Influenza A
Influenza B
Adenovirus 4
Adenovirus 5
Adenovirus 7
Parainfluenza
Rhino virus
RSV
West Nile Virus
Coronavirus
S. pneumoniae
S. pyogenes
M. pneumoniae
N. meningitis
B. Pertussis
C. pneumoniae
B. anthracis
Variola Major Virus
Ebola Zaire
Lassa Virus
F. tularensis
Y. pestis
A. Thaliana
Adf Vac

Fig. 1

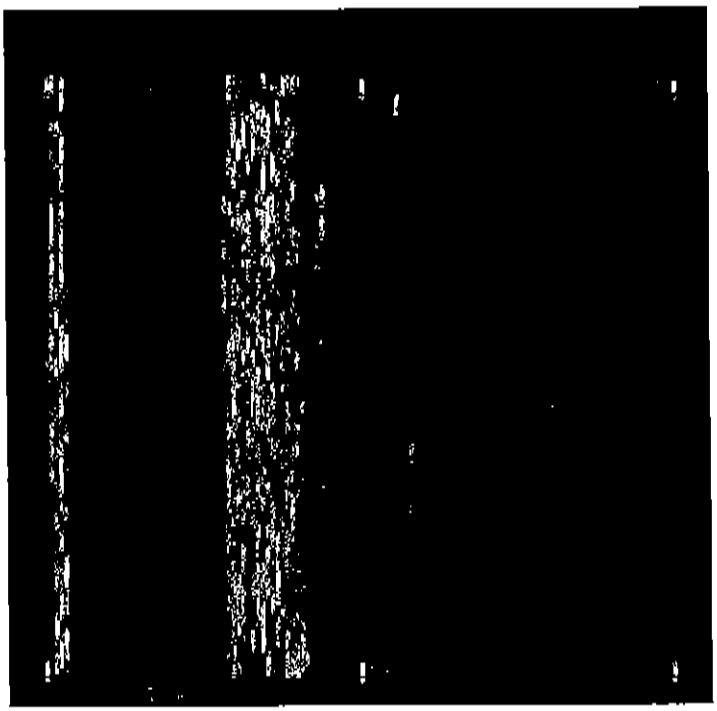


Fig. 2B

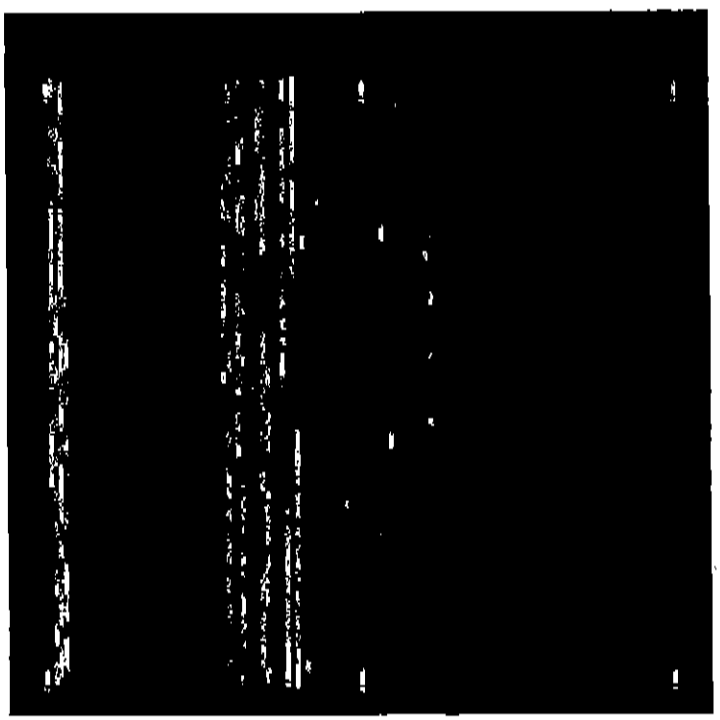


Fig. 2A

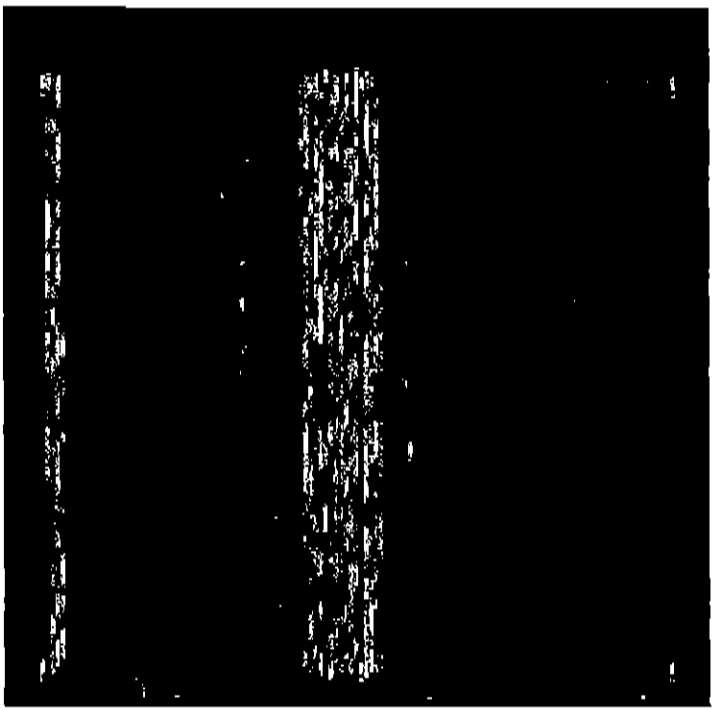


Fig. 3B

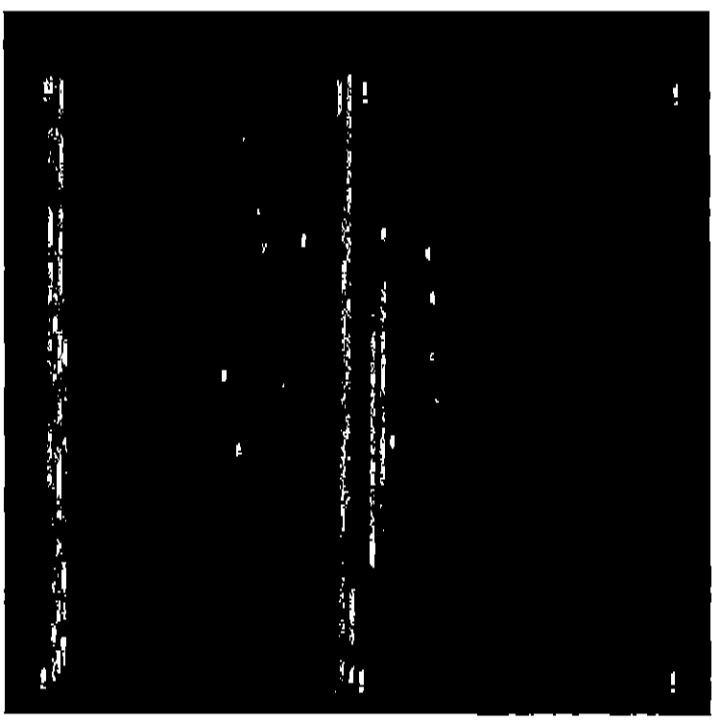


Fig. 3A

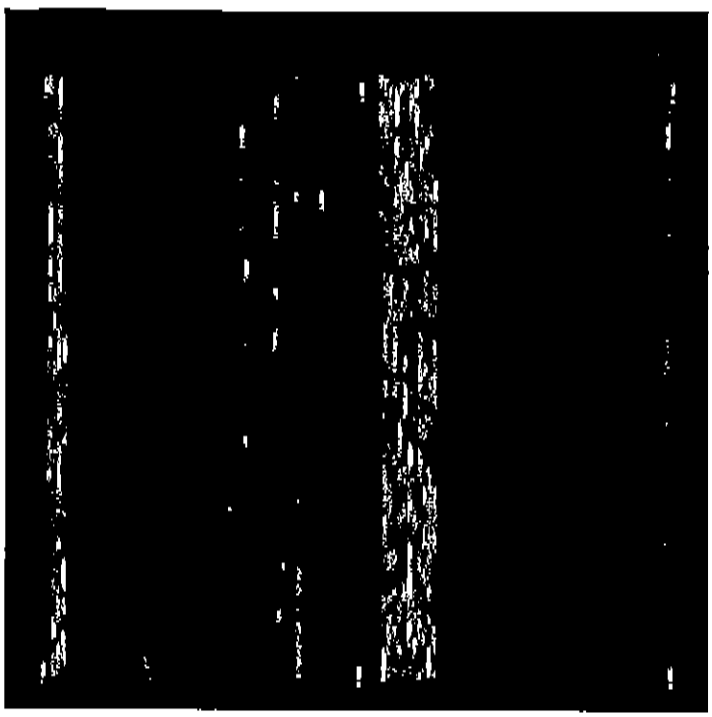


Fig. 3D

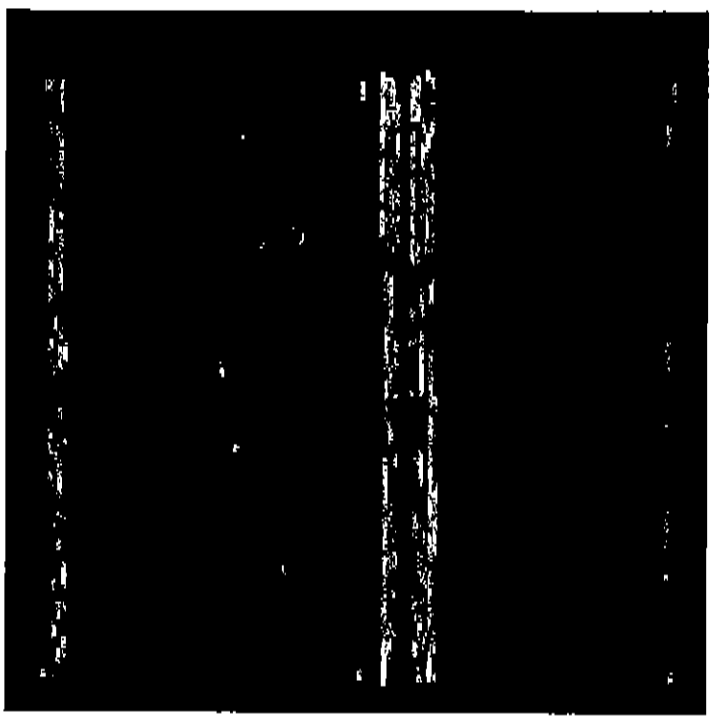


Fig. 3C

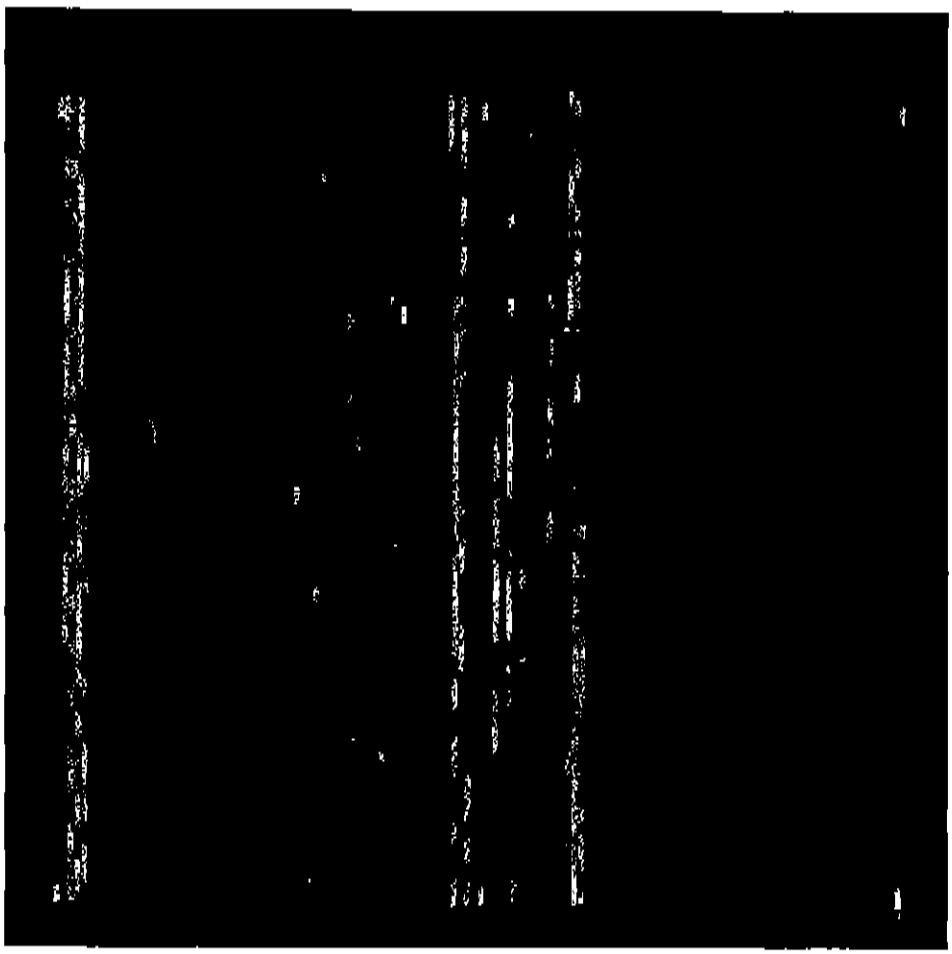


Fig. 4

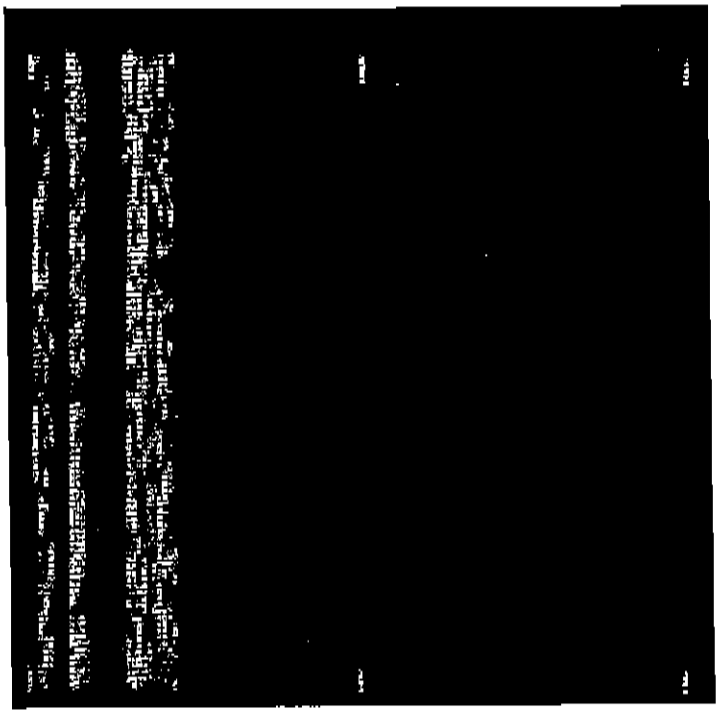


Fig. 5B

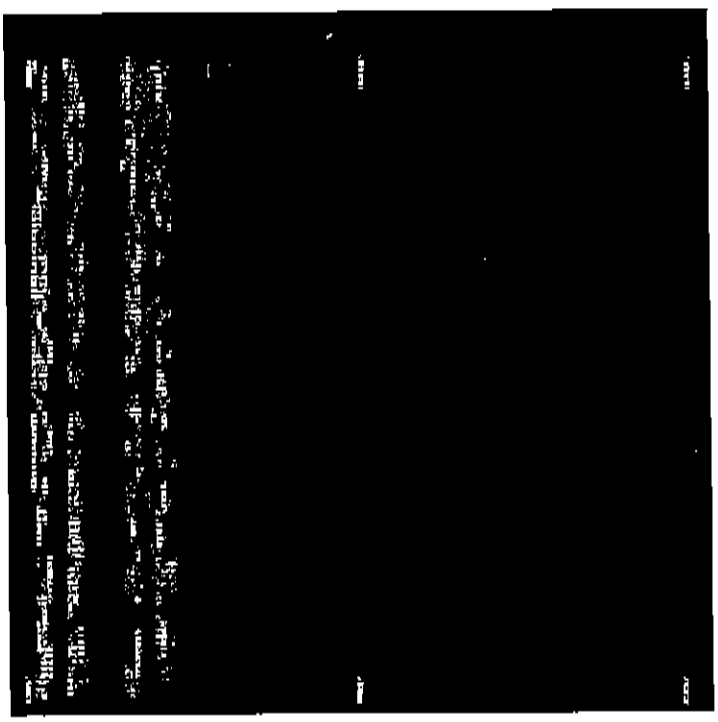


Fig. 5A

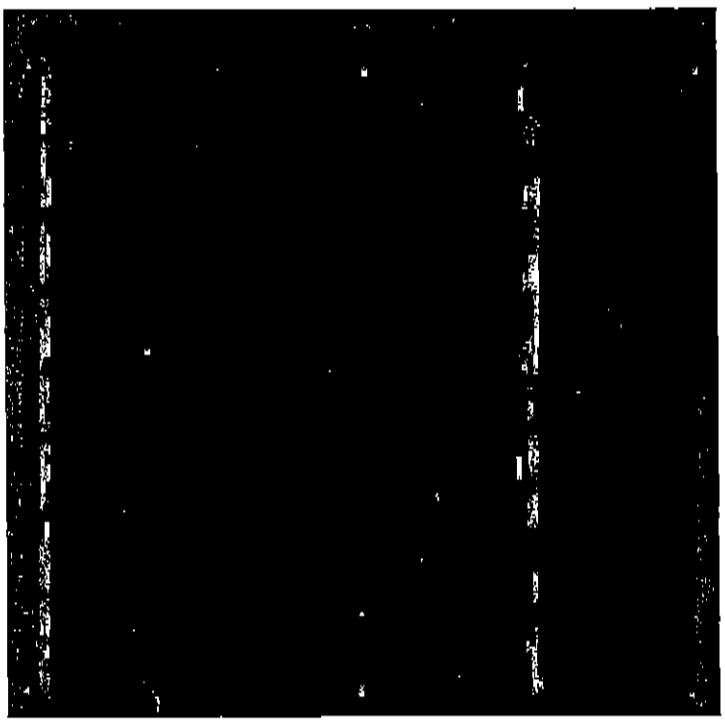


Fig. 6B

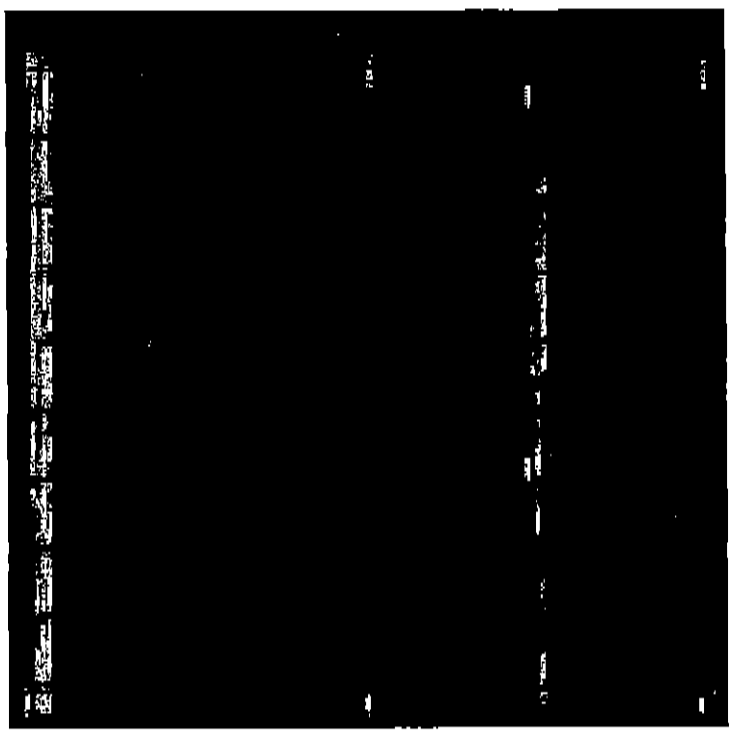


