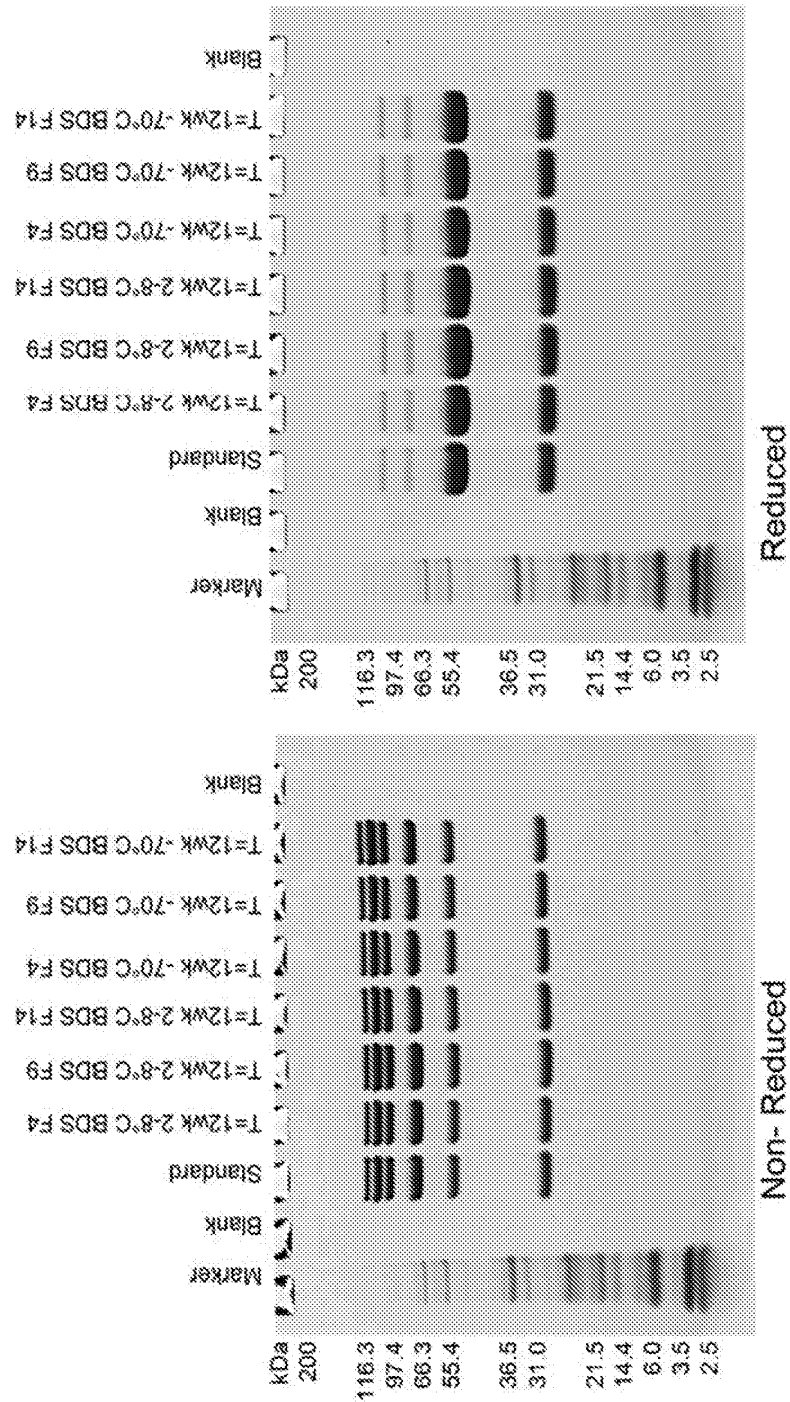


FIG. 3E

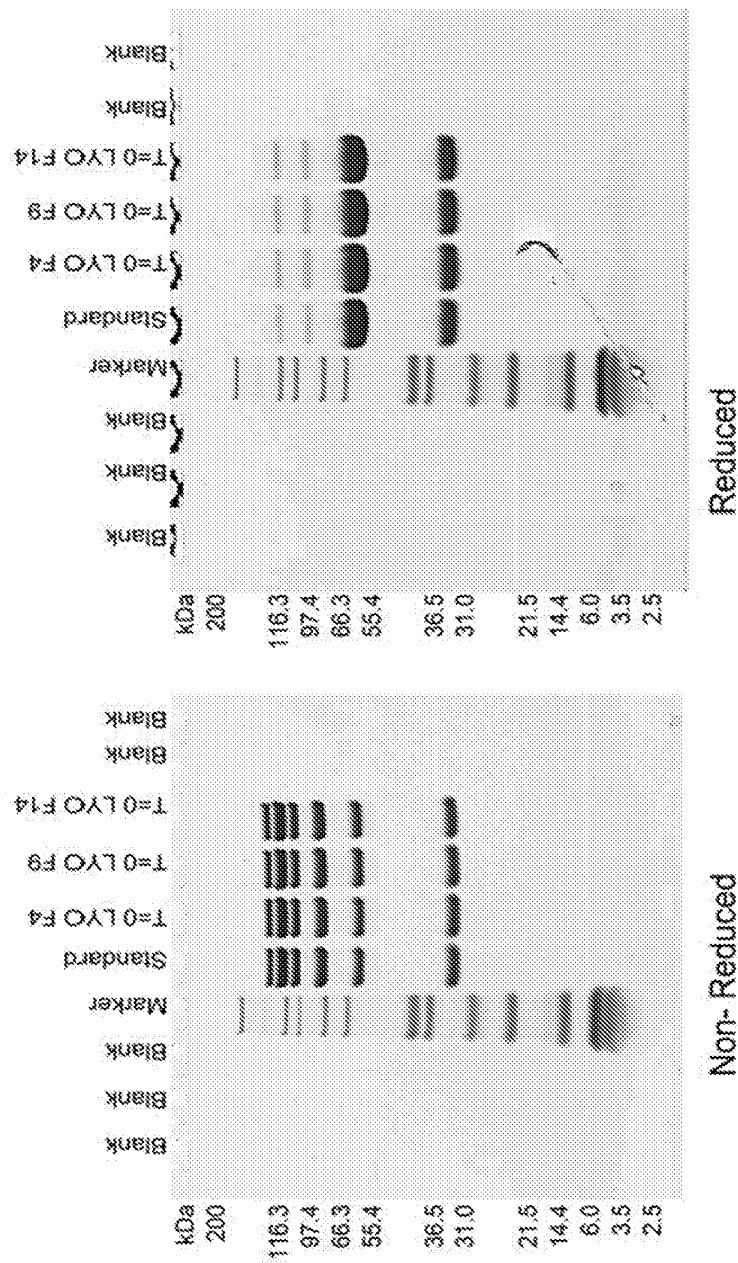


FIG. 3F

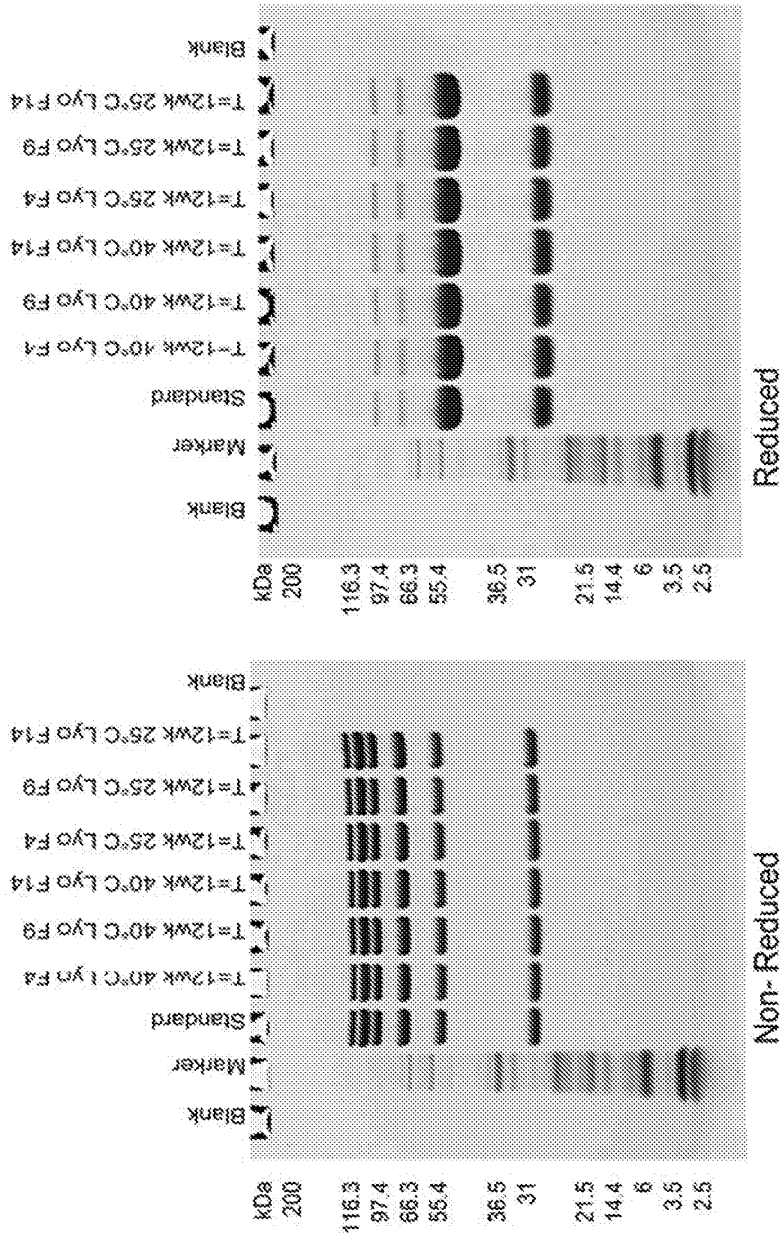


FIG. 3G

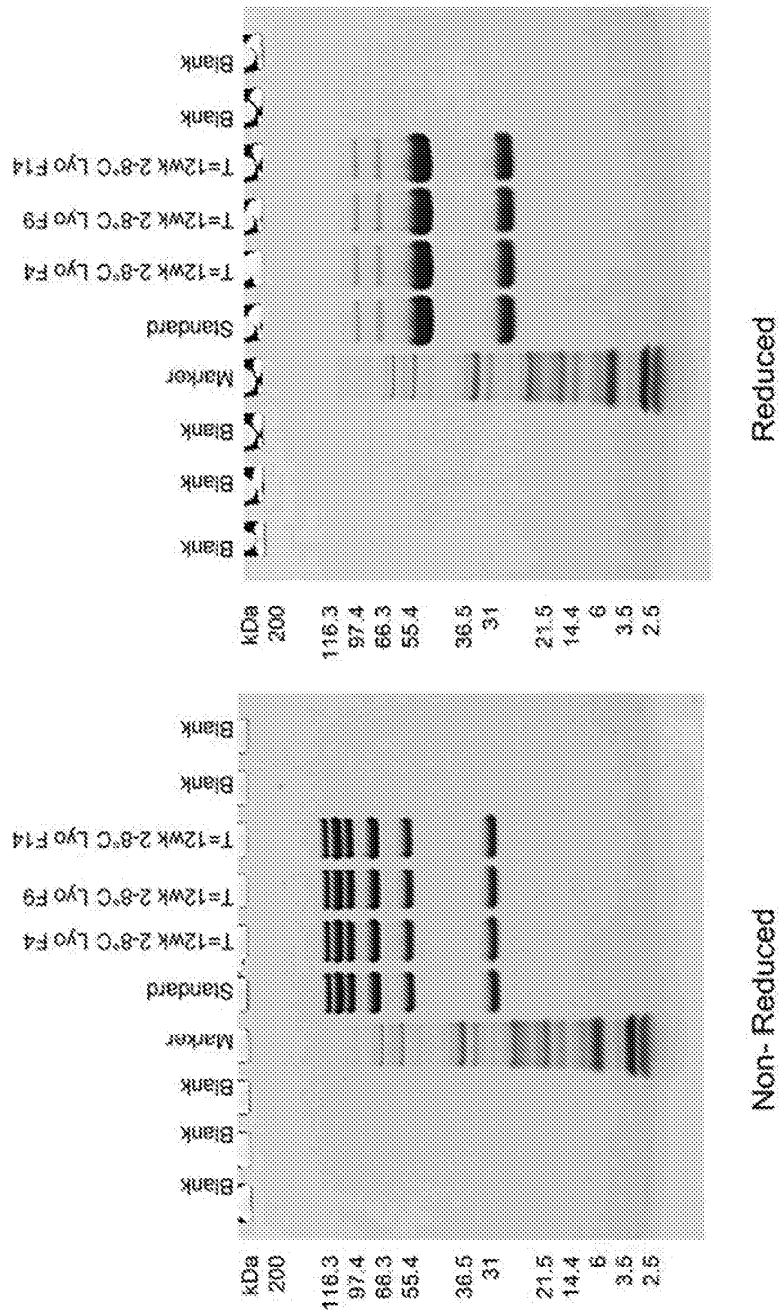


FIG. 3H

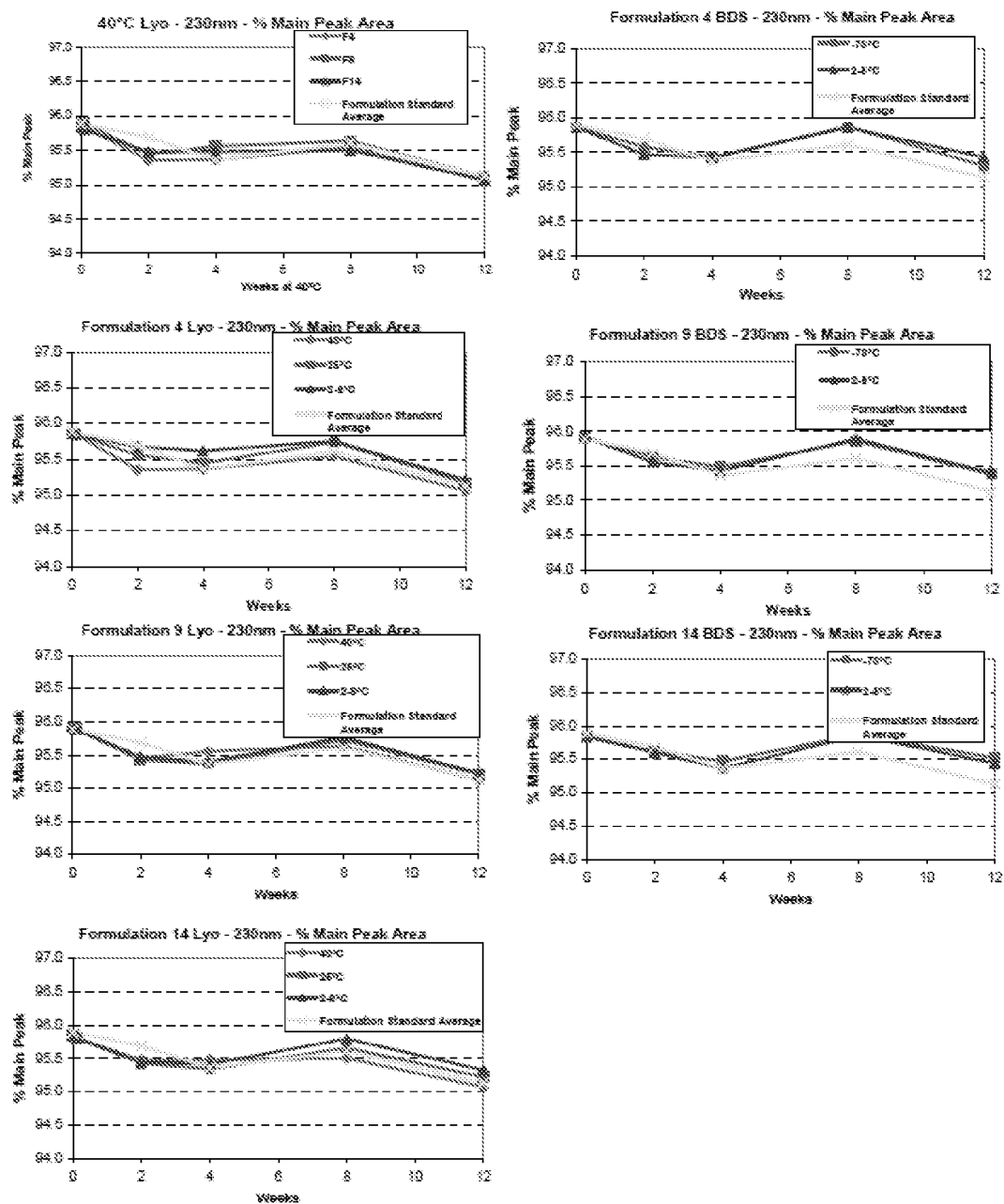


FIG. 31

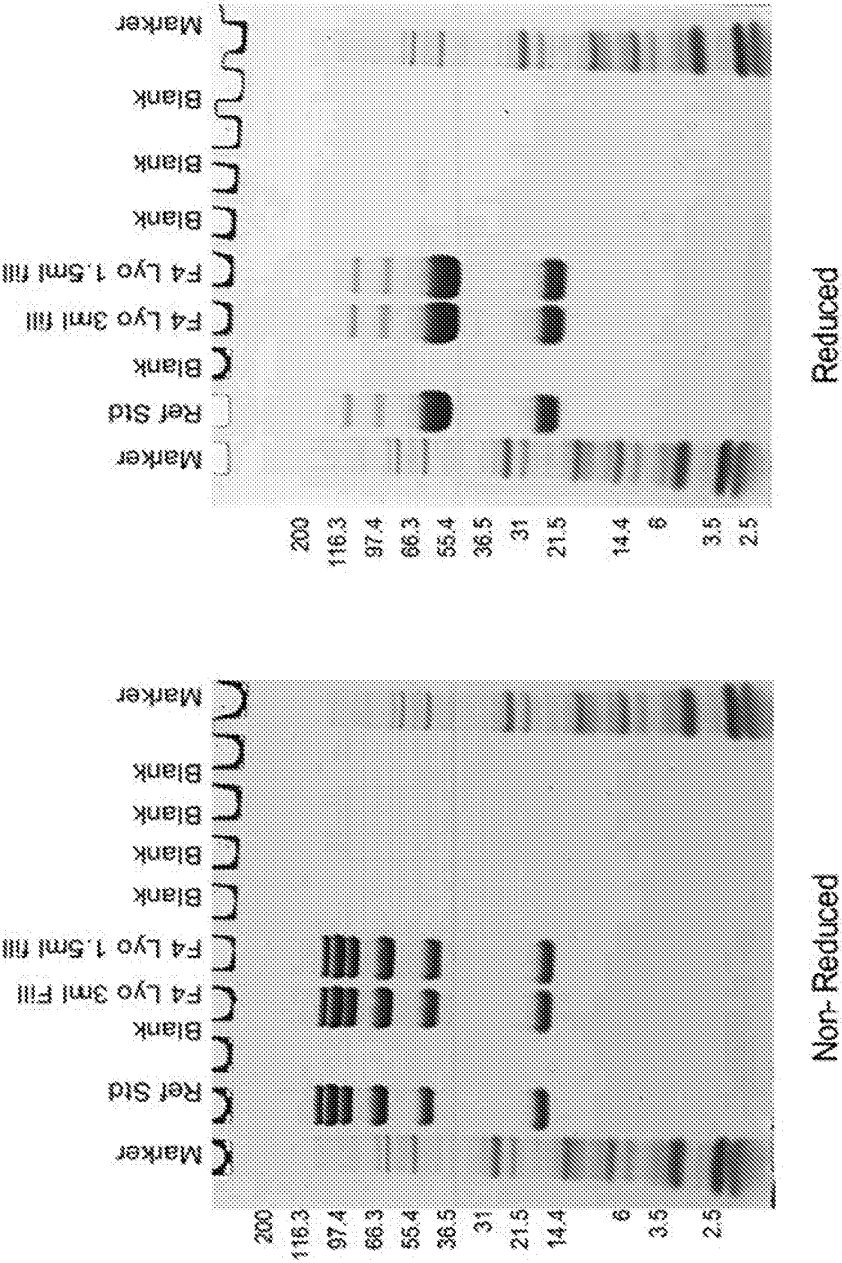


FIG. 4

The cDNA (SEQ ID NO:1) and amino acid sequence (SEQ ID NO:2) of 191P4D12. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

```

