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Key Words and Phrases
Select the link below to go directly to the specific topic:

- Bands
- Cold Agglutinin
- Correcting CBC, DIFF and RET Parameters for Dilution Factor When Doing Manual Dilution
- Correcting RBC Parameters for Extreme Leukocytosis
- Hyaluronidase and Synovial Fluids
- Interfering Substances
- MCHC Troubleshooting Chart
- NRBC Correction
- Plasma Replacement
- Platelet Clumping
- Pseudothrombocytopenia and Approaches for Managing Platelet Clumping
- Vortexing of Sample and Platelet Clumps
- Warm Agglutinin
Introduction

The XN-L Series Flagging Interpretation Guide is designed to serve many objectives including:

- Providing users with an explanation of criteria used for the XN-L Series Interpretive Program (IP) Messages.
- Suggesting actions to be taken when samples generate IP Messages.
- Suggesting actions to resolve sample related problems.

The following sections introduce the IP Messages. Definitions and examples of each message are presented with suggested actions to be taken by qualified personnel to verify the presence of specific cell types and obtain a correct result when interference occurs. These action steps are merely suggested guidelines and not requirements. Always follow your local laboratory procedures for repeat testing or confirmation of results.

The XN-L Series analyzers are designed to aid in the separation of specimens into POSITIVE and NEGATIVE categories according to preset criteria. The system bases its judgments on comprehensive surveys of numerical data, particle size distributions, and scattergrams and provides easy-to-understand flags and messages indicating the analyzer’s findings. These flags and messages are referred to as IP Messages. The IP Messages may be classified as either Suspect IP Messages or Abnormal IP Messages. The IP Messages generated by the analyzer determine if the sample is judged as POSITIVE or NEGATIVE.

Suspect IP Messages are generated by analyzer software algorithms. Abnormal IP Messages are based on numerical user defined settings.

A specimen is judged NEGATIVE when there are no IP messages generated. NEGATIVE does not necessarily indicate a normal sample; however, the results are generally reported without review.

The XN-L Series analyzers will generate a POSITIVE when an IP Message is present. ERROR will be generated when there is an analysis error. These judgments indicate the possibility of sample abnormality. These results should be reviewed carefully and may require further examination in accordance with your local laboratory protocol.
All analyzer flags, error messages and results must be interpreted together and in consideration of the patient’s clinical condition prior to results being reported from the laboratory. Any asterisk (*) next to a parameter indicates these results may be unreliable and should be confirmed according to your laboratory protocol prior to reporting. Protocols for comparison of current results to previous results (delta checking) as well as critical value alerts are also useful for identifying potentially erroneous results prior to reporting to the clinician.

NOTE: System configuration, analysis mode and discrete testing mode used may determine availability of certain IP messages. Refer to the Instructions for Use for detailed list of IP Messages.

The XN-L Series Data Browser Main Tab lists flags present for the sample. IP messages are only intended for use in the clinical laboratory and are not for patient diagnosis. For Q-Flags, the Q-Flag result converted to a numerical value from 0 to 300 (in increments of 10) is displayed. The Q-Flag numerical value does not relate to a quantity of abnormal cells or the degree of abnormality present in a given sample.

Data Browser Flag Field Example
(Q-Flag numerical value highlighted)
Abnormal, WBC Abn Scattergram

The WBC Abn Scattergram IP message is generated whenever clustering in the WDF scattergram is abnormal. Dashes may appear in place of data that was not calculated.

This is a non-specific flag which can be generated for a variety of reasons including increased numbers of abnormal cells, poor separation of differential subpopulations, unlysed RBCs, high numbers of platelet clumps or other interfering substances or conditions.