Fig. 6A

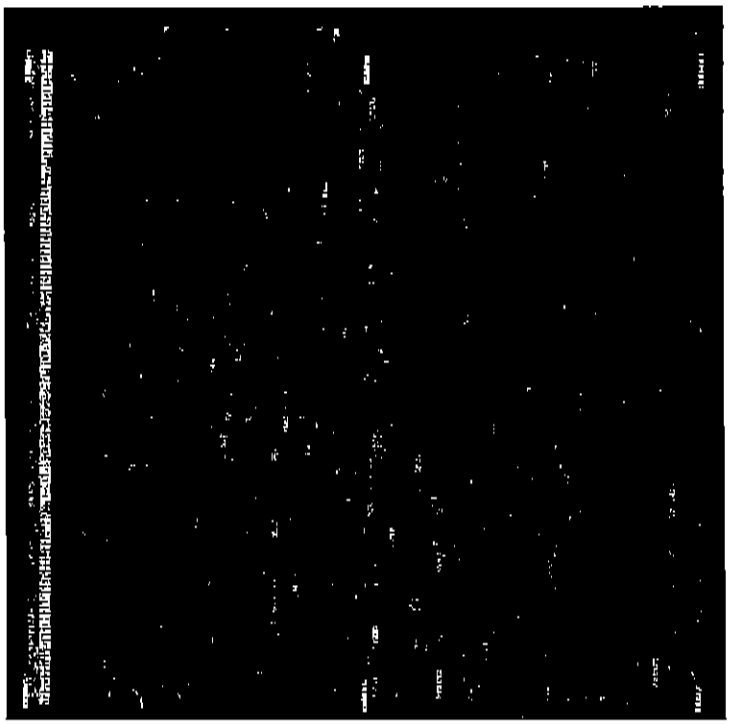


Fig. 7B

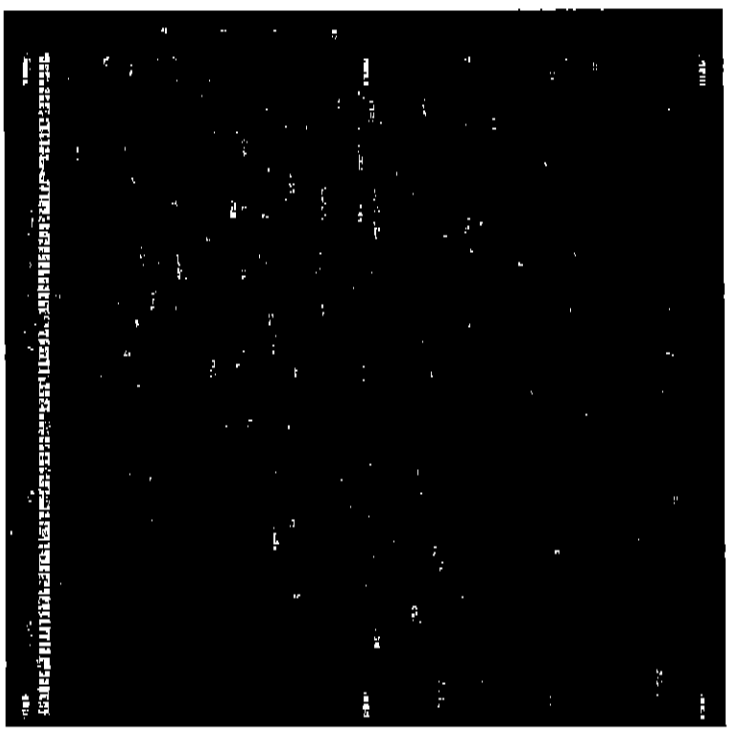


Fig. 7A

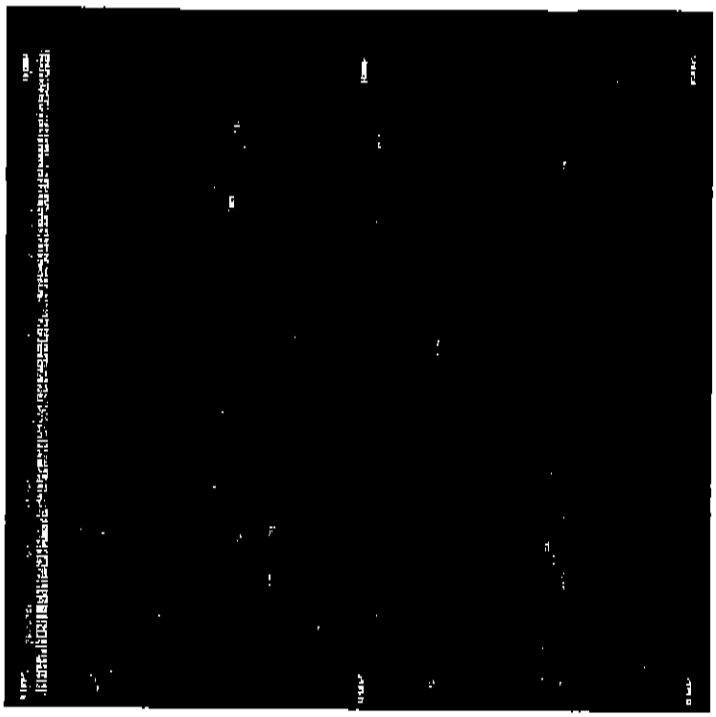


Fig. 7D

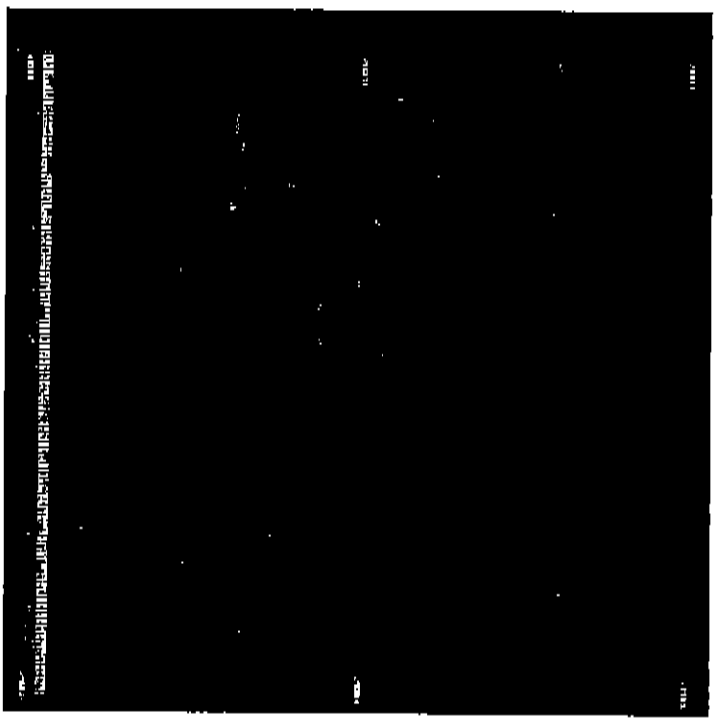


Fig. 7C

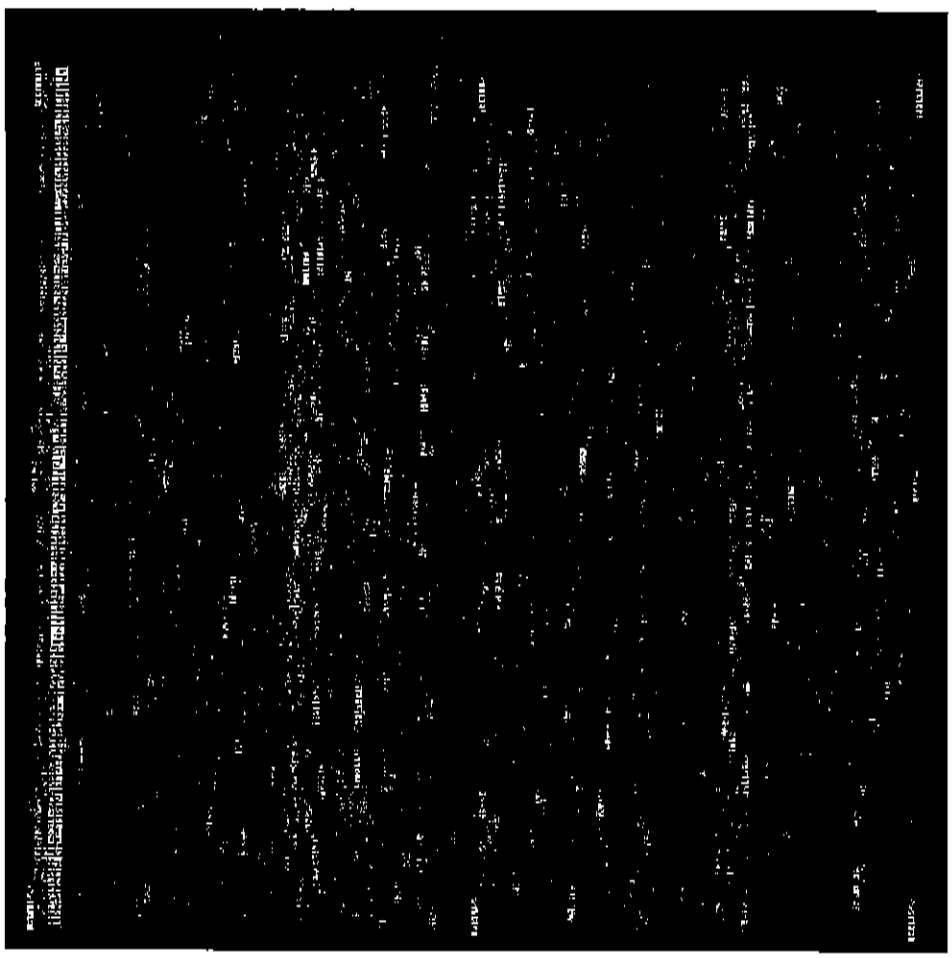


Fig. 7E

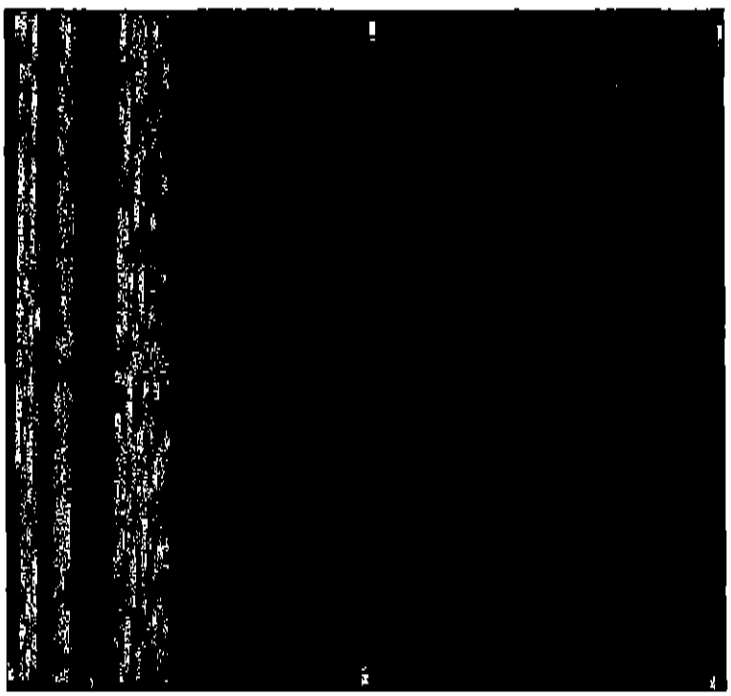


Fig. 8B

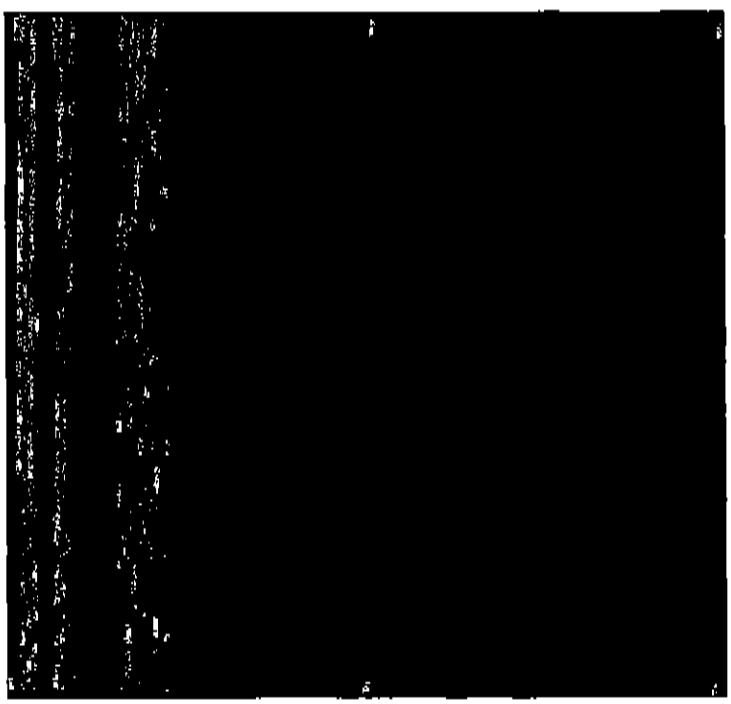


Fig. 8A

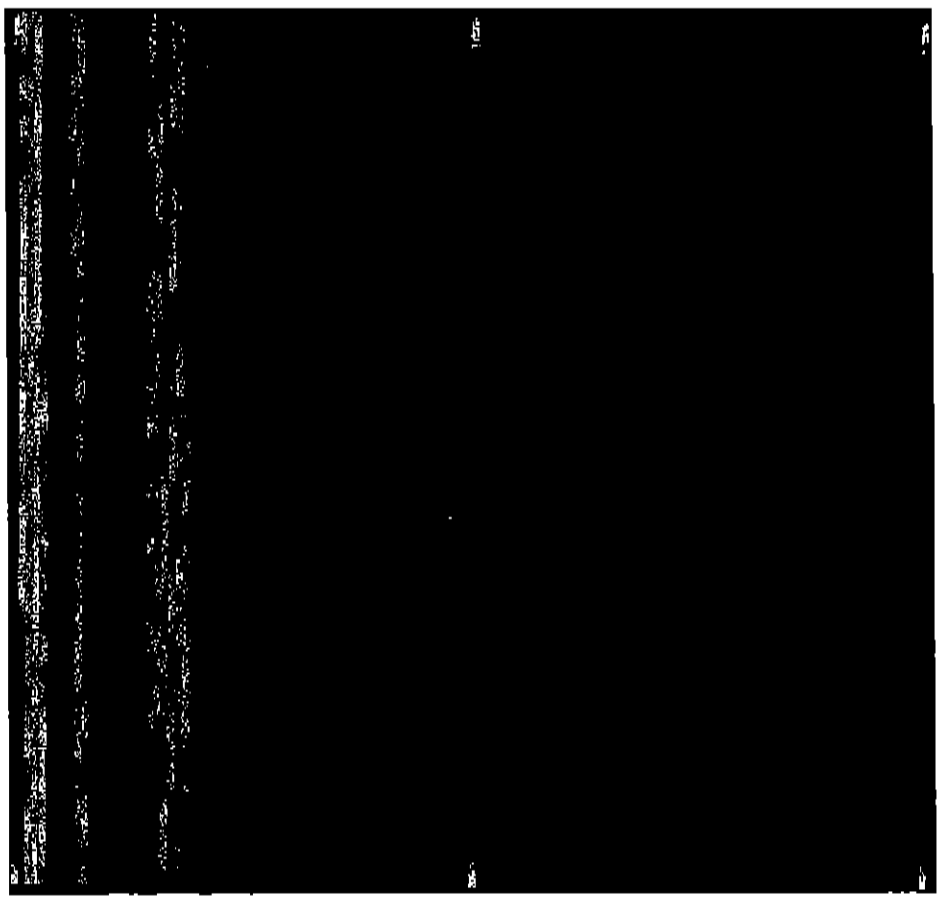


Fig. 8C

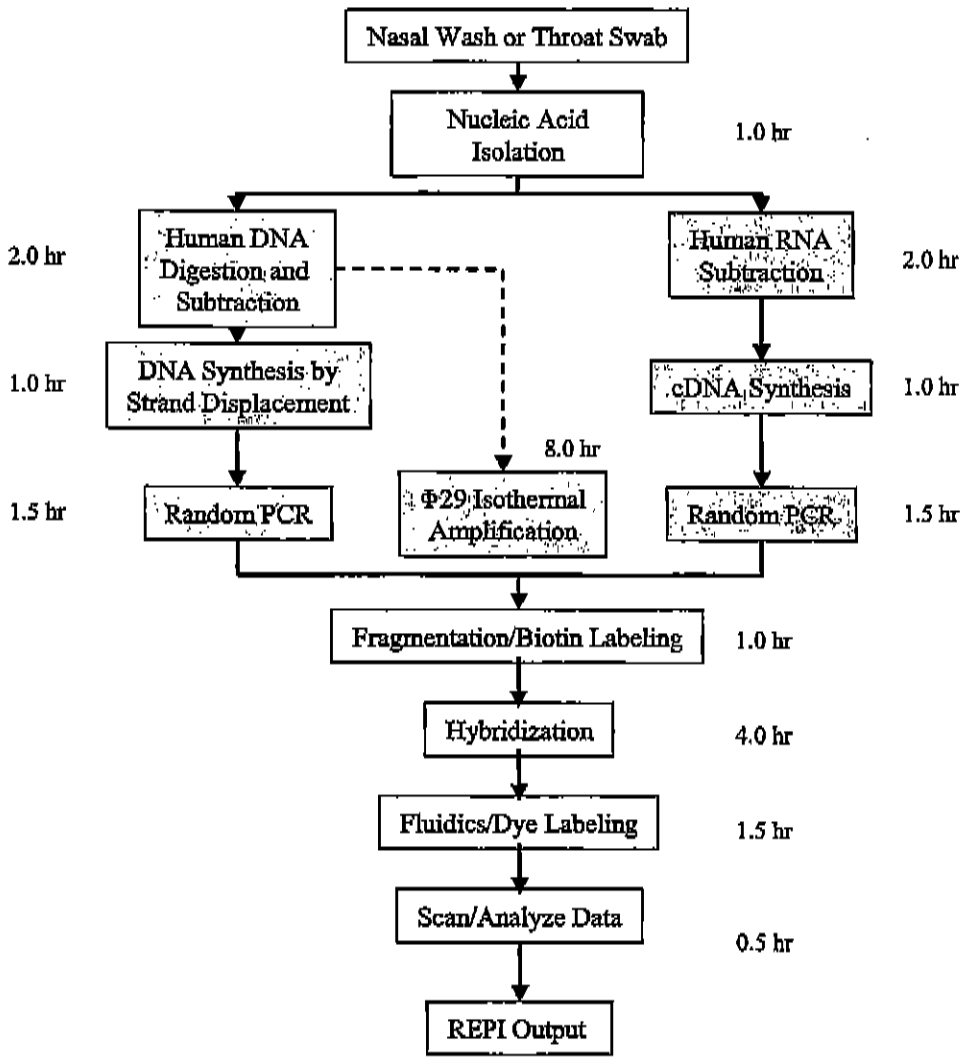

Nasal Wash or Throat Swab
Nucleic Acid Isolation
1.0 hr
Human DNA Digestion and Subtraction
2.0 hr
Human RNA Subtraction
2.0 hr
DNA Synthesis by Strand Displacement
1.0 hr
cDNA Synthesis
1.0 hr
8.0 hr
Random PCR
1.5 hr
Φ29 Isothermal Amplification
Random PCR
1.5 hr
Fragmentation/Biotin Labeling
1.0 hr
Hybridization
4.0 hr
Fluidics/Dye Labeling
1.5 hr
Scan/Analyze Data
0.5 hr
REPI Output