1  ggccgctcgttgttggccacagcgtgaggagcagctctgggggagctcggagctcccgatc
61  acggcttcttgggggtagctacggctgggtgtgttagaaggggcccgggctggggctggg
121  tcccttagtggagacccsagtgagagagggcaagaactctgcagcttccgtgccttctgggt
181  cagttcccttattcaagtcctgcagccggctcccgaggagatctcgggtggaacttcagaaac
1      M P L S L G A E M W Q P E
241  gctggggcagtcctgcctttcaaccATGCCCCGTGTCCTGAGGAGCCGAGATGTGCCCCCTG
14  A W L L L L L L L A S F T G R C P A G E
301  AGGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
24  L E T S D V V T V V L G Q D A K L P C F
361  ASCTGGAGAGCTTACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
54  Y R G D S G E Q V G Q V A W A R V D A G
421  TCTACCCAGGGGACTCCGGGAGCAAGTGGGGCAAGTGGCATGGGCTGGGGTGGACCCGG
74  E G A Q E L A L L H S K Y G L H V S P A
481  GCGAAGGCGGCCAGGAAGTACGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
94  Y E G R V E Q P P P P R N F L D G S V L
541  CTTACGAGGGGCGCGCTGGAGCAGCCCGCCCGCCCGCCAGCCAACTCCCTGGAGCGCTCAGTGC