XN-L Series Results

Abnormal WDF Scatter (Close-Up)  Normal WDF Scatter (Reference)
Abnormal, WBC Abn Scattergram (continued)

Suggested Action Steps:

1. Dashes (— —) in place of numeric data:
   - Verify WBC, differential and PLT results according to your laboratory’s policy. Possible actions may include:
     - repeating the sample
     - performing a manual differential

2. Asterisk (*) next to results:
   - Verify WBC, differential and PLT results according to your laboratory’s policy. Possible actions may include:
     - scanning the slide for abnormal cells or platelet clumping and to estimate the WBC and PLT counts
     - performing a manual differential if abnormal cells are observed
   - If no abnormalities are found when reviewing the smear, the WBC estimate is consistent with the analyzer reported WBC and the PLT estimate is consistent with the analyzer reported PLT, the results with asterisks (*) may be reported.

NOTE: It is suggested to verify the WBC, differential and PLT results according to your laboratory’s policy whenever the WBC Abn Scattergram flag is present even in the absence of asterisks (*) next to results or dashes (— —) in place of numeric data.
Suspect NRBC?

The NRBC? IP Message is generated when clustering is detected in the NRBC area between the lymphocytes and the RBC ghosts on the WDF scattergram. An asterisk (*) will appear next to the % and # for the Neutrophils, Lymphocytes, Monocytes, Eosinophils, Basophils and Immature Granulocytes. The asterisk (*) indicates these results may be unreliable and should be confirmed according to your laboratory protocol prior to reporting.

XN-L Series Results
Suspect, NRBC?
(continued)

Abnormal WDF Scatter
(Close-Up)  Normal WDF Scatter
(Reference)

Suggested Action Steps:
1. Review results according to your laboratory protocol. This may include scanning the peripheral smear for the presence of NRBCs or other abnormal cells. Report any NRBCs or abnormal cells according to your laboratory protocol.

2. If a 100-cell differential is performed and NRBCs or megakaryocytes are counted, the WBC result may be corrected using the following equation if indicated by your laboratory protocol.

   \[
   \text{Corrected WBC (x } 10^3/\mu L) = \frac{(\text{WBC x 100})}{(\text{NRBC + 100})}
   \]

   NOTE: It is up to the laboratory to determine the NRBC or megakaryocyte count which would necessitate correction of the WBC count.

3. If no abnormalities are found when reviewing the smear and analyzer results are consistent with smear review findings, the results with asterisks (*) may be reported.
**IG Present Message**

XN-L Series analyzers report a 6-part differential that is comprised of Neutrophils, Lymphocytes, Monocytes, Eosinophils, Basophils and Immature Granulocytes. The Immature Granulocyte % / # results include metamyelocytes, myelocytes and promyelocytes.

The threshold for the IG Present message is user defined and programmable. It only appears when the IG% or IG# exceeds the programmed limit. It is suggested that the IG Present message threshold be set at 5% or 0.5 x10^3/µL.

The IG Present message alerts the operator to the presence of cells accurately quantitated by the analyzer. When this message is present, it is suggested to review a smear to detect other clinically relevant findings and report the analyzer differential results. If indicated, based on smear review, perform a manual differential or comment on clinically relevant findings as described in your laboratory protocol.

**XN-L Series Results**
IG Present Message
(continued)

Abnormal WDF Scatter
(Close-Up) Normal WDF Scatter
(Reference)

(IG population circled)

Suggested Action Steps:
When the IG Present message is displayed:

1. Review results according to your laboratory protocol. This may include scanning the peripheral smear for the presence of:
   - immature granulocytes – promyelocytes, myelocytes and metamyelocytes
   - band cells in increased numbers
   - toxic granulation or vacuolation of neutrophils
   - other abnormal cells
   Report any abnormal cells according to your laboratory protocol.

2. If the IG% or IG# has an asterisk (*), verify differential results according to your laboratory’s policy. Possible actions may include:
   - scanning the slide for abnormal cells
   - performing a manual differential if abnormal cells are observed

3. If no abnormalities are found when reviewing the smear and analyzer results are consistent with smear review findings, the results with asterisks (*) may be reported.
Suspect, Blasts/Abn Lympho?

The Blasts/Abn Lympho? IP message indicates that the analyzer has detected abnormal clustering in the region for blasts and abnormal lymphocytes in the WDF scattergram.