Fig. 9

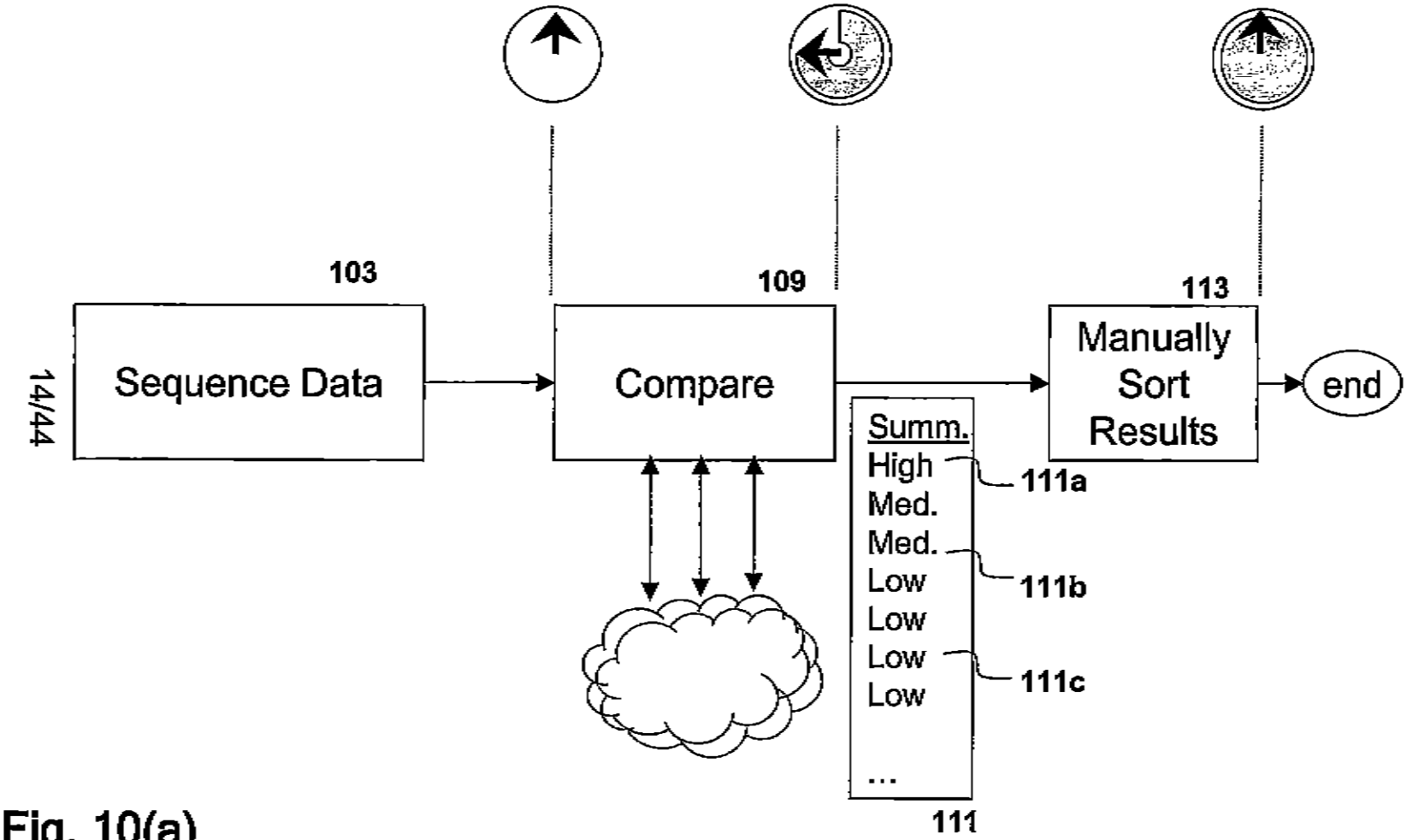


Fig. 10(a)
Background Art

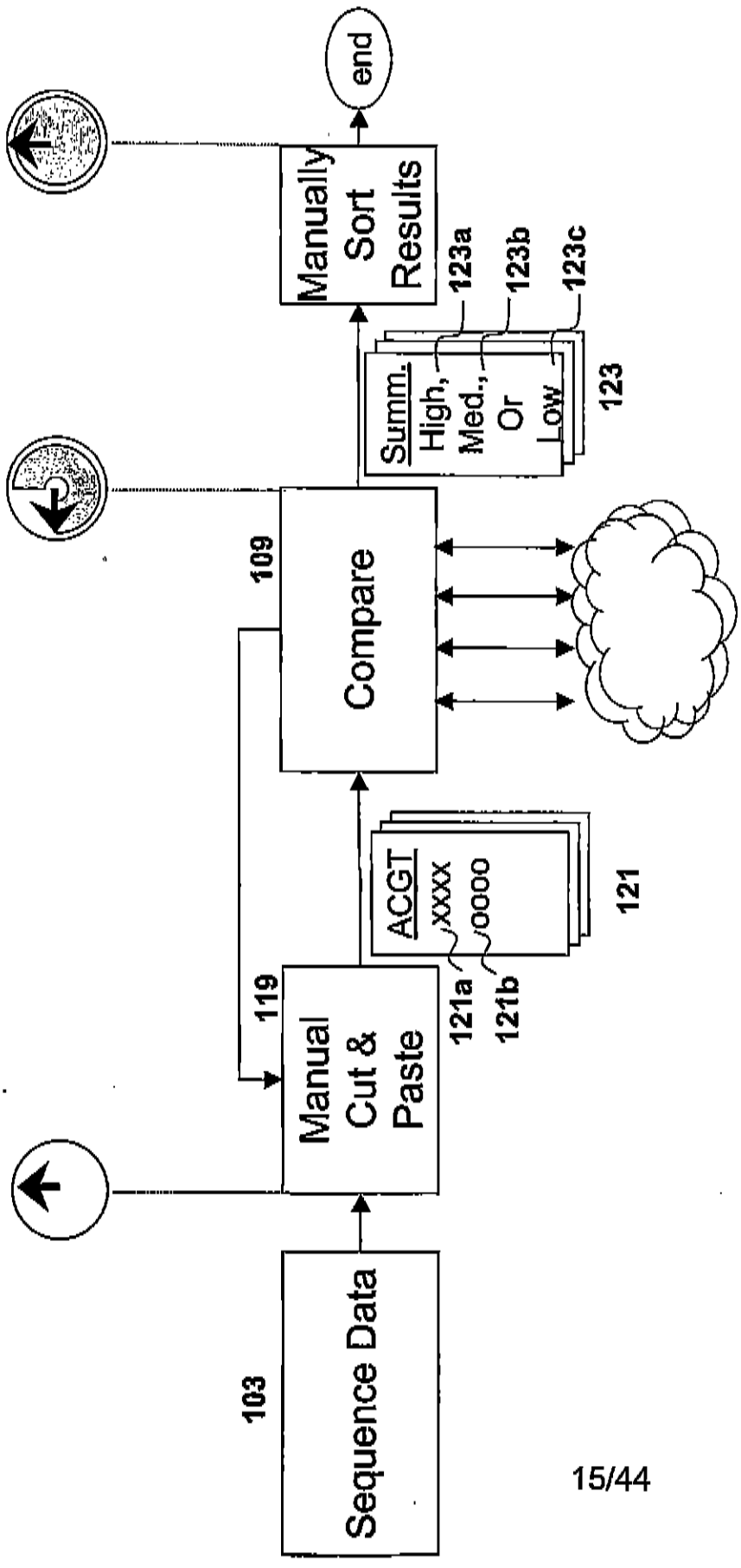


Fig. 10(b)
Background Art

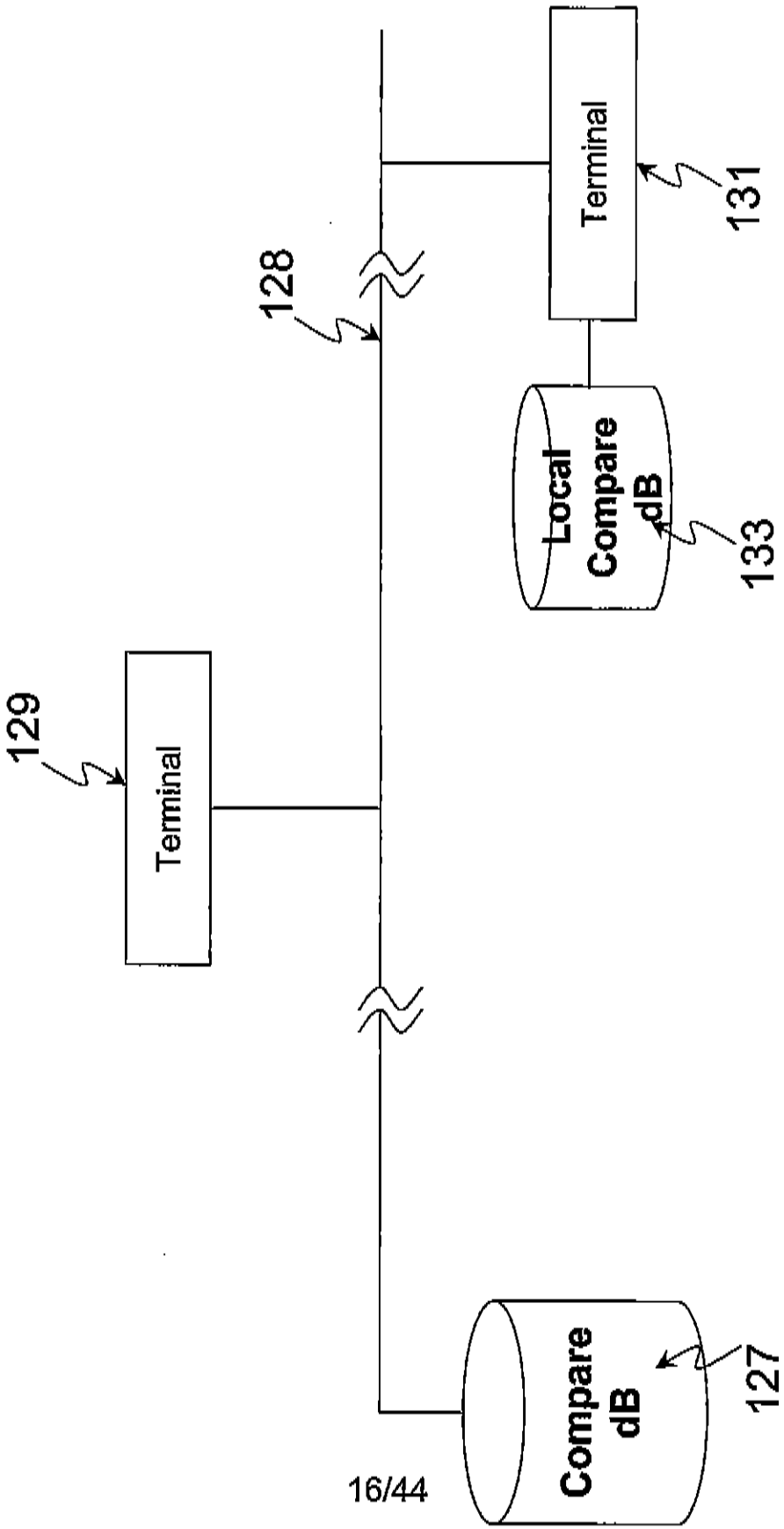


Fig. 10(c) Background Art

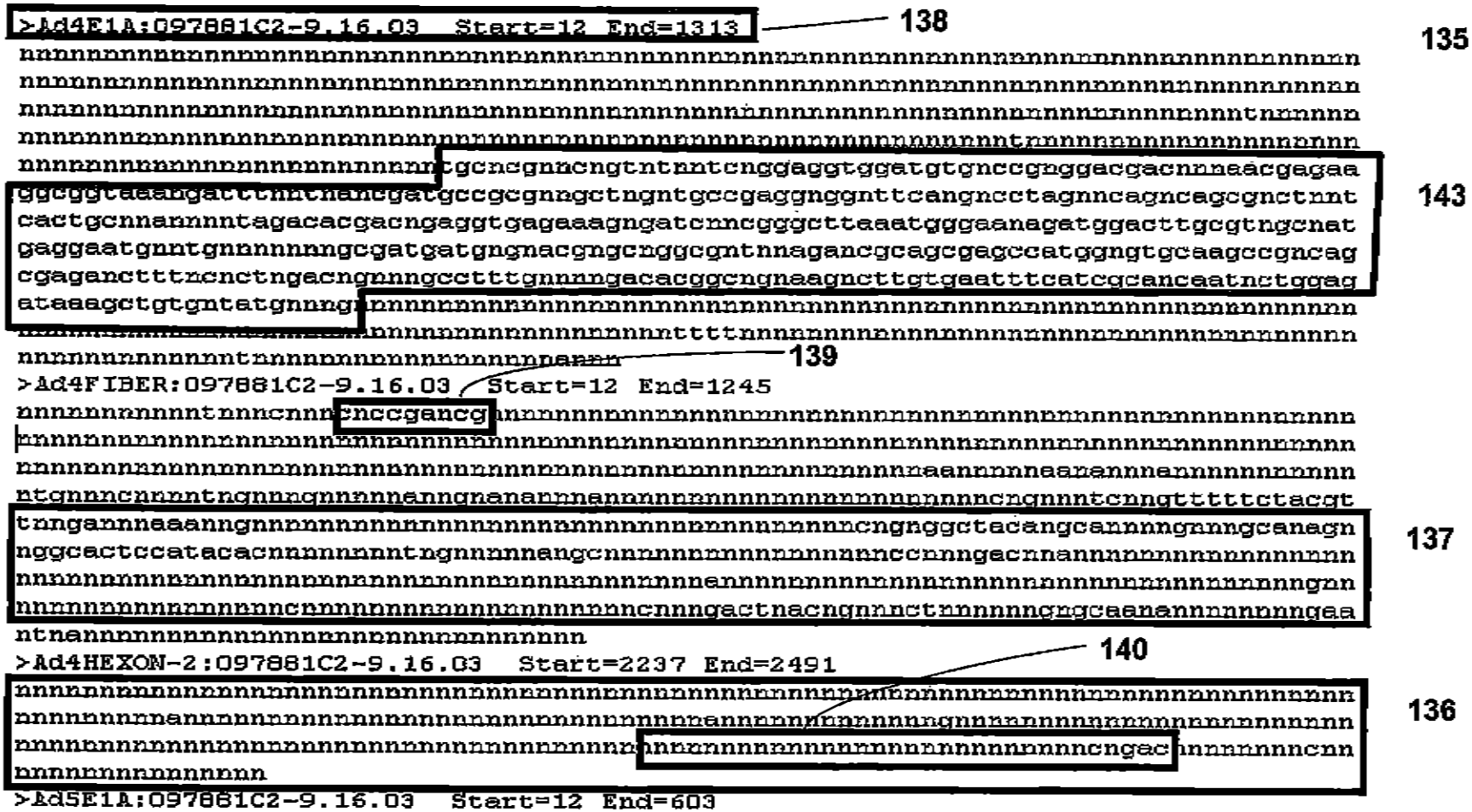


Fig. 10(d)
Background Art

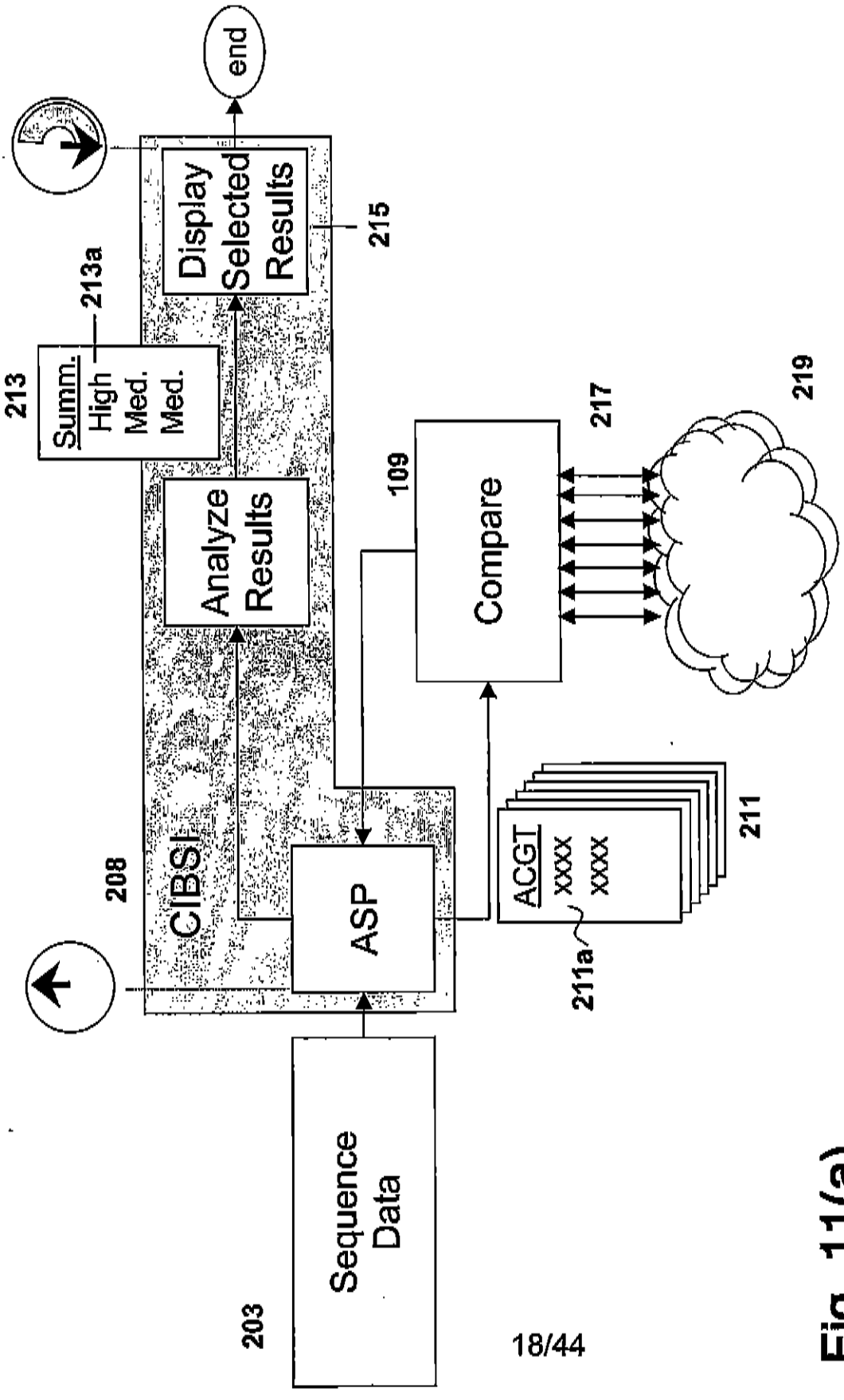

end
Display Selected Results
215
213a
213
Summ.
High
Med.
Med.
Analyze Results
CIBSI
208
109
Compare
217
219
ASP
ACGT
XXXX
XXXX
211
211a
Sequence Data
203

Fig. 11(a)