114  L R N A V Q A D E G E Y E C R V S T F P
601  TCTTCCCGCAAGCACTGCGAGCGGAGTGGAGGGGAGTGGAGTGGCGGCTCAGGACCTTCC
134  A G S P Q A R L E L R V L V P P L P S L
661  CCGCCGCGCAGCTTCCAGGGCGCGCTGCGGCTTCCGAGTGGCTGGTGGCTCCCTTCCCTCAG
154  N P G P A L E E G Q G L T L A A S C T A
721  TGAATCCTGGTCCAGCACTAGAAAGAGGGCCAGGGCTGAGCCCTGGCAGCCCTCCTGCACAG
174  E G S P A P S V T W D T E V K G T T S S
781  CTGAGGGCAGGCGGAGCGCGGAGCTGAGCTGGGACAGGAGGTCAAAGGCACACCTCCA
194  R S F E H S R S A A V T S E F H L V P S
841  GCGCTTCTTCAAGCACTGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
214  R S M N G Q P L T C V V S H P G L L Q D
901  GCGCCAGCAGTAATGGGCGAGTACTGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
234  Q R I T H I L N V S F L A E A S V R G L
961  ACCAAAGGATCAGCCACATGCTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
254  E D Q N L W H I G R E G A M L K C L S E
1021  TTGAGAGCCAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGGCTGAGTG
274  G Q F P P S Y N W T R L D G P L P S G V
1081  AAGGCGAGCCCGCTTCCCTCATACAACTGGACAGGCTGGATGGGCTTCTGCCCCAGTGGGG
294  R V D G D T L G F P F L T T E H S G I Y
1141  TACGAGTGGATGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCCACAGCGGCATCT
314  V C H V S N E F S S R D S Q V T V D V L
1201  AGGTCTGCCATGTACGAATGAGTCTCTCTCAAGGGATCTTCAGGTCACCTGTGGATGTTT
334  D P Q E D S G K Q V D L V S A S V V V V