An asterisk (*) appears next to the % and # for the Neutrophil, Lymphocyte, Monocyte and Immature Granulocytes. The asterisk (*) indicates these results may be unreliable and should be confirmed according to your laboratory protocol prior to reporting.

XN-L Series Results
Suspect, Blasts/Abn Lympho?  
(continued)

Suggested Action Steps:
1. Review results according to your laboratory protocol. This may include scanning the peripheral smear for the presence of:
   - blasts – lymphoblasts, myeloblasts, and myelomonoblasts
   - immature granulocytes – promyelocytes, myelocytes, metamyelocytes
   - atypical or immature lymphocytes
   - other abnormal cells

   Report any abnormal cells according to your laboratory protocol.

   NOTE: Reviewing the feathered edge and sides of the peripheral smear is suggested as blasts and other large cells may migrate to this area during smear preparation.

2. If no abnormalities are found when reviewing the smear and analyzer results are consistent with smear review findings, the results with asterisks (*) may be reported.

3. If dashes (— —) are in place of numeric data, verify differential results according to your laboratory’s policy. Possible actions may include:
   - repeating the sample
   - performing a manual differential
Suspect, Left Shift?

The Left Shift? IP message indicates that the analyzer has detected abnormal clustering in the region for left shift (bands) in the WDF scattergram. When bands are present, they are included in the neutrophil population.

An asterisk (*) appears next to the % and # for the Neutrophil, Eosinophil and Immature Granulocytes. The asterisk (*) indicates these results may be unreliable and should be confirmed according to your laboratory protocol prior to reporting.

Judgement for Left Shift? is not performed when WBC is less than 0.50 x 10^9/µL in the Whole Blood mode or less than 0.20 x 10^9/µL in the Pre-Dilution mode.

XN-L Series Results
Suspect, Left Shift? (continued)

WDF Scatter (Close-Up)  Normal WDF Scatter (Reference)

Suggested Action Steps:
1. Review results according to your laboratory protocol. This may include scanning the peripheral smear for the presence of:
   - band cells in increased numbers
   - toxic granulation or vacuolation of neutrophils
   - other abnormal cells
   Report any abnormal cells according to your laboratory protocol.

2. If no abnormalities are found when reviewing the smear and analyzer results are consistent with smear review findings, the results with asterisks (*) may be reported.

3. If dashes (— —) are in place of numeric data, verify differential results according to your laboratory’s policy. Possible actions may include:
   - repeating the sample
   - performing a manual differential
Suspect, Atypical Lympho?

The Atypical Lympho? IP message indicates that the analyzer has detected significant clustering in the region for atypical lymphocytes that is located in the upper left lymphocyte region on the WDF scattergram.

An asterisk (*) appears next to the % and # for the Neutrophil, Lymphocyte, Monocyte and Immature Granulocytes. The asterisk (*) indicates these results may be unreliable and should be confirmed according to your laboratory protocol prior to reporting.

XN-L Series Results
Suspect, Atypical Lympho?
(continued)

WDF Scatter
(Close-Up)

Normal WDF Scatter
(Reference)

Suggested Action Steps:

1. Review results according to your laboratory protocol. This may include scanning the peripheral smear for the presence of:
   - atypical or variant lymphocytes
   - abnormal or atypical monocytes
   - immature lymphocytes, such as seen in ALL or CLL
   - immature monocytes
   - smudge cells
   - other abnormal cells
   Report any abnormal cells according to your laboratory protocol.

2. If no abnormalities are found when reviewing the smear and analyzer results are consistent with smear review findings, the results with asterisks (*) may be reported.

3. If dashes (— —) are in place of numeric data, verify differential results according to your laboratory’s policy. Possible actions may include:
   - repeating the sample
   - performing a manual differential
Abnormal, RBC Abn Distribution

The RBC Abn Distribution IP Message is generated when the histogram pattern from the RBC channel is abnormal or when RBC < 0.50 x 10^6/μL. Judgement for other RBC IP Messages is not performed when RBC is < 0.50 x 10^6/μL.