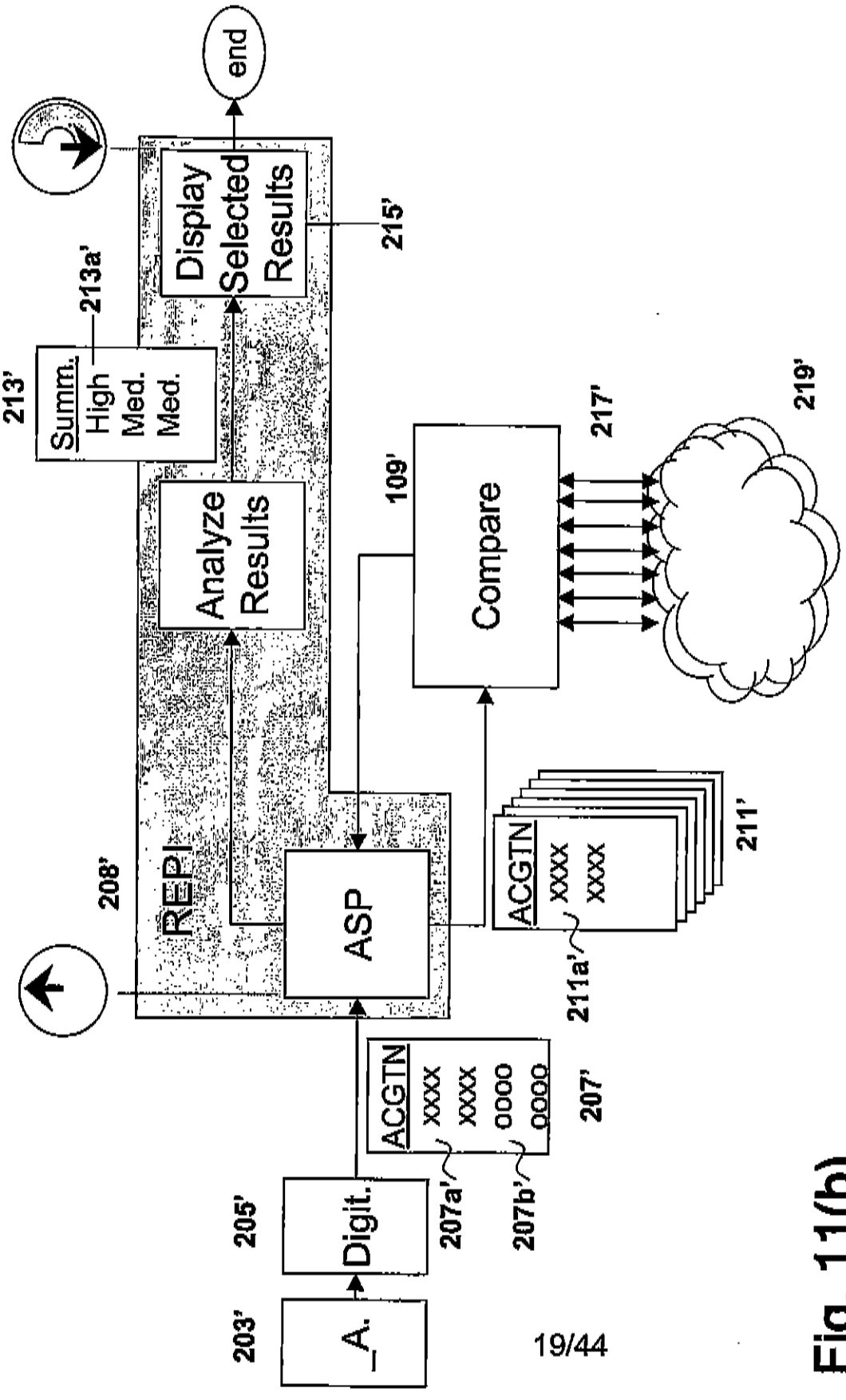

203'
_A_
205'
Digit.
207a'
207b'
ACGTN
XXXX
XXXX
0000
0000
207'
208'
REPI
ASP
211a'
ACGTN
XXXX
XXXX
211'
109'
Compare
217'
219'
Analyze Results
213'
Summ.
High
Med.
Med.
213a'
Display Selected Results
215'
end

Fig. 11(b)

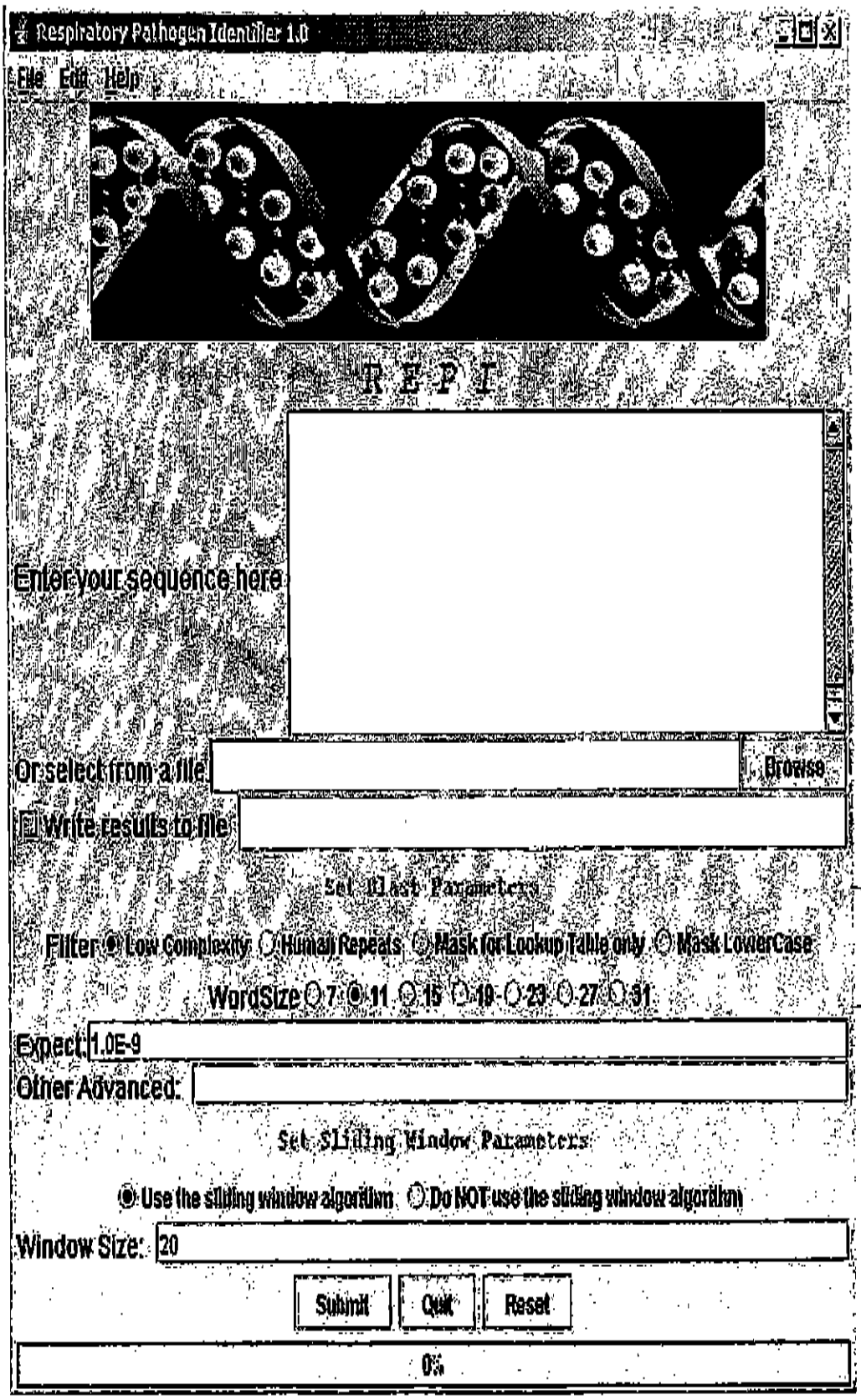

Respiratory Pathogen Identifier 1.0
File Edit Help
R E P I
Enter your sequence here
Or select from a file:
Browse
Write results to file:
Set Blast Parameters
Filter: Low Complexity Human Repeats Mask for Lookup Table only Mask LowerCase
WordSize: 7 11 15 19 23 27 31
Expect: 1.0E-9
Other Advanced:
Set Sliding Window Parameters
Use the sliding window algorithm Do NOT use the sliding window algorithm
Window Size: 20
Submit Quit Reset
0%
251
253

Fig. 11(c)

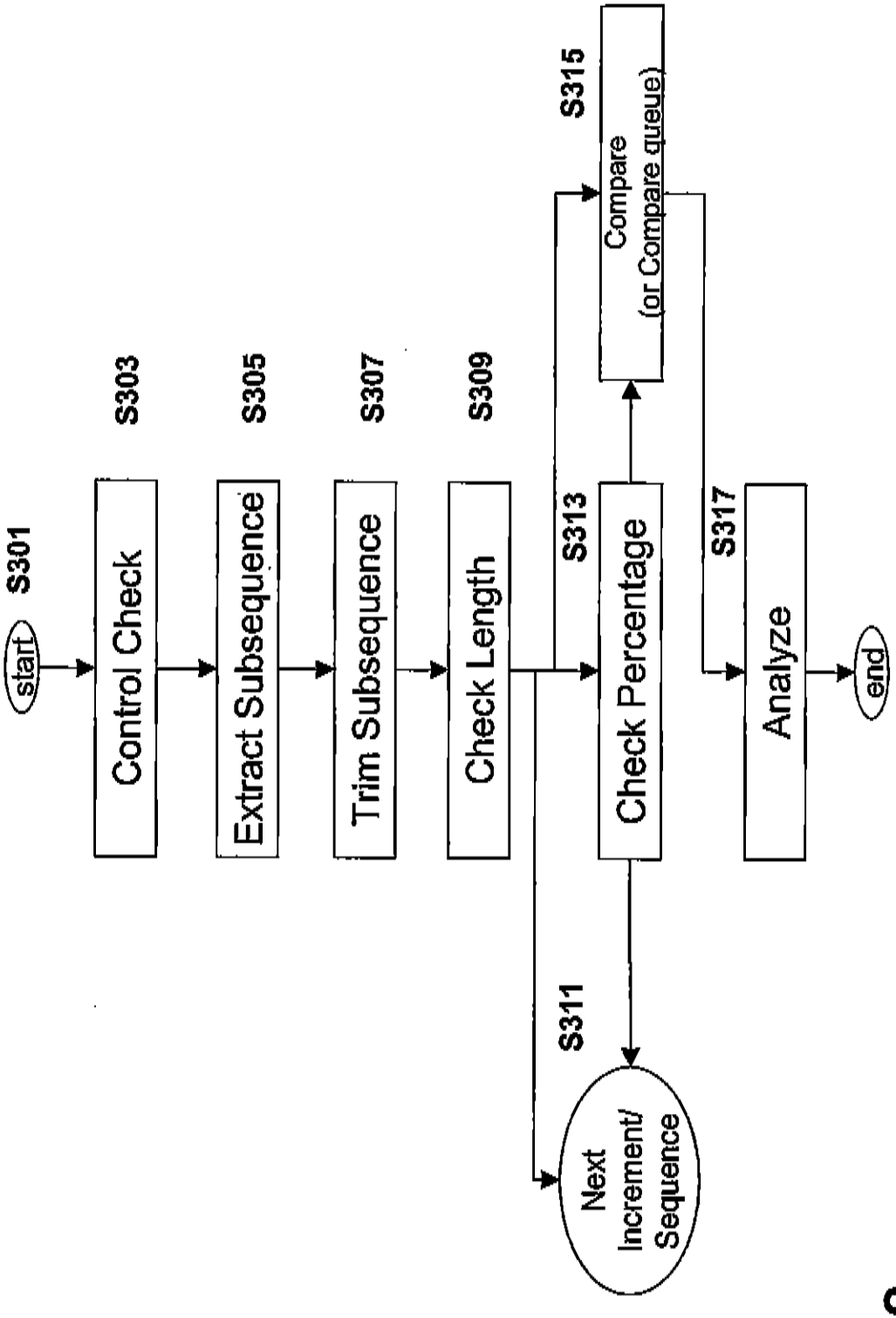

S301
start
Control Check
S303
Extract Subsequence
S305
Trim Subsequence
S307
Check Length
S309
S313
Check Percentage
S315
Compare
(or Compare queue)
S317
Analyze
end
S311
Next
Increment/
Sequence

Fig. 12

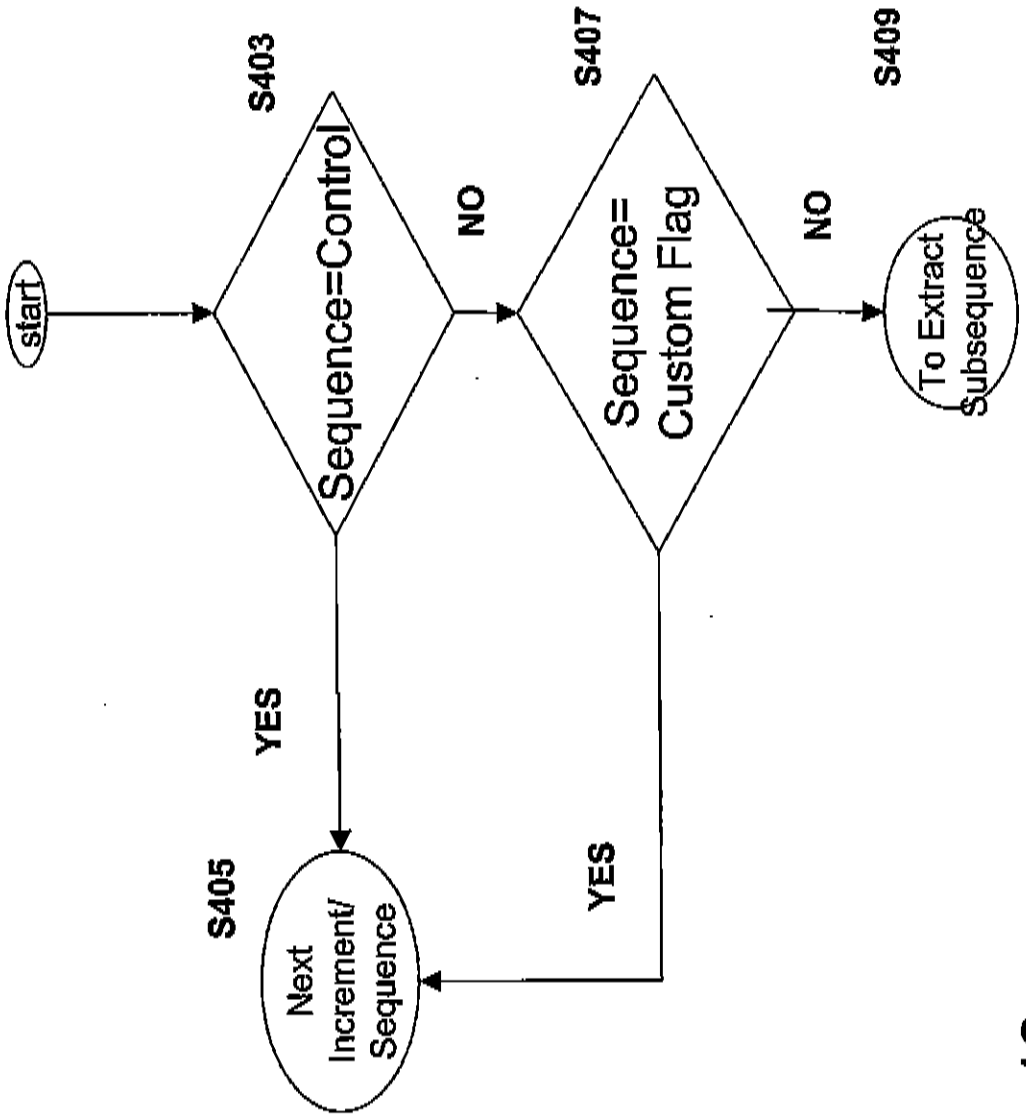

start
S403
Sequence=Control
NO
S407
Sequence= Custom Flag
NO
S409
To Extract Subsequence
YES
S405
Next Increment/ Sequence
YES

Fig. 13

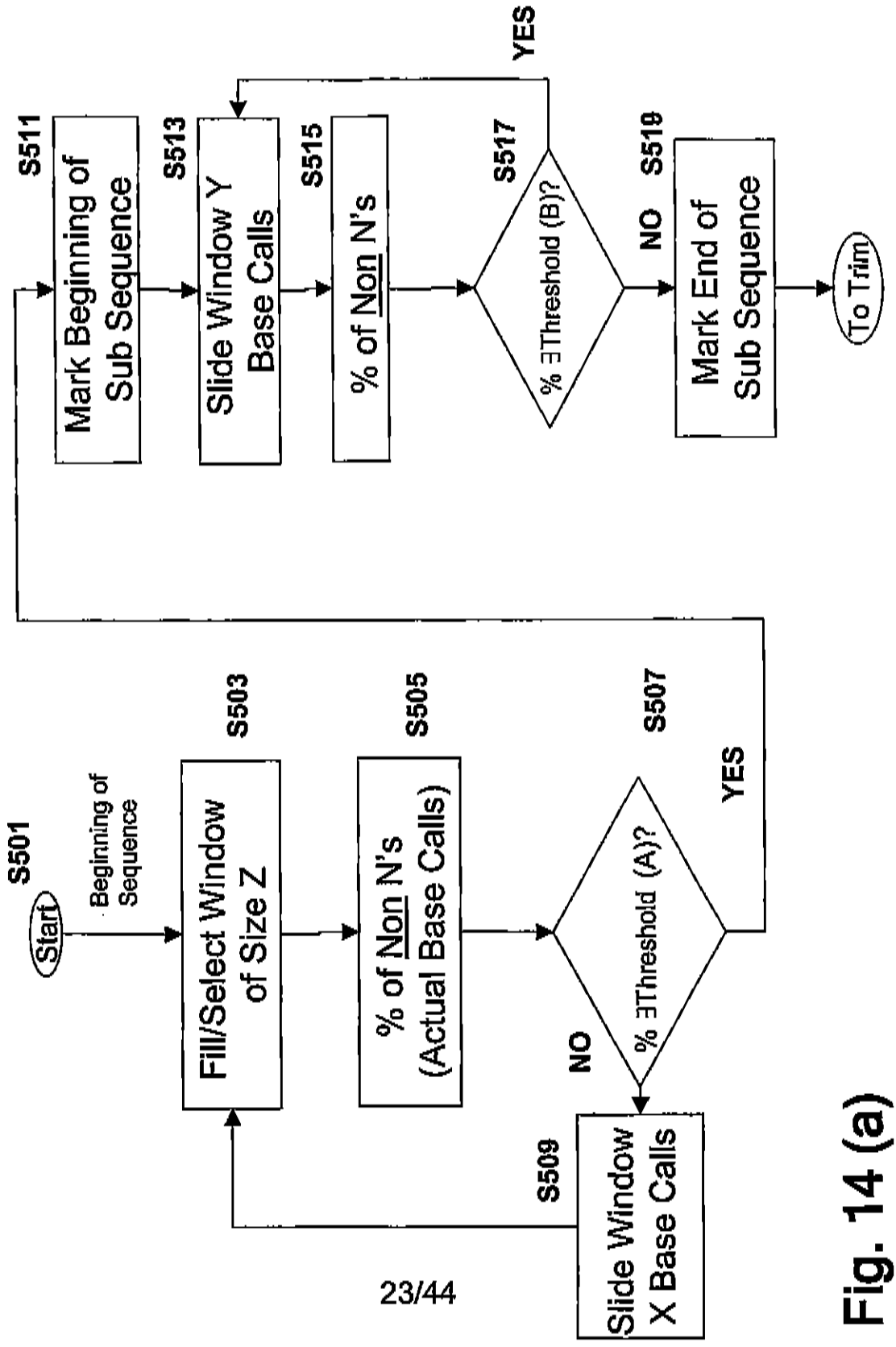

S501
Start
Beginning of Sequence
S503
Fill/Select Window of Size Z
S505
% of Non N's (Actual Base Calls)
S507
% ∃Threshold (A)?
NO
YES
S509
Slide Window X Base Calls
S511
Mark Beginning of Sub Sequence
S513
Slide Window Y Base Calls
S515
% of Non N's
S517
% ∃Threshold (B)?
YES
NO
S519
Mark End of Sub Sequence
To Trim