```

FIG. 5A

```

1261 TTGACCCCCAGSAAGACTCTGTGGAAACAGCTGACCTACTGTTCAGCCTCGGTGCTGCTGG
354 G V T A A L L F C L L V V V V V L M S R
1321 TGGGTGTGATCCCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
374 Y H R R K A Q Q M T Q K Y E E E L T L T
1381 GATACCATCCGGCGCAAGGCCCAAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCCTGA
394 R E N S I R R L H S H H T D F R S Q P E
1441 CCAAGGAGAACTCCATCCCGGAGCCTGCATTCCCATCAACCGGACCCCGAGGAGCCAGCCGG
414 E S V G L R A E G H P D S L K D N S S C
1501 AGGAGAGTGTAGSSECTGAGAGGCCGAGGGCCACCTGATAGTCTCAAGGACAAACAGTAGCT
434 S V M S E E P E G R S Y S T L T T V R E
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCCGCAGTCACTCCACGCTGACCAACGGTGAGGG
454 I E T Q T E L L S P G S G R A E E E E D
1621 AGATAGAAACACAGACTGAACTGCTCTCTCTCCAGGCTCTGGGGGGGGGAGGAGGAGGAGG
474 Q D E G I K Q A M N H F V Q E N G T L R
1681 ATCAGGATGAAGGCATCAAAACAGGCCATGAACCATTTCTTTCAGGAGAAATGGGACCCCTAC
494 A K P T G N G I Y I N G R G H L V *
1741 GGGCCAAAGCCCAAGGCCAATGSCATCTACATCAATGGGGGGGACACCTGCTCTGAACCA
1801 ggccctgcctcccttccctaggccctggcctccctctgttgcacatgggagatcttagctcctc
1861 ttggggggccctcccttcaaacaccccccatttcttggggagagatgctcccccattccactgactg
1921 cttgaccccttaccctccaaacccctctgttccctggggagggctcccccatttgcgtctctcc
1981 ccccatgcaatgcaggctccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
2041 tctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
2101 ctgttcatacagagtcaggctgactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
2161 gggcaaacctgtcaggggtttggcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
2221 aaagcaggtattttctcagaccccccagagcaggtattaatgatgcagaggtttggaggagaga
2281 ggtggagactgtgtgtcagaccccccaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
2341 ggtgtgagggaaacctgtctccctccacacttcaggagccatgggggcaagtggtgagcagcca
2401 gtccctgggtcagccagagggcttgaactgttacagaagccctctgcccctctgggtggcctc
2461 tgggctgctgcctgtacatattttctgtaaatatcatgcgcggggagctctcttgcagg
2521 aatactgctccgaatccacttttaattttttcttttttttttttttttttttttttttttttttt
2581 tgtatttttttatttatttttatttttttttttttttttttttttttttttttttttttttttttt
2641 tcaggctgggcttgaactccctgggctcaagcgaatccctccctgctccagcctcccttagtagc
2701 tgggactttaagtgtaacccactgtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
2761 attaaagaaagccttttagatttatccaatgtttactactgggattgcttaagtgaggcc
2821 cctccaaacacccaggggttaattccctgtgattgtgaaaggggtacttccaaaggcatctt
2881 catgcaggcagccctctggggagggcaccctgagagctggttagagctctgaaattagggatgt
2941 gagcctcgtggttactgagtaaggtaaaaattgcacccaccattgtttgtgataccttagg
3001 gaattgcttggacctggtgacccgggctccctgttcaatagtgtgtgttggggagagagaga
3061 gcagtgatttatagacagagagagtaggagttgaggtgaggtgagggaggtgctgggggtg
3121 agaattgtgcctttcccccctgggttttggatccctcaatccaaaggctcttctggatgtttc
3181 tctgggttggggctggagttcaatgaggtttatttttttagctggcccccacccagatacactc
3241 agccagaatacctagatttagtaccacaaactcttcttagctctgaaactctgctggattctt
3301 ggccctaaaggagagggctcccatccttctgttccccagccagcctaggacttcgaatgttgg
3361 gctggaagatcctaagatccataacatgtacatttttatgtaaatatgtgcataatttgcacat
3421 aaatgtattctgtttttaaataaacagaccccaacttgaaaaa

```

FIG. 5A (con't)

The amino acid sequence (SEQ ID NO:7) of Ha22-2(2,4)6.1 heavy chain. Double-underlined is the leader sequence, underlined is the heavy chain variable region, and underlined with a dashed line is the human IgG1 constant region.

```

1  MEFLGLCNVELVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFS
51 YNMNVVRQAPGRCLEWVSYISSSSSSTIYYADSVKGRFTIGRDMAKNSL
101 QMNSLRQESTAVYYCARAYYYCMQDVWQQTTVTVSSASTEGPSYTFLAFF
151 AKSTSGGTAALGCLVYEDYFPEPVTVSWNSGALTSCVHTFPAVLQSSGLYS
201 LSSEVYTFPSGSLSTQTXICNVNKKFSTKVDKRVKPKSCQKSTSTCPKCPA
251 PELLGGPSVFLFPPKPKDTLMISRTFEVTCVVVDVSHEDPEVEFNWYVDG
301 VEVHNAAKTKEREEDYNSTYRVVSVLTVLHQDWLNGKEYKCKVHREALDAP
351 TEKTIQKAAEQGPRPDQVYTLPPSRHEEMTKNQVSLTCLVKGFYPSDIAVEW
401 ESNGQPFNNYKTTTPPYLDSDGSFFLYSKLTVDKSRWQQGNVFPSCSVNHEA
451 LNNHYTQKSLGLSPCK

```

The amino acid sequence (SEQ ID NO:8) of Ha22-2(2,4)6.1 light chain. Double-underlined is the leader sequence, underlined is the light chain variable region, and underlined with a dashed line is the human kappa constant region.

```

1  MMNRVFPACILGLILLKFPSSRCDIQNTQSPSSVSASVGDENVITCRASQC
51 ISENLAWYDCKPKAKPKFLIYAASTLQSGVPSRPFGSGSGGTGFTLTISL
101 QPEDFATYYCQDANSFPPTFGGCTHVEIKRTVAAPSYTIFPPSPDQLKSG
151 IASVYCIANNFYPSBAKVQNKVDNALQSGNSQESVTEQDSKASTYRASSC
201 LTLSKADYEKHKMVAACEVTHQGLSSPVTKSFNGEC

```

FIG. 5C