Dashes appear in place of affected results. For example, if there are multiple peaks present on the RBC histogram, there would be dashes in place of results for the RDW-SD and RDW-CV. Sometimes this IP Message may cause the RBC, HCT, MCV, MCH, MCHC, RDW-SD and RDW-CV to be marked with an asterisk (*). The asterisk (*) indicates these results may be unreliable and should be confirmed according to your laboratory protocol prior to reporting.

XN-L Series Results
Abnormal, RBC Abn Distribution
(continued)

Suggested Action Steps:

1. Review results according to your laboratory protocol. This may include scanning the peripheral smear for the presence of abnormal RBC morphology such as:
   1. increased anisocytosis
   2. multiple RBC populations
   3. fragmented RBCs
   4. poikilocytesis
   5. rouleaux or RBC agglutination (refer to suggested action for “RBC Agglutination?” if present)

Report any abnormal RBC morphology according to your laboratory protocol.

2. If no abnormalities are found when reviewing the smear and analyzer results are consistent with smear review findings, the results with asterisks (*) may be reported.

3. If dashes (— —) are in place of numeric data, verify results according to your laboratory’s policy. Possible actions may include repeating the sample or reporting RBC morphology from smear review.

NOTE: If necessary, follow your laboratory protocol for reporting results that cannot be measured or calculated. In most laboratory information systems, this is done by using a code for “do not report” or “not measured” in place of the RDW results.

4. If the RBC morphology is normal and the MCHC is abnormal (<30 or >37.5 g/dL) an interfering substance or condition may be present. Refer to the suggested guidelines for the Turbidity/HGB Interference? IP Message.
Abnormal, Dimorphic Population

The Dimorphic Population IP Message is generated when there are multiple peaks in the RBC histogram pattern. This message may occur with the RBC Abn Distribution IP Message.

Dashes appear in place of results for the RDW-SD and RDW-CV. This message may cause certain RBC parameters to be marked with an asterisk (*). The asterisk (*) indicates these results may be unreliable and should be confirmed according to your laboratory protocol prior to reporting.

XN-L Series Results

![XN-L Series Results](image)

**RBC Histogram (Close-Up)**

![RBC Histogram](image)

**Normal RBC Histogram (Reference)**

![Normal RBC Histogram](image)
Abnormal, Dimorphic Population (continued)

The RBC count and MCV for the two populations shown on the RBC histogram can be found in the Service tab of the Browser Screen if needed.

NOTE: Results from the Service Tab are not directly reportable by the laboratory and must be confirmed prior to reporting.
Abnormal, Dimorphic Population (continued)

Suggested Action Steps:

1. Review results according to your laboratory protocol. This may include scanning the peripheral smear for the presence of abnormal RBC morphology such as:
   - increased anisocytosis
   - multiple RBC populations (sometimes seen in patients who have received numerous recent packed red blood cell transfusions or other therapies)
   - fragmented RBCs
   - poikilocytosis
   - rouleaux or RBC agglutination (refer to suggested action for “RBC Agglutination?” if present)

   Report any abnormal RBC morphology according to your laboratory protocol.

2. If no abnormalities are found when reviewing the smear and analyzer results are consistent with smear review findings, the results with asterisks (*) may be reported.

3. If dashes (— —) are in place of numeric data, verify results according to your laboratory’s policy. Possible actions may include repeating the sample or reporting RBC morphology from smear review.

   NOTE: If necessary, follow your laboratory protocol for reporting results that cannot be measured or calculated. In most laboratory information systems, this is done by using a code for “do not report” or “not measured” in place of the RDW results.

4. If the RBC morphology is normal and the MCHC is abnormal (<30 or >37.5 g/dL) an interfering substance or condition may be present. Refer to the suggested guidelines for the Turbidity/HGB Interference? IP Message.
**Suspect, RBC Agglutination?**

The RBC Agglutination? IP Message is determined by calculation and size comparison of certain RBC items (MCHC, MCH, RBC, Upper RBC histogram discriminator [RU%]*).

*The RU% is not a reportable parameter, but it is used in the RBC Agglutination algorithm.