Fig. 14 (a)

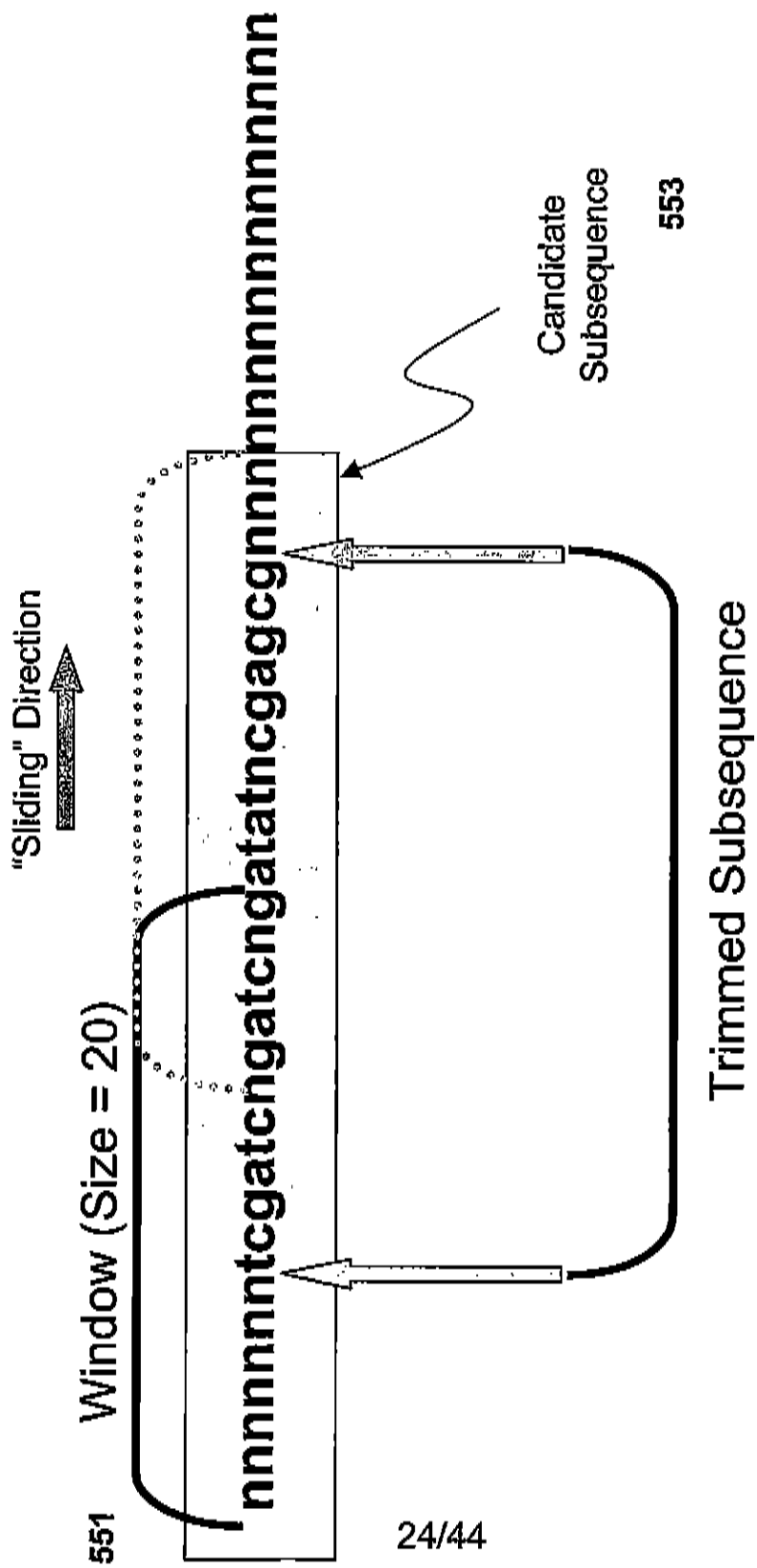

"Sliding" Direction
Window (Size = 20)
551
nnnnnntcgatcngatatncgagcgnnnnnnnnnnnnnnn
Candidate Subsequence
553
Trimmed Subsequence

Fig. 14 (b)

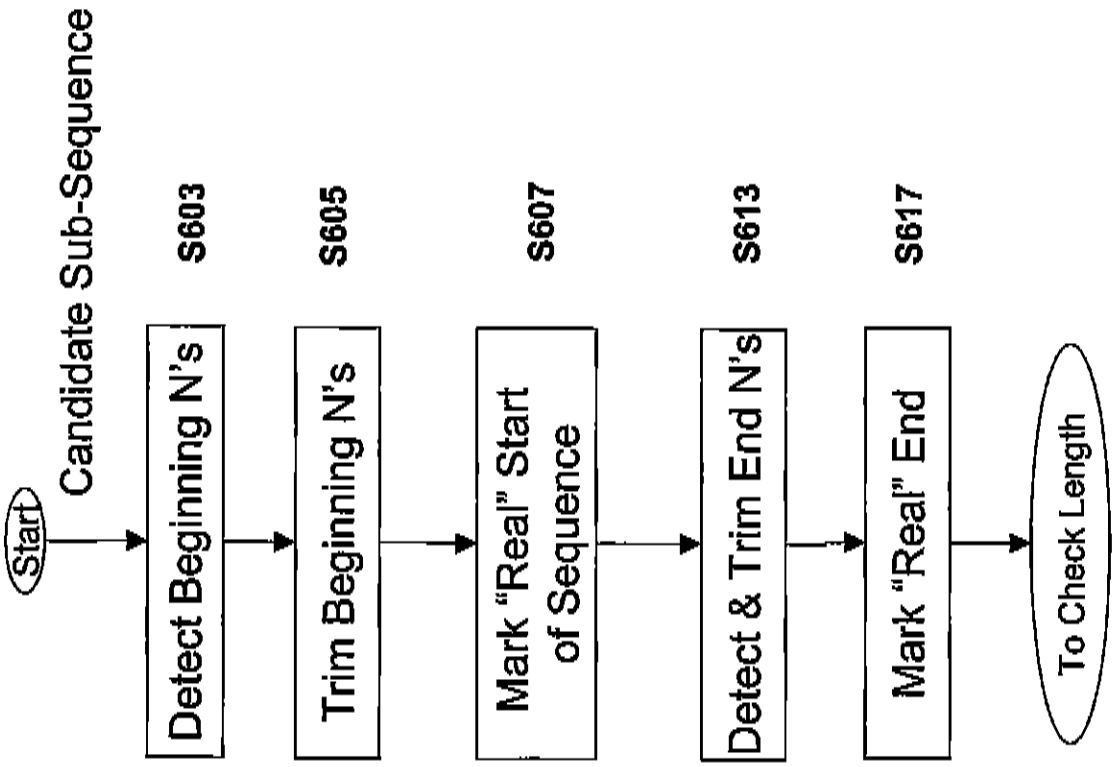

Start
Candidate Sub-Sequence
S603
Detect Beginning N's
S605
Trim Beginning N's
S607
Mark "Real" Start of Sequence
S613
Detect & Trim End N's
S617
Mark "Real" End
To Check Length

Fig. 15

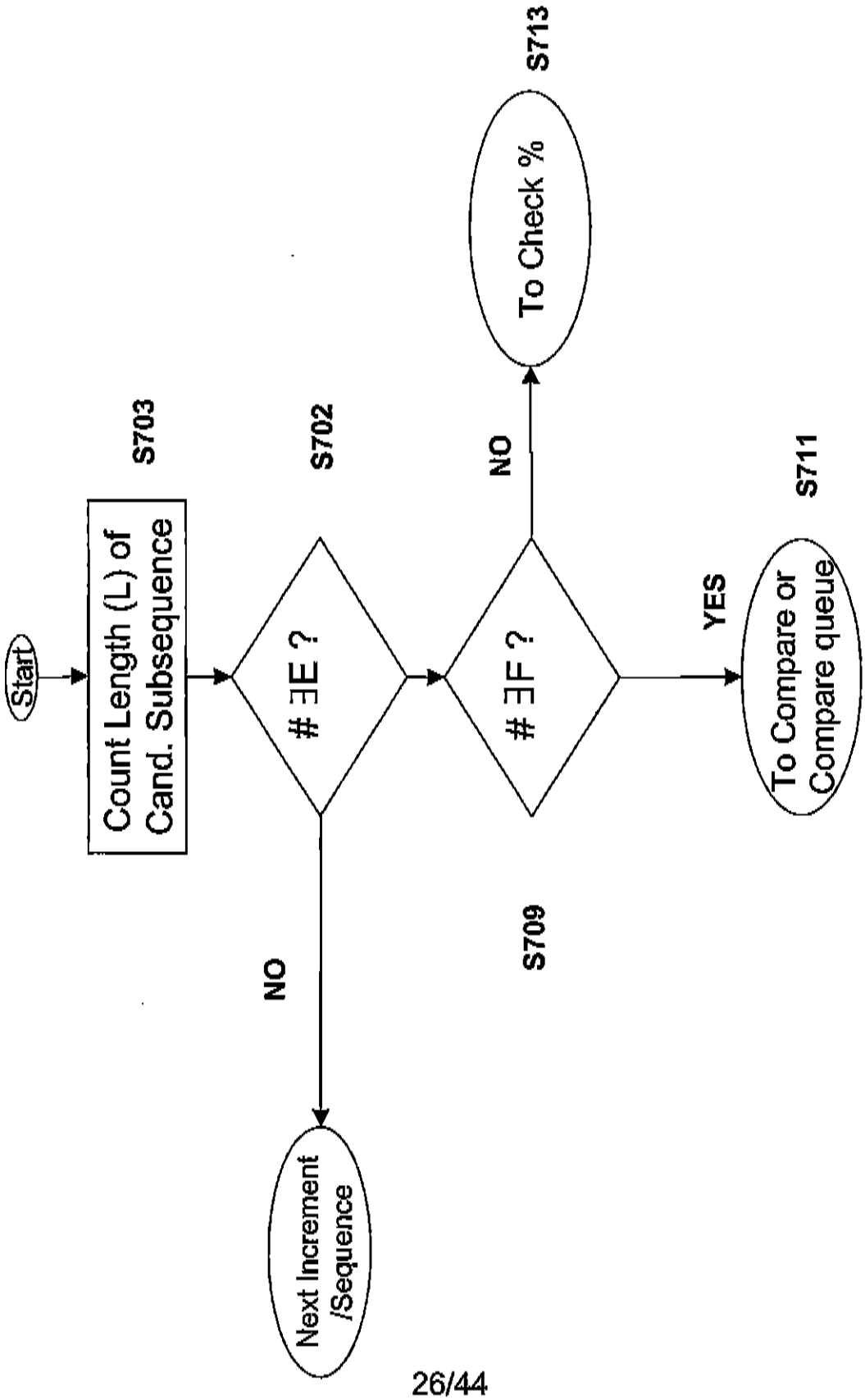

Start
Count Length (L) of Cand. Subsequence
S703
∃E ?
S702
NO
∃F ?
S709
NO
To Check %
S713
YES
To Compare or Compare queue
S711
Next Increment /Sequence

Fig. 16

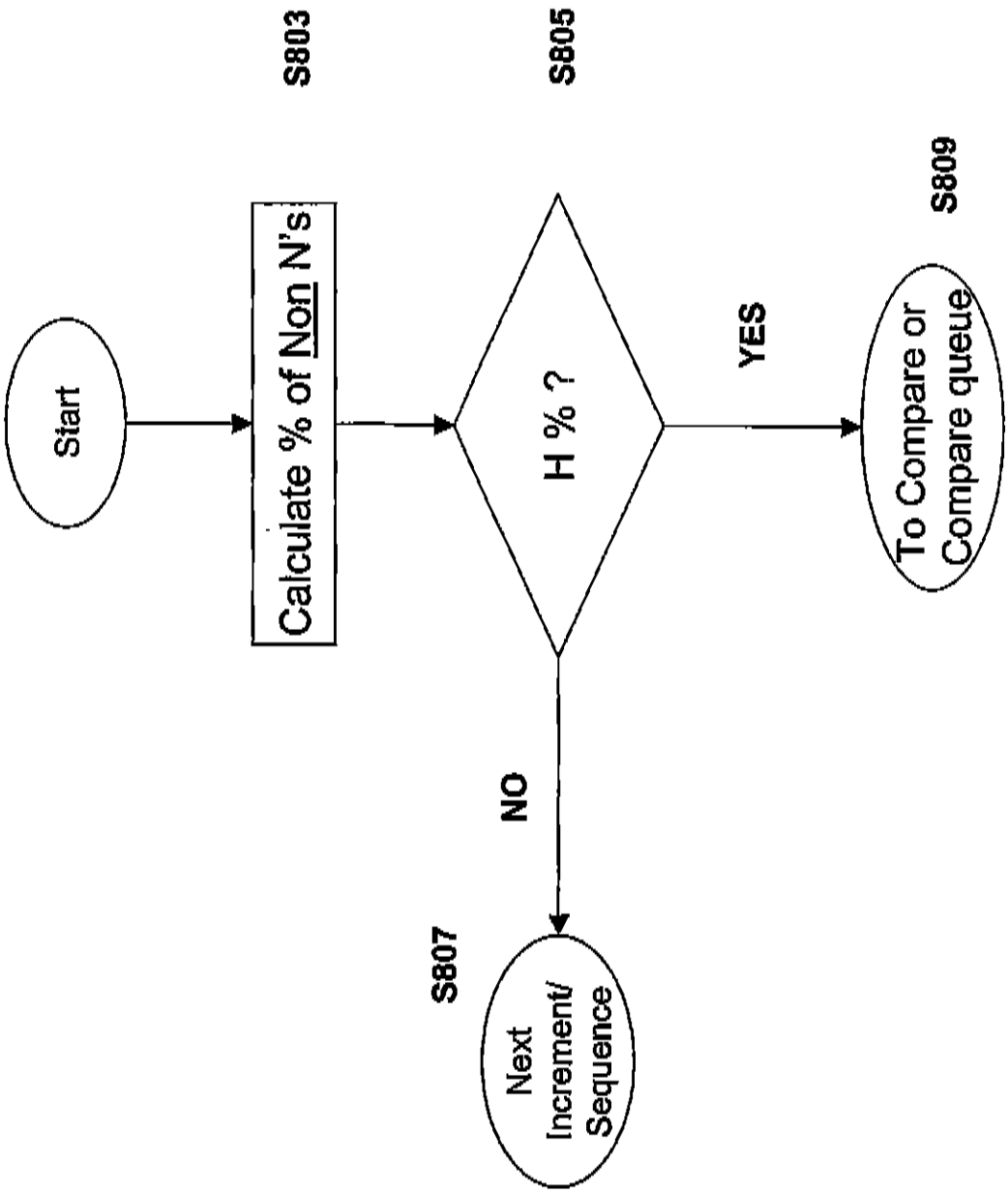

Start
Calculate % of Non N's
S803
H % ?
S805
YES
To Compare or Compare queue
S809
NO
Next Increment/ Sequence
S807

Fig. 17

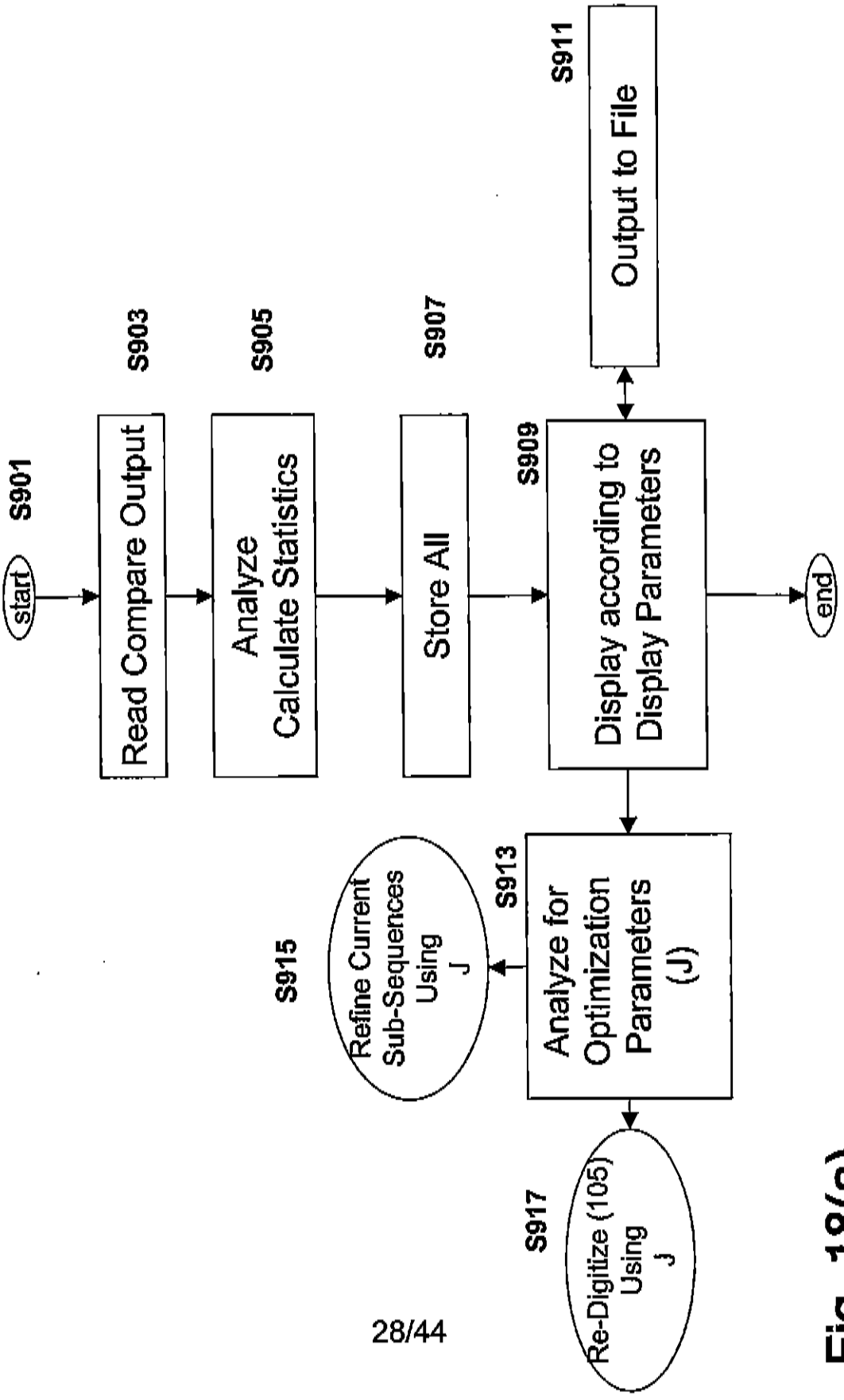

S901
start
S903
Read Compare Output
S905
Analyze
Calculate Statistics
S907
Store All
S909
Display according to
Display Parameters
S911
Output to File
end
S913
Analyze for
Optimization
Parameters
(J)
S915
Refine Current
Sub-Sequences
Using
J
S917
Re-Digitize (105)
Using
J