Asterisks (*) appear next to the RBC, HCT, MCV, MCH, MCHC and RET# parameters. The asterisk (*) indicates these results may be unreliable and should be confirmed according to your laboratory protocol prior to reporting.

**NOTE:** Availability of RET analysis function depends on system configuration.

**XN-L Series Results (initial run)**

<table>
<thead>
<tr>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>WBC</td>
<td>6.16</td>
<td>10^3/μL</td>
</tr>
<tr>
<td>RBC</td>
<td>0.72</td>
<td>10^6/μL</td>
</tr>
<tr>
<td>HGB</td>
<td>8.4</td>
<td>g/dL</td>
</tr>
<tr>
<td>HCT</td>
<td>8.8</td>
<td>%</td>
</tr>
<tr>
<td>MCV</td>
<td>122.2</td>
<td>fl</td>
</tr>
<tr>
<td>MCH</td>
<td>116.7</td>
<td>pg</td>
</tr>
<tr>
<td>MCHC</td>
<td>95.5</td>
<td>g/dL</td>
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<tr>
<td>PLT</td>
<td>20</td>
<td>10^3/μL</td>
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</table>

<table>
<thead>
<tr>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>NEUT#</td>
<td>4.18</td>
<td>10^3/μL</td>
</tr>
<tr>
<td>LYMPH#</td>
<td>1.04</td>
<td>10^3/μL</td>
</tr>
<tr>
<td>MONO#</td>
<td>0.74</td>
<td>10^3/μL</td>
</tr>
<tr>
<td>ECH#</td>
<td>0.82</td>
<td>10^3/μL</td>
</tr>
<tr>
<td>BASO#</td>
<td>0.88</td>
<td>10^3/μL</td>
</tr>
<tr>
<td>RET%</td>
<td>1.48</td>
<td>%</td>
</tr>
<tr>
<td>RET#</td>
<td>0.0107</td>
<td>10^6/μL</td>
</tr>
<tr>
<td>IRF</td>
<td>10.1</td>
<td>%</td>
</tr>
<tr>
<td>RET-He</td>
<td>34.5</td>
<td>pg</td>
</tr>
</tbody>
</table>

**Flag(s)**

- Bl/Abn Ly?(110)
- Atypical Ly?(300)
- RBC Abn Dist
- Dimorph Pop
- Macro
- RBC Agglut?(230)
Suspect, RBC Agglutination? (continued)

Initial Run RBC Histogram (Close-Up)  Normal RBC Histogram (Reference)

XN-L RBC Histogram (after warming at 37°C) (Close-Up)

Suggested Action Steps:
1. Follow your laboratory protocol and scan the peripheral smear for the presence of agglutinated RBCs or visually check the sample tube for agglutination.

2. If agglutinated RBCs are present, warm the sample at 37°C for 15-30 minutes according to your laboratory policy. Reanalyze the warmed sample in the manual mode after mixing by manual inversion 10 times. Make a new peripheral smear from the warmed sample if agglutination is severe and WBCs and PLTs cannot be accurately assessed.

NOTE: Sometimes agglutination can be so severe that warming the sample does not enable accurate analysis.
Suspect, RBC Agglutination?
(continued)

3. In cases with high cold agglutinin titers, a dilution or plasma replacement using warm CELLPACK™ DCL may be necessary to reduce the interference from the antibody. Further warming post-dilution or plasma replacement may also be necessary.

   a. To perform a plasma replacement
      i. Centrifuge an aliquot of blood from the primary tube to separate the cells from the plasma.
      ii. Using a pipette, remove a measured amount of plasma, removing as much plasma as possible without disturbing the buffy coat.
      iii. Add back the same amount of CELLPACK DCL as the volume of plasma removed in step ii. (Example: If 0.5 mL of plasma is removed then add back 0.5 mL of CELLPACK DCL.)
      iv. Cap the tube and mix the sample by manual inversion until the cells are fully re-suspended in the CELLPACK DCL.
      v. Reanalyze the sample in the manual mode.

4. In cases where a warm-reacting antibody has caused agglutination, a plasma replacement may reduce the interference from the antibody. Room temperature CELLPACK DCL may be used to replace the plasma.
Suspect, Turbidity/HGB Interference?

The Turbidity/HGB Interference? IP Message occurs when the MCHC is >37.5 g/dL and indicates that turbidity may be present in the diluted and lysed sample. This turbidity could interfere with the HGB detection light path and falsely increase the HGB value. Other interfering substances or conditions may impact the hemocrit and also cause an increased MCHC.

Asterisks (*) appear next to the HGB, MCH and MCHC parameters. The asterisk (*) indicates these results may be unreliable and should be confirmed according to your laboratory protocol prior to reporting.

XN-L Series Results

<table>
<thead>
<tr>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>WBC</td>
<td>5.43</td>
<td>10^3/μL</td>
<td>NEUT#</td>
<td>3.71</td>
<td>10^3/μL</td>
</tr>
<tr>
<td>RBC</td>
<td>0.55</td>
<td>10^6/μL</td>
<td>LYMPH#</td>
<td>0.86</td>
<td>10^3/μL</td>
</tr>
<tr>
<td>HGB</td>
<td>8.9</td>
<td>g/dL</td>
<td>MONO#</td>
<td>0.74</td>
<td>10^3/μL</td>
</tr>
<tr>
<td>HCT</td>
<td>6.7</td>
<td>%</td>
<td>EO#</td>
<td>0.01</td>
<td>10^3/μL</td>
</tr>
<tr>
<td>MCV</td>
<td>121.8</td>
<td>fL</td>
<td>BASO#</td>
<td>0.04</td>
<td>10^3/μL</td>
</tr>
<tr>
<td>MCH</td>
<td>161.8</td>
<td>pg</td>
<td>NEUT%</td>
<td>68.4</td>
<td>%</td>
</tr>
<tr>
<td>MCHC</td>
<td>132.8</td>
<td>g/dL</td>
<td>LYMPH%</td>
<td>15.8</td>
<td>%</td>
</tr>
<tr>
<td>PLT</td>
<td>12</td>
<td>10^3/μL</td>
<td>MONO%</td>
<td>13.6</td>
<td>%</td>
</tr>
<tr>
<td>RDW-SD</td>
<td>-----</td>
<td>fL</td>
<td>EO%</td>
<td>0.2</td>
<td>%</td>
</tr>
<tr>
<td>MPV</td>
<td>12.6</td>
<td>fL</td>
<td>BASO%</td>
<td>0.7</td>
<td>%</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>IG#</td>
<td>0.07</td>
<td>10^3/μL</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>IG%</td>
<td>1.3</td>
<td>%</td>
</tr>
</tbody>
</table>

NOTE: MCHC results up to 37.5 g/dL may indicate a normal specimen on the high end of normal range in which case no action is needed. This may occur more often in samples with higher hemoglobin and hematocrit results.

Consider the MCHC and the MCV together when evaluating results and the reasons for the interference. Refer to the following table for possible interferences and corrective actions.

The Turbidity/HGB Interference troubleshooting chart provides suggestions for resolving common conditions or substances that may interfere with RBC, HGB or HCT measurement. These include cold agglutinins, icteric or lipemic plasma, electrolyte imbalances or markedly increased glucose. These procedures can assist in equilibration of red cells with isotonic reagents and allow proper measurement in such specimens.
Suspect, Turbidity/HGB Interference? (continued)

<table>
<thead>
<tr>
<th>Pattern of Results</th>
<th>Encountered in</th>
</tr>
</thead>
<tbody>
<tr>
<td>Low or Normal MCV</td>
<td>• Hemolysis</td>
</tr>
<tr>
<td>High MCHC (&gt;37.5 g/dL)</td>
<td>• Plasma electrolyte abnormalities (i.e., low sodium) affecting hematocrit results</td>
</tr>
<tr>
<td></td>
<td>• Severe lipemia</td>
</tr>
<tr>
<td></td>
<td>• Icterus</td>
</tr>
<tr>
<td></td>
<td>• Severe leukocytosis affecting hemoglobin measurement</td>
</tr>
<tr>
<td></td>
<td>• Abnormal plasma protein precipitation affecting hemoglobin measurement</td>
</tr>
<tr>
<td></td>
<td>Refer to Troubleshooting Chart</td>
</tr>
<tr>
<td>High MCV</td>
<td>• RBC Agglutination</td>
</tr>
<tr>
<td>High MCHC (&gt;37.5 g/dL)</td>
<td>• Rouleaux</td>
</tr>
<tr>
<td></td>
<td>Refer to Troubleshooting Chart</td>
</tr>
</tbody>
</table>