Fig. 18(a)

>Ad4E1A:Ad4 Prototype-serial dilution1 Start=12 End=1313
Subsequence:
cacctncgctgcncgancngtatgatctggnggtggatgtgnccgaggacgacnncaacgagaaggcggtacaatgatttatttagcgatgccg
cgctgctagctgncgaggnggcttcaagncctagcttcagacagcgactcttcactgcatacccctagncacgncagaggtggagaaagagatcc
ccgggcttaaatgggaaaagntggacttgcgttgctatgaggaatgnctgnnnncaagcgatgatgaggacgagcnggcgnttcdgancgcag
cgagccatgnagtgcaagccgtcagcgagagctttgcactggacngcccgcctttgcncggcacggctgtaagtcttgtgattttcatcgca
ncaatactggagataaagctgtgttatgtgcgctttgctatatgagagcgnacaaccattgtgtttncagtaagtgtgattaagtgaactttn
aanggaggcaaanagtagngtgactnngtgatgactnnttttnttttntntntntntttttttwtntnnktnynnttttythnnnnnnnntknt
Subsequence Percentage of Target: 43%
Subsequence Length: 556
Number of Subsequence Base Calls: 493
Percentage of Subsequence Base Calls: 89%
lcl|ad4 No definition line found; Length = 35990
evalue: 0.0 for Ad4E1A
gi|209874|gb|M14918.1|ADRDE1AA Adenovirus type 4 E1A region; Length = 2042
evalue: 0.0 for Ad4E1A
gi|17105037|gb|AF394196.1|AF394196 Simian adenovirus 25, complete genome; Length = 36521
evalue: 2.63705E-155 for Ad4E1A
gi|33694802|tpg|BK000413.1| TPA: Simian adenovirus 25, complete genome; Length = 36519
evalue: 2.63705E-155 for Ad4E1A
lcl|ad4_vaccine No definition line found; Length = 35119
evalue: 1.11896E-123 for Ad4E1A
lcl|ad4_Navy_Fieldstrain No definition line found; Length = 35090
evalue: 1.03083E-43 for Ad4E1A
lcl|ad4_AirForce_Fieldstrain No definition line found; Length = 35089
evalue: 1.60947E-42 for Ad4E1A

>Ad4FIBER:Ad4 Prototype-serial dilution1 Start=12 End=1245
Subsequence:
gnnannnnncnccaccgancgtgnccttcatcaacnctcccttcnnnnnnttcagntggattccaagaaaagcccctggnggtgttgtccn
nngggnntgnncgacnctgtcncnccaagaatgggaaattaccctcaagntnnnnnannnnnnnganctgncgnctcgggnaanctcattg
caaaacncagnaaacaaggccattgnnnntctcagttttycccaacaaccacgtttnnnnttaacatggntacccctttatbcaccaaagatgg
aaaactancettacaagtttctncccaccantaagnannttaagancaacaattttgaatncannannnnnnctttggctcaggtttaggnc
tcagtgncagcgnccctgncagtacagttagcctctccaacttncatttgntgataaagggaatgtaaagattaccctaaacaggngnttgcatg
ttncancaggagntgcaattgaaagcaacatcagttgggctaaaggtataaaatttgaagntggtgccatagctacaaacattggtaagnnsn
nnngnktnggaaccagnagtncagaaacaggagttaataatgcttatccaatccaagttaaacttggctctggtctcagctttgncagcacag
gaggccataatggctggcaataaagnctatgataaattgacttttgtggacaacgcctgacccatcaccaaactgncaaatactngcagaaaatg
ntgcaaaactancactttgcnnaannaannnngacagncaaatnctggccactgtakcngntttggntgttagaagtggaaacttaaacccaa
ttactggcacagtaagcagtgctcaagtttttctacgttttgatgcaaatggtgttctttaacagaacactcnannennaaaaaatnctgggg
gctacaagcaaggagatagcatagntggcactncatacaccaatgctgttggttttatgcccaattcaacagcttatccaaagacccaaagtt
ctactnntaaaaataatagtgggtcaagtatacatgaatggagntgtttcaaaaccccatgcttcttactataactcttaatggtactgatg

Fig. 18(b)

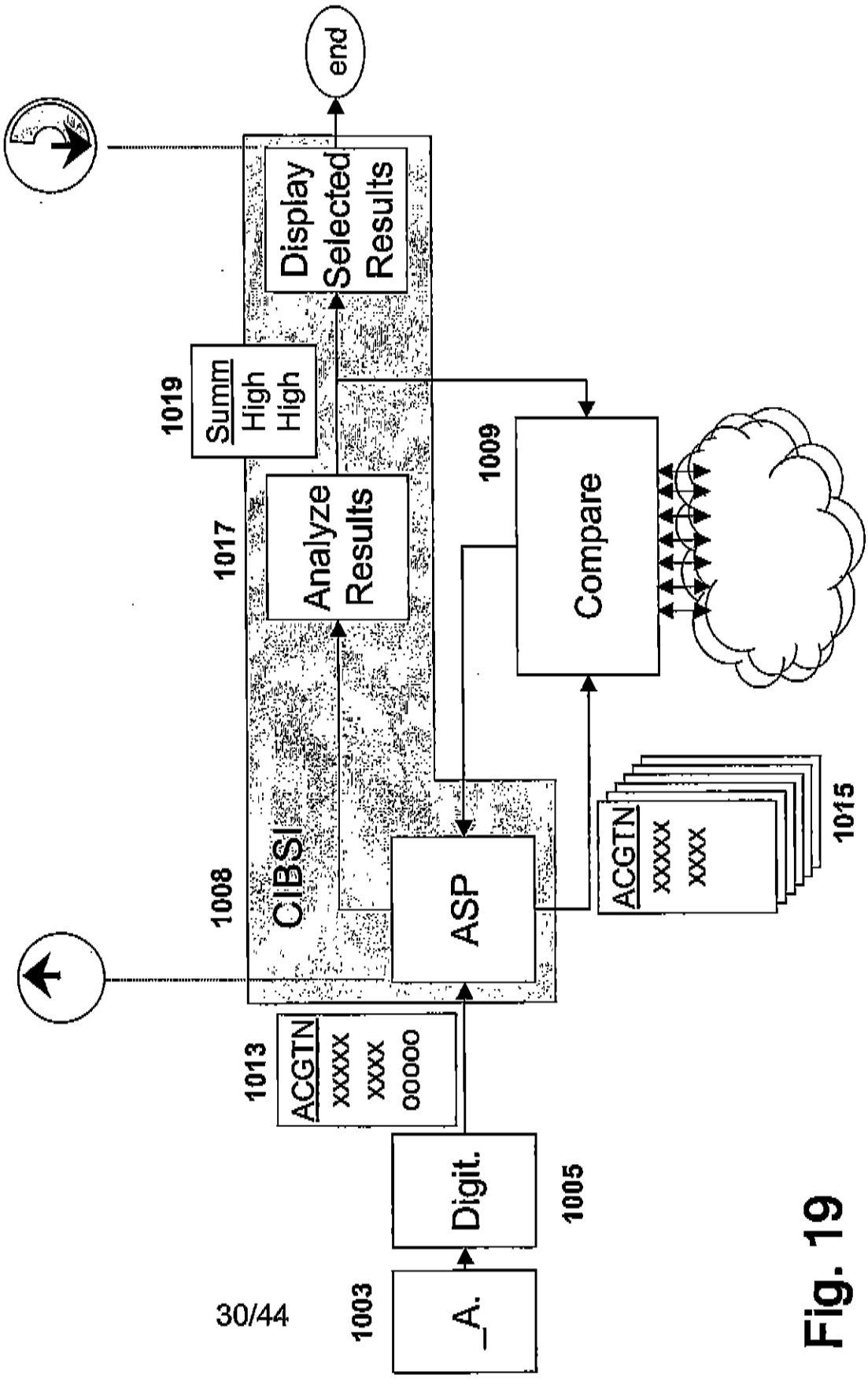

1003
_A.
Digit.
1005
1013
ACGTN
xxxxx
xxxx
ooooo
1008
CIBSI
ASP
1015
ACGTN
xxxxx
xxxx
1009
Compare
1017
Analyze Results
1019
Summ
High
High
Display Selected Results
end

Fig. 19

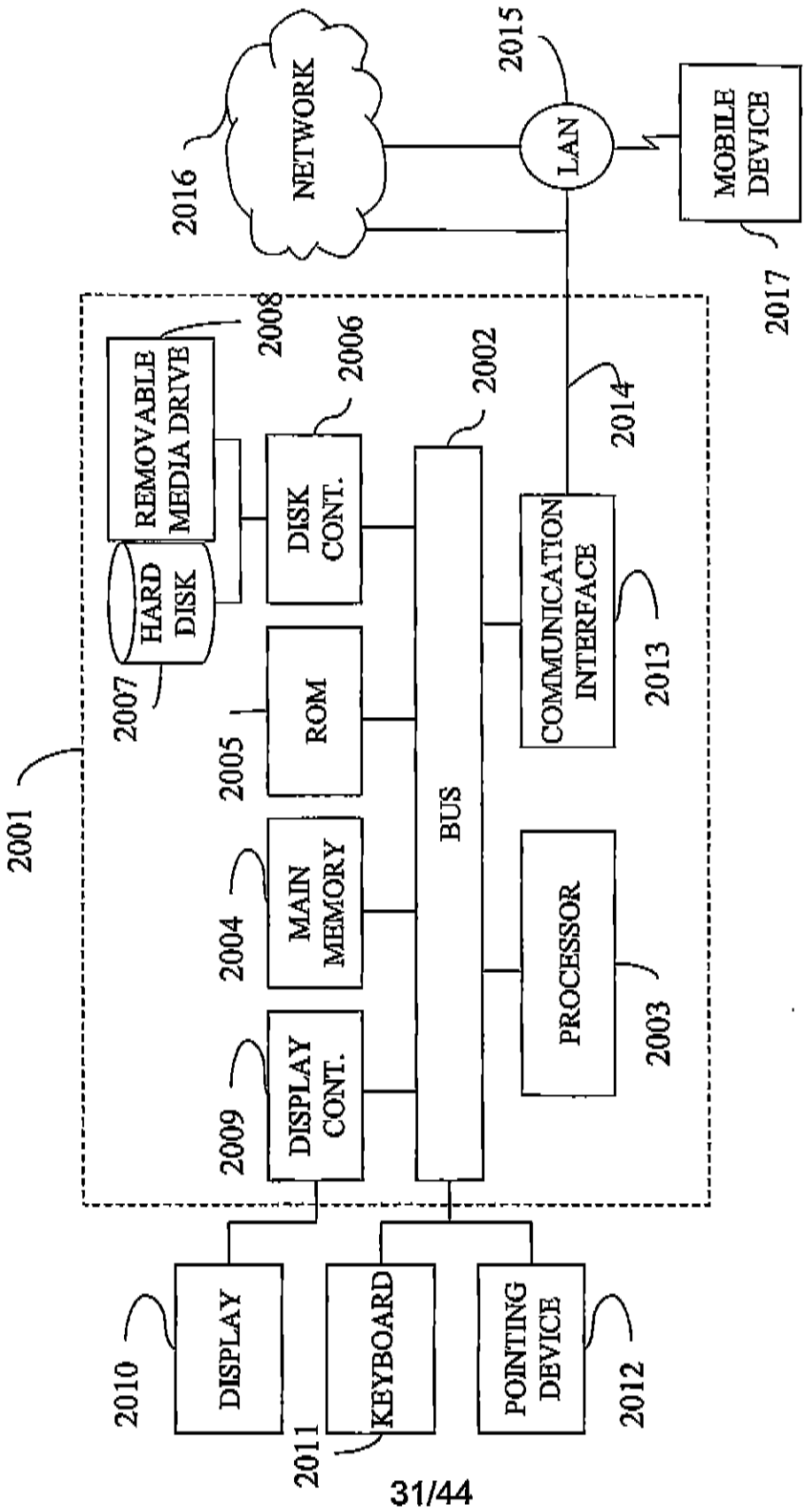

2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
REMOVABLE MEDIA DRIVE
HARD DISK
DISK CONT.
ROM
MAIN MEMORY
DISPLAY CONT.
BUS
PROCESSOR
COMMUNICATION INTERFACE
LAN
NETWORK
MOBILE DEVICE
DISPLAY
KEYBOARD
POINTING DEVICE

Fig. 20

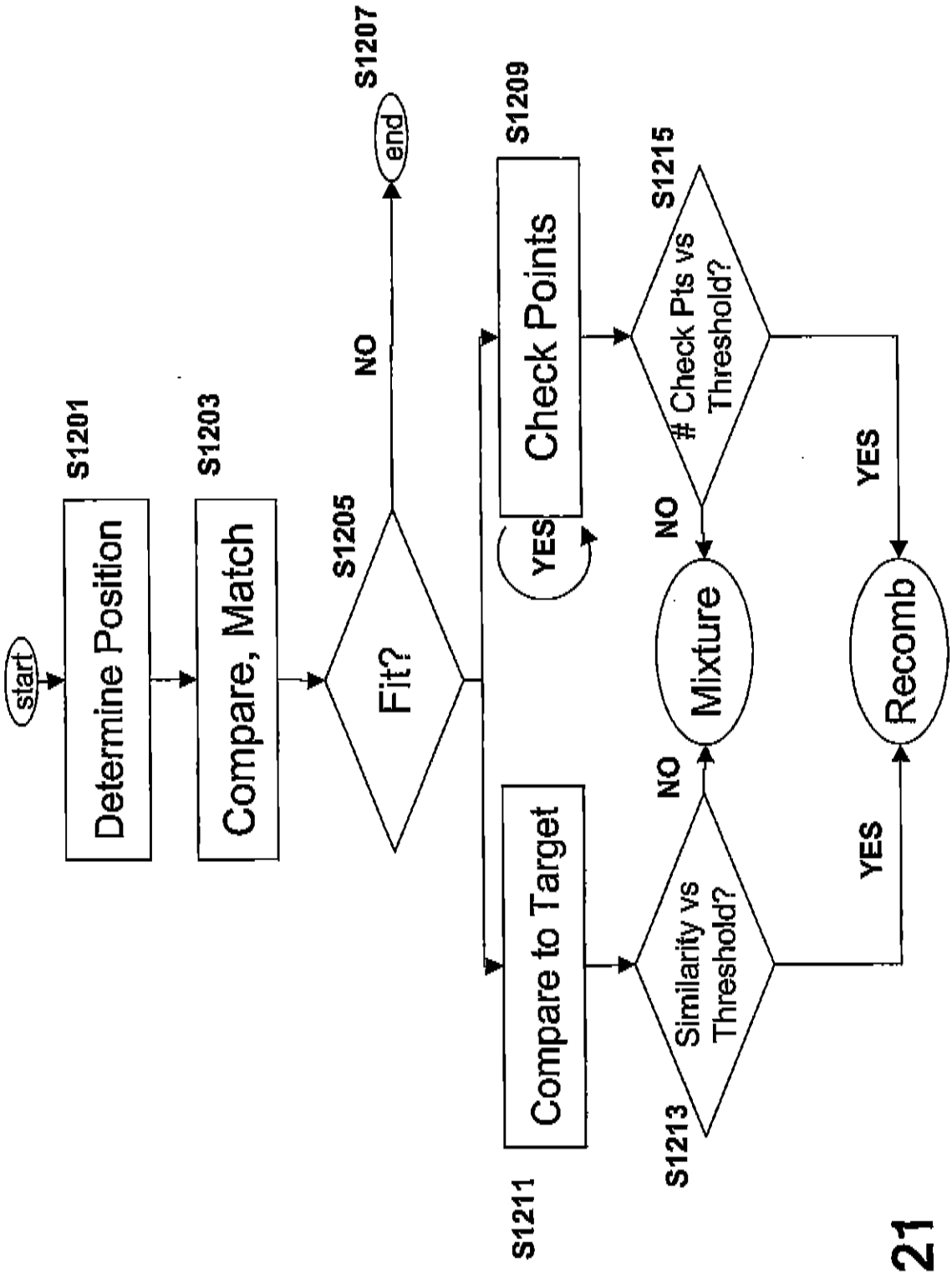

start
S1201
Determine Position
S1203
Compare, Match
S1205
Fit?
NO
S1207
end
YES
S1209
Check Points
S1215
Check Pts vs Threshold?
NO
YES
Mixture
Recomb
NO
YES
S1213
Similarity vs Threshold?
S1211
Compare to Target

Fig. 21

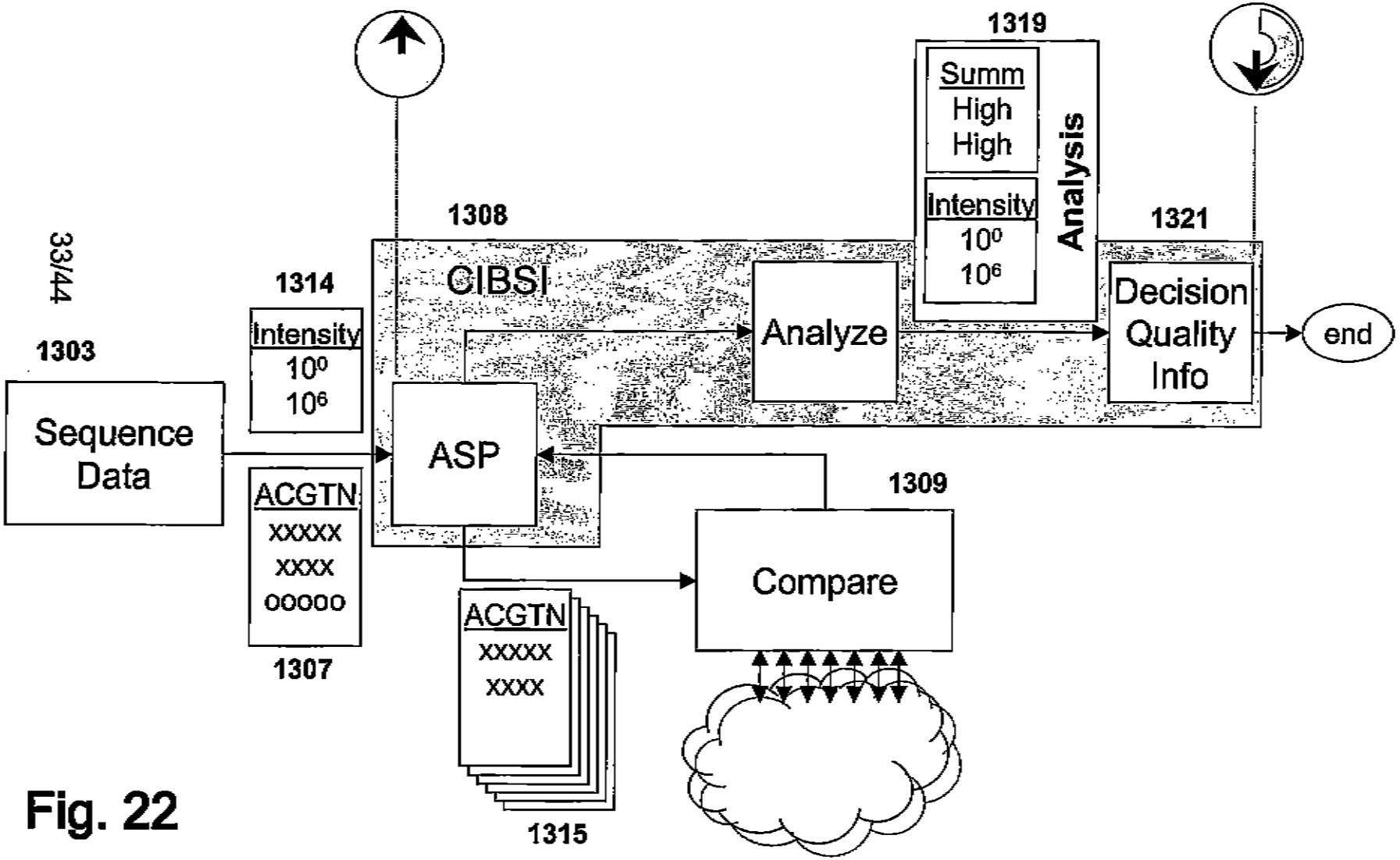

1319
Summ
High
High
Intensity
10^0
10^6
Analysis
1308
CIBSI
1321
1314
Intensity
10^0
10^6
Analyze
Decision
Quality
Info
end
1303
Sequence
Data
ASP
ACGTN
XXXXX
XXXX
OOOOO
1307
1309
Compare
ACGTN
XXXXX
XXXX
1315

Fig. 22

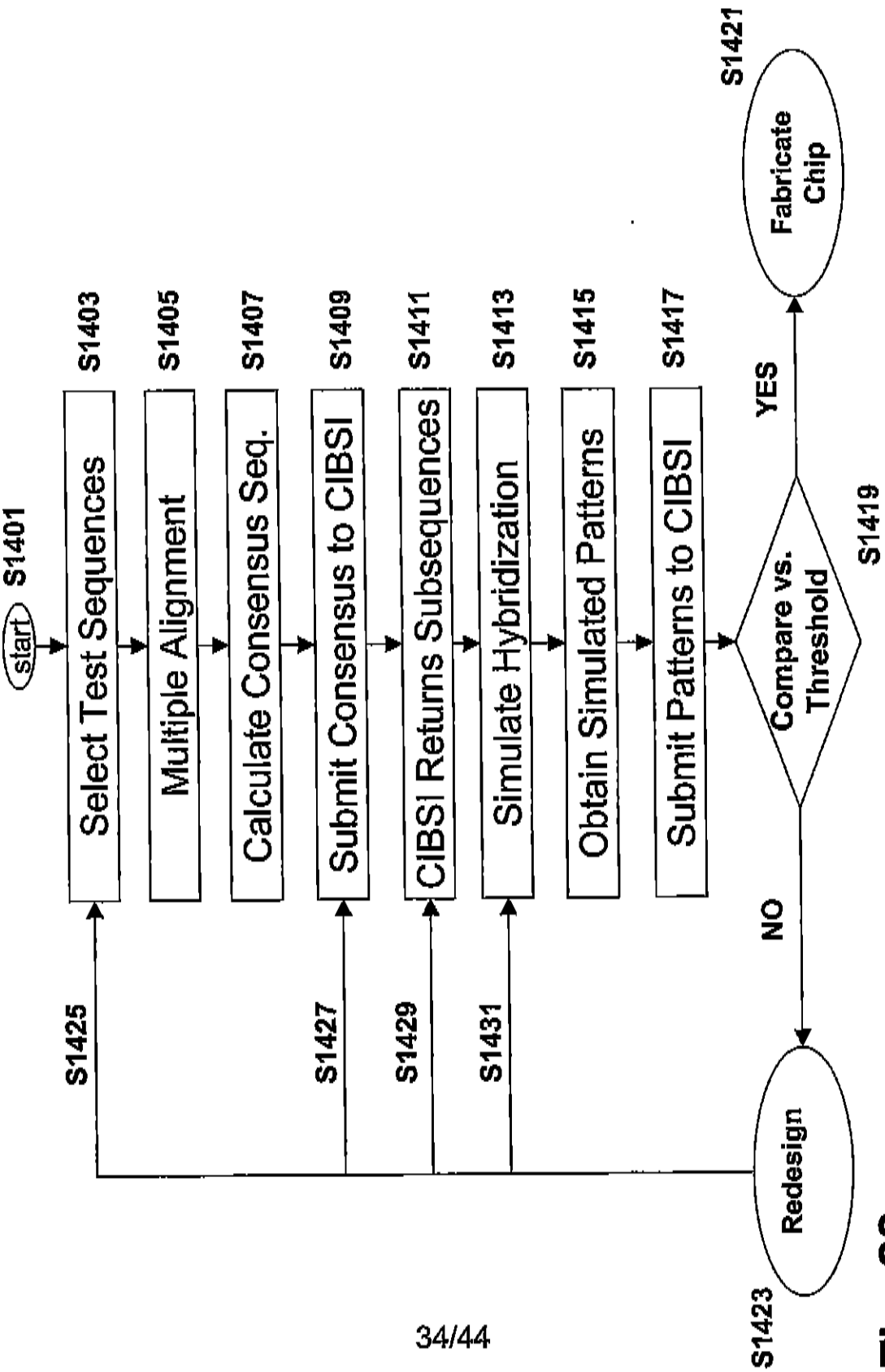

start
S1401
Select Test Sequences
S1403
Multiple Alignment
S1405
Calculate Consensus Seq.
S1407
Submit Consensus to CIBSI
S1409
CIBSI Returns Subsequences
S1411
Simulate Hybridization
S1413
Obtain Simulated Patterns
S1415
Submit Patterns to CIBSI
S1417
Compare vs. Threshold
S1419
YES
Fabricate Chip
S1421
NO
Redesign
S1423
S1425
S1427
S1429
S1431

Fig. 23

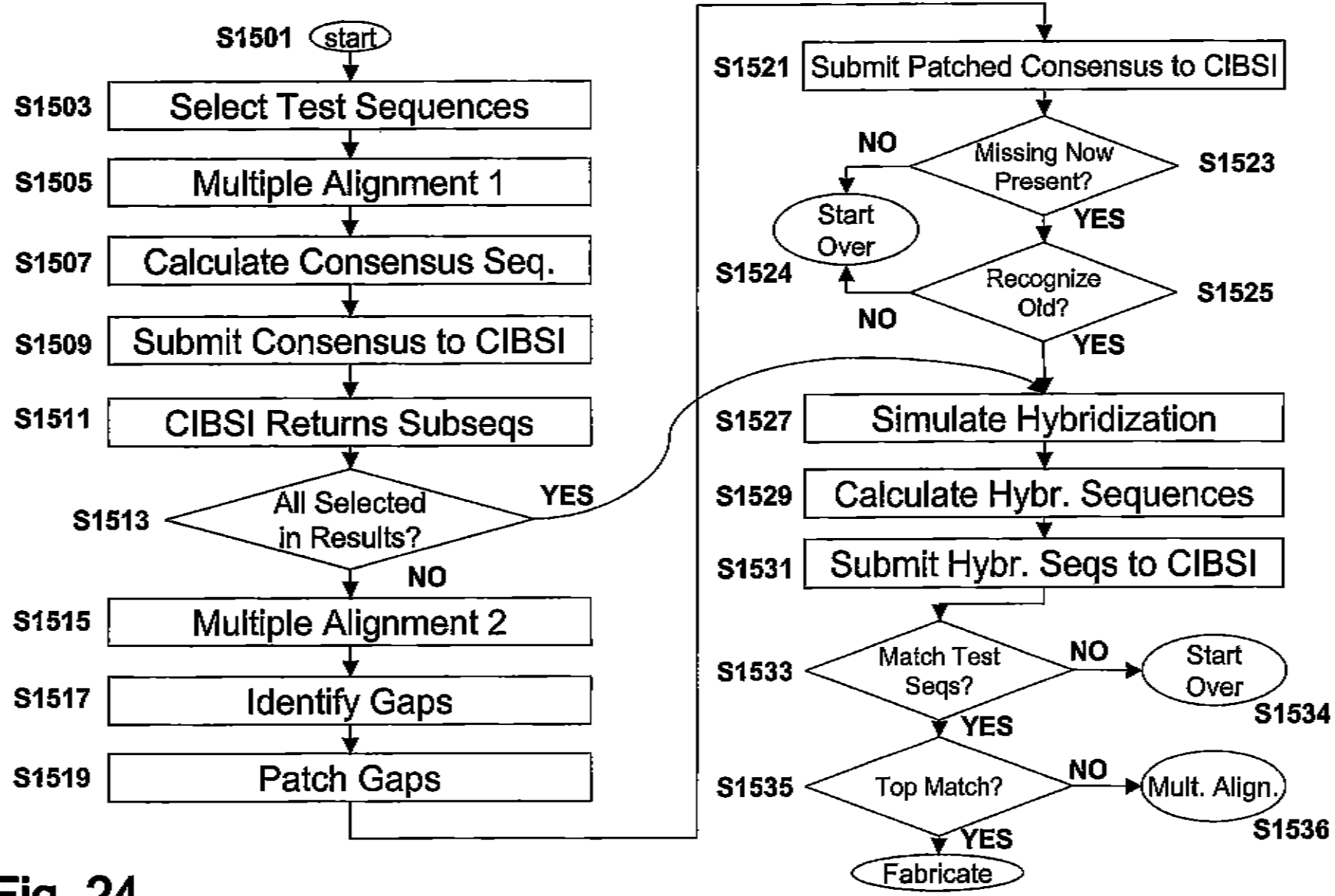

S1501
start
S1503
Select Test Sequences
S1505
Multiple Alignment 1
S1507
Calculate Consensus Seq.
S1509
Submit Consensus to CIBSI
S1511
CIBSI Returns Subseqs
S1513
All Selected in Results?
YES
NO
S1515
Multiple Alignment 2
S1517
Identify Gaps
S1519
Patch Gaps
S1521
Submit Patched Consensus to CIBSI
S1523
Missing Now Present?
NO
YES
S1524
Start Over
S1525
Recognize Old?
NO
YES
S1527
Simulate Hybridization
S1529
Calculate Hybr. Sequences
S1531
Submit Hybr. Seqs to CIBSI
S1533
Match Test Seqs?
NO
S1534
Start Over
YES
S1535
Top Match?
NO
S1536
Mult. Align.
YES
Fabricate

Fig. 24

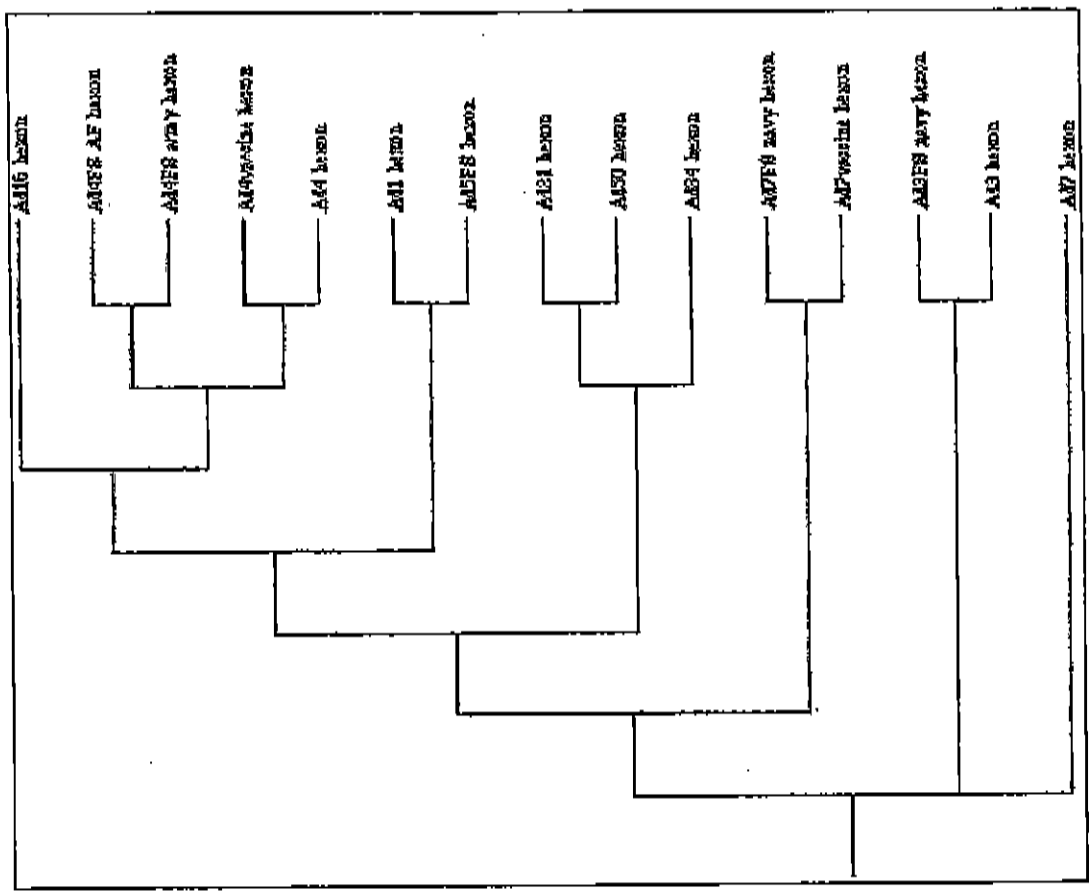

A116 locus
A1058 AF locus
A1058 arm Y locus
A1058 Y locus
A64 locus
A11 locus
A1058 locus
A121 locus
A150 locus
A124 locus
A1058 arm locus
A1Pmarine locus
A1058 army locus
A13 locus
A17 locus

Fig. 25

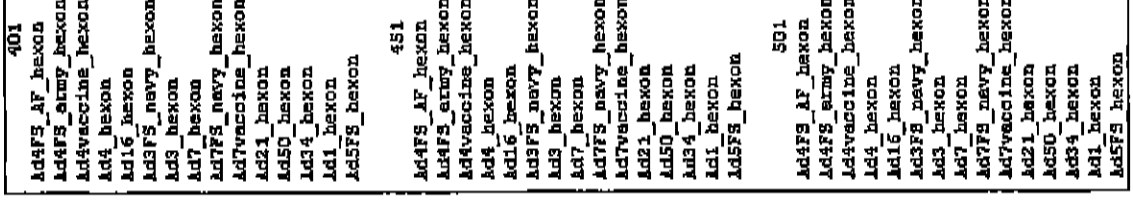


Fig. 26

Fig. 27


Ad34_hexon TGGTACGGCTTACAACTCCCTGGCTCCTAAAGGCGCTCCAAATGCATCTC
Ad1_hexon CGGCACTGCCTACAACGCTCTAGCCCCCAAAGGCGCTCCCAATTCCTGCG
Ad5FS_hexon TGGCACTGCCTACAACGCCCTGGCTCCCAAGGGTGCCCCAAATCCTTGCG
401
450
Ad4FS_AF_hexon AGTGG.....AAGGAT
Ad4FS_army_hexon AGTGG.....AAGGAT
Ad4vaccine_hexon AGTGG.....AAGGAT
Ad4_hexon AGTGG.....AAGGAT
Ad16_hexon AGTGG.....AAGGAT
Ad3FS_navy_hexon AGTGGAT.....AGTTAC.....AACGAAT
Ad3_hexon AGTGGAT.....AGTTAC.....AACAAAT
Ad7_hexon AGTGGAT.....AGTTAC.....AGCAGGA
Ad7FS_navy_hexon AGTGGAT.....AGTTAC.....AACGGGA
Ad7vaccine_hexon AGTGGAT.....AGTTAC.....AACGGGA
EMBOSS_001 AGTGGATGGATACAGANNNTACTCAGGA.....AATGGNN
Ad21_hexon AGTGGATTGCTGAAGGCGT.AAAAAAA.....GAAGAT
Ad50_hexon AGTGGCTTAATAAGGG....AGATGAA.....GAGGAT
Ad34_hexon AGTGGTTGGATAAGGGAGTTACAAGCACTGG.....CCTAGTGGACGAC
Ad1_hexon AGTGGGAACAAGAAGAACCAACTCAGGAAATGGCTGAAGAACTTGAAGAT
Ad5FS_hexon AATGGGATGAAGCTGCTACTGCTCTTGAAAT.....AAACCTAGAAGAA
451
500
Ad4FS_AF_hexon GC.....TAACAGCAAA.....AT.....GCATACC
Ad4FS_army_hexon GC.....TAACAGCAAA.....AT.....GCATACC
Ad4vaccine_hexon TC.....TGACAGCAAA.....AT.....GCATACC
Ad4_hexon TC.....TGACAGCAAA.....AT.....GCATACC
Ad16_hexon TC.....TGACAGCAAA.....AT.....GCATACC
Ad3FS_navy_hexon CG.....AGACAATGCAGTAACTACCA.....CCAC.....AAACACA
Ad3_hexon GG.....GGACAATGCAGTAACTACCA.....CCAC.....AAACACA
Ad7_hexon GA.....AGAAAGAGCAGTAACTACCA.....CCAC.....AAACACA
Ad7FS_navy_hexon GA.....AGACAATGC.....CA.....CCAC.....ATACACA
Ad7vaccine_hexon GA.....AGACAATGC.....CA.....CCAC.....ATACACA
EMBOSS_001 NNANAACTNGACAATGCNGNAACTGNCA.....CCACGGAAGANGNANA
Ad21_hexon GGGGGATCTGACGAAGAGGAAGAGAAAAATCTCACCAC.....TTACACT
Ad50_hexon GGGGAA...GACGACCAACAAG.....CTAC.....ATACACT
Ad34_hexon GGCAATACTGATGATGGGGAAGAAGCCAAAAAAGCAAC.....ATACACT
Ad1_hexon GAGGAGGAGGCAGAGGAGGAGGAGGCAGAGGAGGAGGC...AGAAGCACC
Ad5FS_hexon GAGGACGATGACAACGAAGACGAAGTAGACGAG.....

Fig. 28

>Manually modified cons to include missing Ad5/1
AACAGGATGCTTCGGAGTACCTGAGTCCGGGTCTGGTGCAGTTCGCCCGCG
TGGCCACCCCATCGATGATGCCCCAGTGGGCATACATGCACATCGCCGG
CCACAGACACCTACTTCAGTCTGGGGAACAAGTTTAGAAACCCCACGGTG
GCGCCCACCCACGATGTGACCACCGACCGTAGCCAGCGGCTGATGCTGCG
CTTCGTGCCCGTTGACCGGGAGGACAATACCTACTCTTACAAAGTGCGCT
ACACGCTGGCTGTGGGCGACAACAGAGTGCTGGACATGGCCAGCACATTC
TTTGACATTCGGGGGCGTGCTGGATAGAGGCCCTAGCTTCAAGCCCTACTC
CGGCACTGCTTACAACTCACTGGCTCCTAAGGGCGCGCCCAATACATCTC
AGTGGATGGATACAGANNNTACTCAGGAAATGGCTGAAGAACTAATGGNN
NNANAACTNGACAATGCNGNAACTGNCAAGGAGG CCACGGAAGANGNANA
NNANGNNNNNNNNNCNACATACACCTATTGGCATNNNNNNAATGCTGCCA
TG CCAATTGGAATAGATATTACTNCTACTGAAGGAGANGACAAACCAATTTA
AAAGGTGAGACNCGTTNNNCTGGGAAAATTACTAAAGATGAAGGTCTG
CCAATTGGAATAGATATTACTNCTACTGAAGGAGANGACAAACCAATTTA
TGCTGATAAAACTTATCAACCAGAACCTCAAGTTGGAGAAGAAACTTGGA
CTGACACTGATGGAACAAATGAAAAATATGGANGCAGAGCTCTAAAACC
AGCTACTAAAATGAAACCCTGCTACGGGTCTTTTGCCAAACCTACAAACA
TAAAAGGGGGTCAGGCTAAAATAAAAGNAATCAAAAACAACAACCGAAGG
AGCCATNGATCCTGAGTATCCAGATATTGATATGNGAATTTTTTGACGGT
AAAAATACTGTTGNAGCTGACTTCGATCCTGAAATTGTAATGTACACAGA
AAATGTTGATTTGGAAACTCCAGACACTCATGTTGTATACAAACCTGGAA
CTTCGGATGCNAGCTCTCATGCAAATTTGGGTCAACAAGCCATGCCTAAC
AGACCCAACTACATTGGCTTCAGGGACAACTTTATCGGGCTCATGTACTA
CAACAGTACTGGCAATATGGGAGTTCTGGCCGCCCAAGCATCTCAGCTGA
ATGCAGTGGTTGACTTGCAGGACAGAAACACTGAACTGTCATATCAGCTC
TTGCTTGATTCTCTGGGTGACAGAACCAGATACTTCAGTATGTGGAATCA
GGCTGTGGACAGCTATGATCCTGATGTGCGCATTATTGAAAATCATGGTG
TGGAGGATGAACTGCCAAACTACTGCTTTCCGTTGGATGGTGTAGGTCNA
CCAACAGACACTTACCAAGGTATTAAAGTTAAAACAGATGAAANTNCTGA
ATNNNNNNNNNNNNAGTGGGACAAAGATGNTAACGCAGT
TAGAACTGCTAATGAAATAGCTGTAGGCAATGCTTTTGCCATGGAAATTA
ACATCCAAGCCAACCTGTGGAGAAGTTTCCTGTATTCCAATGTGGCTGTG
TATCTGCCAGATAATTACAAATACACGCCAGCCAACATCACTCTGCCCAC
TAACACCAACACCTACGAGTACATGAACGGGCGGGTGGTGGCCCCATCGC
TGGTGGATTCCTACATTAACATTGGCGCCAGGTGGTCTCTGGACCCCATG
GACAATGTCAATCCATTCAACCACCACCGCAATGCTGGCCTGCGCTACCG
GTCCATGCTTCTGGGCAATGGTCGTTATGTGCCTTTCCACATACAAGTGC
CTCAGAAATTCTTTGCTGTCAAGAACCTACTGCTTCTACCCGGCTCCTAC
ACCTACGAGTGGAACTTCAGAAAGGATGTGAACATGGTCCTGCAGAGTTC
CGTTGGAAATGACCTCCGAACAGATGGTGCCACCATAAGTTTCACCAGCA
TCAAGCTCTATGCCACCTTCTTCCCCATGGCTCACAACACCGCCTCCACC
CTTGAAGCCATGCTGCGCAACGACACCAATGATCAGTCATTCAACGACTA
CCTCTCTGCAGCGAACATGCTCTACCCCATCCCTGCCAATCCAACCAACG
TTCCCATCTCCATCCCCTCTCGCAACTGGGCCGCCTTCAGCGGCTGGTCC
TTCACCAGAACTCAAAACCAAGGAGACTCCCTCTCTGGGATCAGGGTTCGA
CCCCTACTTCGTCTACTCTGGCTCTATTCCCTACCTGGATGGCACCTTTT
ACCTTAACCACACTTTCAAGAAGGTCTCCATCATGTTTGACTCTTCAGTC
AGCTGGCCTGGCAATGACAGGCTGCTGACTCCAAACGAGTTTGAAATCAA
GCGCAGTGTGGACGGGGAAGGATACAACGTGGCCCAATGCAACATGACCA
AAGACTGGTTCCTGGTCCAGATGCTTGCCAACTACAACATTGGCTACCAG
GGCTTCTACATCCCTGAGGGATACAAGGATCGCATGTACTCCTTCTTCAG
AAACTTCCAGCCCATGAGCAGGCAGGTGGTTGATGAGGTTAATTACAAGG
ACTACAAAGCCGTCACCTTACCCTACCAACACAACAACTCTGGCTTTGTA
GGTTACCTTGCGCCTACTATGCGACAAGGGCAACCCTACCCCGGCAACTA
CCCATACCCGCTCATGGGAACTACTGCCGTTAACAGTGTCACCCAGAAAA
AGTTCGTGTGCGACAGGACCATGTGGCGCATTCCCTTCTCCAGCAAGTTC
ATGTCCATGGGCGCCCTTACCGACCTGGGACAGAACATGCTCTATGCCAA
CTCCGCCCATGCGCTGGACATGACTTTTGAGGTGGATCCCATGGATGAGC
CCACCCTGCTTTATGTTCTTTTCGAAGTCTTCGACGTGGTCAGAGTGCAC
CAGCCACACCGCGGCGTCATCGAGGCCGTCTACCTGCGCACACCGTTCTC
GGCCGGCAACGCCACCACATAA

Fig. 29

>EMBOSS_001_modified_hexon_cons
Subsequence:
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TTTAGAAACCCCACgGTGGCGCCcACCCACGATGTGACCACCGACCGtAGCCAGCGgCTGATGCTGCGCTTCGTGCCCGTTGACCGGGAGGACAATACCTACTCtTACAAAGTGCGcTACACgCTGGCtGTGGGC
GACAACAGAGTGCTGGACATGGCCAGCACaTTCTTTGACATTCGgGGcGTGCTGGATAGaGGcCCTAGCTTCAAGCCcTAcTCCGGCACtGCtTACAACtCaCTGGCTCCtAAGGGCGCGCCCAATACaTclCAGTG
GAlgGATaCaGannntactcAggAAATGGCTGAAGAACTAatggnnnnnanaaclnGAcAATGCngnaactgncaAGGAGGccacggaagangnanannangrnnnnnnnnnnonacatAcACcTaTTGGcAlnnnnnnnaatGCTgCCATGaAaGgtGAgA
CnccttnnnnTGggaAAAttActAAAGAtgaaGGlcTGCcAATTGGaAtAGAtaITACtnCTactgaaGGAganGACAAaCCAATTTATGCtGATAAAACtTATCAaCCAGAACCTCAAGTTGGAGAaGAaactTGGAcTGAcACtGATGG
AACAAATGAAAAATaTGGAnGGcAGAGCTCTaAAAccagCTACtAAAATGAAACCcTGCTACGGgTCTTTTGCcAAACCTACaAACAtAAAAGGgGGtCAgGCTAAAataAaAgnAatcAaaAaCAacaccgaaGGaGccatngAtc
CTgAglATccaGATATtGATaTGnGaaTTtTTTGAcGGtAaAaalAcTGtTGnagctgacTTcgatCCtGAAATTGTaaTGTACACaGAAAATGTtGAtTTGGAAACTCCAGAcACTCATgTtGTATACAAACCtGGAACttCgGAtgcnAg
CTCTcAtGCaAATTTGGGTCAACAAGCCATGCCTAACAGACCCAAcTACATTGGCTTCAGgGAcAAcTTTATcGGgCTcATGTACTACAACAGtACTGGcAATATGGGaGTtCTGGCcGGcCAAGCaTCtCAGCTGAATG
CaGTGGTTGACTTGCAgGACAGAAACACTGAACTGTCATAtCAGCTcTTGCTTGAtTCTCTGGGtGACAGAACCAGATACTTCAGtATGTGGAATCAGGCtGTGGACAGCTATGATCCtGATGTgCGcATTATTGAAAA
TCATGGtGTgGAGGATGAACTGCCaAAcTAcTGcTTTCCgtTGGATGGTGTaGGtcnAccaAcAGACACTTACCAAGGtATTAAAgtTAAAacaGAtGaaanTnCTGaAlnnnnnnnnnnnnnagtGGGAcAAAGATGntAacgcAgtTAg
aactgCTAATGAAATagctgTAGGCAATcctTTGCCATGGAAATTAACATCCAAGCcAACCTgTGGAGAAGTTTcCTgTAtTCCAATGTGGCTCTGTATCTgCCAGATaaaTACAAATACACgCCagCCAACATcACTCTGCC
CaCtAACACCAACACCTAcGAGTACATGAACGGGCGgGTGGTggCcCCATCgCTGGTgGAttCCTACATtAACATTGGcGCCAGgTGGTCTCTGGACCCCATGGACAATGTcAATCCaTTCAACCACCACCGCAATGC
TGGCCTGCGCTACCgGTCCATGCTTCTGGGCAAtGGtCGTTAtGTGCCTTTCCACATaCAAGTGCCTCAGAAATTCTTTGCTGTcAAGAACCTaCTgCTTCTaCCcGGCTCCTACACCTACGAGTGGAACTTCAGaAA
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GCTGCGCAACGACACCAATGATCAGTCATTCAACGACTACCTCTCTGCaGCcAACATGCTcTACCCCATCCCtGCCAAtGCaACCAACgTTCCCATcTCCATCCCcTCTCGCAACTGGGCcGCCTTCAGcGGCTGGT
CCTTCACcAGaCTCAAAACCAAGGAGACTCCcTCTCTGGGaTCaGGGTTCGAcCCCTACTTCGTcTAcTCTGGcTCTATtCCCTACCTGGATGGCACCTTtTACCTtAACCACACTTTCAAGAAGGTCTCCATCATGTT
TGACTCTTCAGTCAGCTGGCCTGGCAATGACAGGCTGCTGACtCCaAAcGAGTTTGAAATCAAGCGCACtGTGGACGGgGAAGGaTACAACGTGGCCCAATGCAACATGACCAAAGACTGGTTCCTGGTcCAGAT
GCTtGCCAACTACAACATTGGCTACCAGGGCTTcTACATcCCtGAGGGaTACAAGGATCGCATGTACTCCTTcTTCAGAAACTTCCAGCCCATGAGCAGgCAGGTGGTTGATGAGGTTAAtTACAAgGACTACAAAG
CCGTCACCtTACCcTACCAACACAACAACTCTGGCTTTGTaGGtTACCTtGCgCCtACtATGCGaCAaGGgCAACCcTACCCcGCCAACTAcCCaTACCCGCTCATcGGAACtACTGCCGTTAAcAGTGTcACCCAGAAAA
AGTTCCTGTGCGACAGGACCATGTGGCGCATtCCcTTCTCCAGCAACTTCATGTCCATGGGcGCCCTTACcGACCTGGGACAGAACaTGCTCTATGCCAACTCcGCCCATGCGCTGGACATGACTTTTGAGGTGG
ATCCCATGGATGAGCCCACCCTGCTTTATCTTCTtTTCGAAGTCTTCGACGTGGTCAGAGTGCACCAGCCACACCGCGGCGTCATCGAGGCCGTCTACCTGCGCACACCGTTCTCGGCCGGCAACGCCACCAC
ATAA
Subsequence Percentage of Target: 100%
Subsequence Length: 2961
Number of Subsequence Base Calls: 2899
Percentage of Subsequence Base Calls: 98%
  lcl|AY599834 | Human Adenovirus Serotype 3 | 35,345bp; Length = 35345
    evalue: 0.0, score: 2296.06 for null
  lcl|AY594255 | Human Adenovirus Serotype 7 | 35,305bp; Length = 35306
    evalue: 0.0, score: 2272.27 for null
  gi|861019|emb|Z48571.1|MAVH7HEXN Mastadenovirus h7 hexon gene; Length = 2916
    evalue: 0.0, score: 2272.27 for null
  gi|11968173|gb|AF065065.3|AF065065 Human adenovirus type 7 pVI core protein (pVI) gene, partial cds; hexon protein (hexon) gene, complete cds; and p23 protease gene, partial cds; Length = 3237
    evalue: 0.0, score: 2272.27 for null
  gi|3841840|emb|X76549.1|AV3HEXO3 Adenovirus type 3 hexon gene; Length = 2835
    evalue: 0.0, score: 2264.34 for null
  lcl|AY601634 | Human Adenovirus Serotype 7, US Navy Field Strain | 35,198bp; Length = 35198
    evalue: 0.0, score: 2258.4 for null

...

Fig. 30

```
>ad4_bl2seq.out
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnntgtaggcaatcctttgccatggaaatnaacatccaagccaac
ctgtggagnannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnntgcccacn
aacaccaacacctacgagtacatgaacggncgggtggtggcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
nnnnnnnnnnnnnnnnnnnnnnnnnnnatccnttcaaccaccaccgcaatgcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnccggntcctacacctacgagtg
gaacttcngnnnnnnnnnnnnnnnnacatgntcctgcagagttcccttggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
nnnacctctangccaccttcttccccatggcncacaacaccgcctccacnnttgangccatgctgcgcaacgacaccaatgancannnn
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnccaacgtncccatctccatcccctcncgcaact
gggccgccttnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncngggttcgacccctacttcgtctact
cnggctcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnaccacacnttcaagaaggtctccatcannnnnnnnnnnnnnnnnnnn
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnngatacaacgtggcccantgcaa
catgaccaangactggttcctggtccagatgctngccnnctacaacatnggctaccagggcttctacnnnnnnnnnnnnnnacaagganc
gcatgtactccttcttcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
nctaccaacacaacaactcnggcttnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncctaccccgccaactacccntaccc
gctcatcggnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnatgtggcgcatncccttctccagcaactt
catgtccatgggcgcnctnnnnnnnnnnnnnnnnnnnnnnnagaacatgctctatgcnaactccgcccannnnnnnnnnnnnnnnnnnnn
nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnagtgcaccagccncaccgcggcgtcatngag
gccgtctacctgcgcacnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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Fig. 31

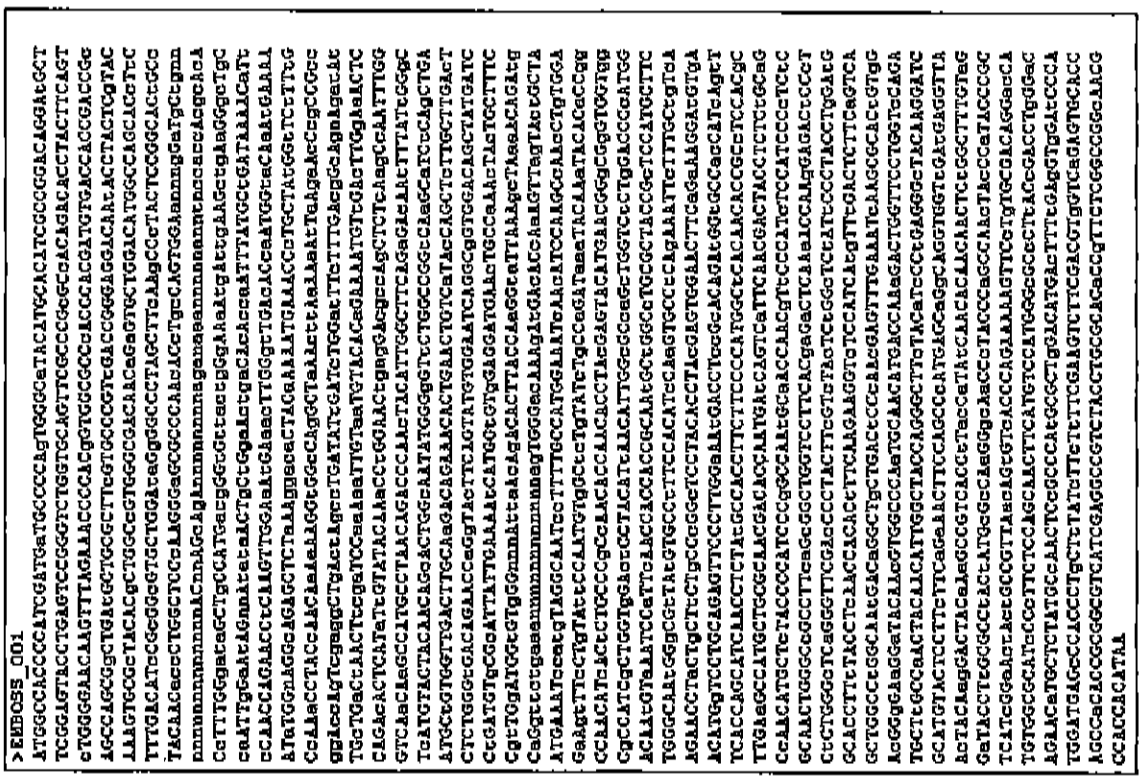


Fig. 32

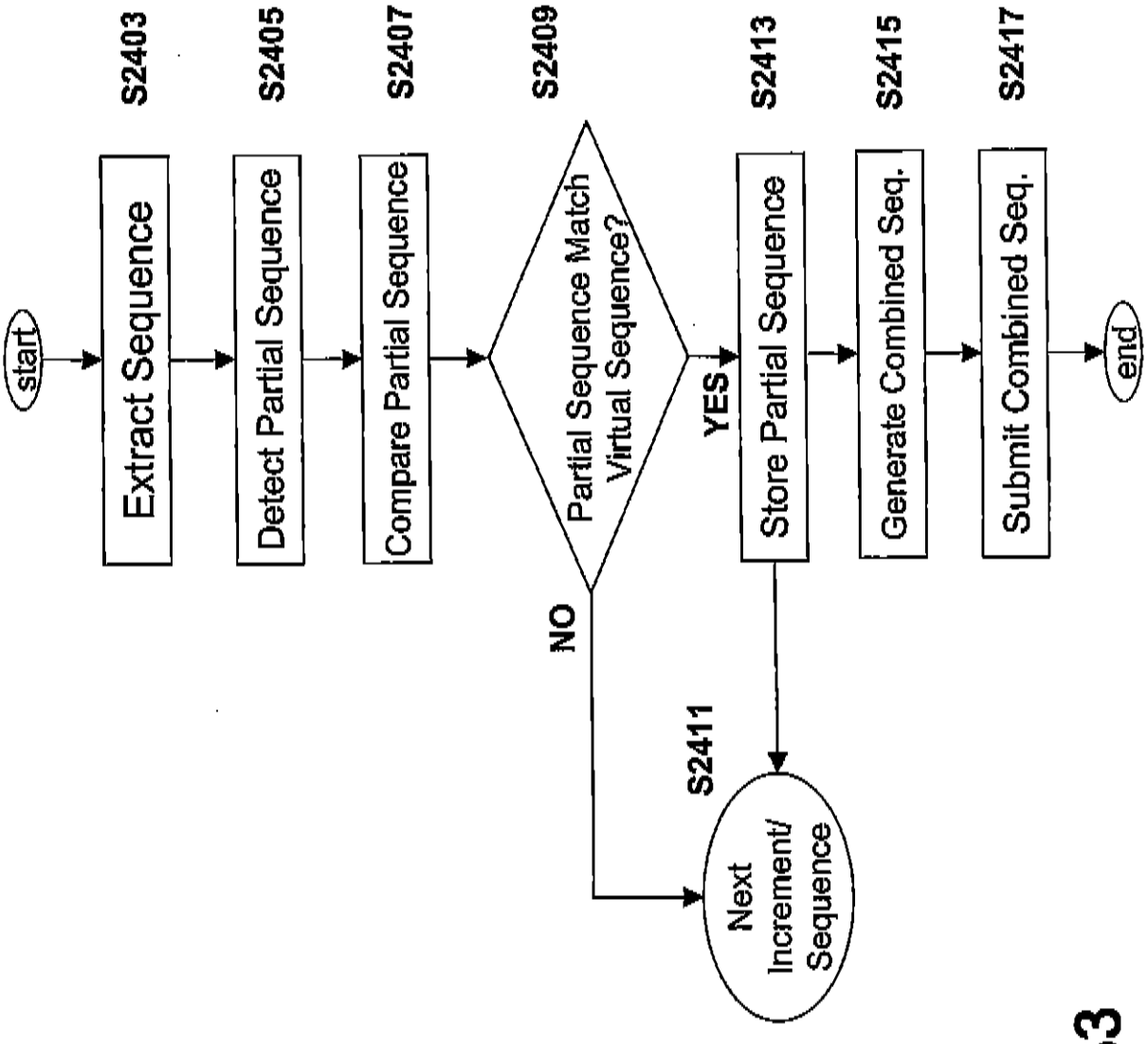

start
Extract Sequence
S2403
Detect Partial Sequence
S2405
Compare Partial Sequence
S2407
Partial Sequence Match Virtual Sequence?
S2409
YES
Store Partial Sequence
S2413
Generate Combined Seq.
S2415
Submit Combined Seq.
S2417
end
NO
S2411
Next Increment/ Sequence

Fig. 33