Troubleshooting Chart
Always follow your local laboratory procedure for repeat testing or rejection of samples

<table>
<thead>
<tr>
<th>Low Sodium Affecting Hematocrit?</th>
<th>RBC Agglutination?</th>
<th>Severe Lipemia, Icterus, Abnormal Protein or Leukocytosis Affecting Hemoglobin Measurement or Hemolysis?</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Perform a 1:5 dilution of sample with CELLPACK DCL</td>
<td>1. Prewarm at 37°C for fifteen to thirty minutes then rerun</td>
<td>1. Perform a 1:5 dilution of sample with CELLPACK DCL</td>
</tr>
<tr>
<td>2. Allow the dilution to equilibrate for ten to fifteen minutes</td>
<td>2. Severe cold agglutinins or rouleaux may require dilution or plasma replacement with CELLPACK DCL.</td>
<td>2. Repeat diluted sample</td>
</tr>
<tr>
<td>3. Rerun after equilibration</td>
<td>3. For severe cold agglutinins, additional incubation at 37°C may be necessary following dilution or plasma replacement.</td>
<td>3. Correct results for dilution factor prior to reporting.</td>
</tr>
<tr>
<td>4. Correct results for dilution factor prior to reporting.</td>
<td>Lipemia or Icterus Only Perform a plasma replacement procedure</td>
<td></td>
</tr>
</tbody>
</table>

NOTE: MCV, MCH, MCHC, RDW-SD, RDW-CV, MPV, Ret-He, IRF and differential percent results are unaffected by dilution and do not require correction.

Hemolysis: Recollect a new sample.
Suspect, Turbidity/HGB Interference?
(continued)

Extreme leukocytosis may interfere with the RBC, HGB, HCT and MCV determinations. The degree of interference depends on the number and size of WBCs present in the sample in addition to the hemoglobin concentration of the sample. Evaluate the MCHC to help identify potential interference. Suggestions for resolving interference and correcting results for extreme leukocytosis include:

RBC: Subtract the WBC count from the RBC count
   Corrected RBC (cRBC) = RBC (x 10^6/μL) – WBC (x 10^3/μL)

HCT:
   Option 1: Perform a spun hematocrit and recalculate the MCV (cMCV) using the spun hematocrit and the cRBC result using the following formula:
   \[
   \text{Corrected MCV (cMCV)} = \frac{\text{HCT} \times 10}{\text{cRBC}}
   \]

   Option 2: Obtain the small cell population (sMCV) from the Service RBC/PLT Browser Tab as described in the Abnormal, Dimorphic Population flag section. Recalculate the HCT with the sMCV and cRBC result using the following formula:
   \[
   \text{Corrected HCT (cHCT)}(\%) = \frac{(sMCV \times cRBC)}{10}
   \]

HGB: Dilute as described in the Troubleshooting Chart.

NOTES:
1. Results from the Service Tab are not directly reportable by the laboratory and must be confirmed first.
2. When performing corrections also recalculate the MCH and MCHC using the results from the corrected parameters.

Certain hemoglobinopathies (Examples: S-C, S-S, C-C, H-S) are known to produce hyper-dense RBCs with increased MCHC values due to altered surface volume and/or deformability of the RBCs. In such cases, cell membrane changes produced by these hemoglobinopathies are not reversible or changeable. In individual patients, the quantity of hyper-dense RBCs may change when they are in crisis or from transfusion and/or drug therapies they are receiving.

Suspect, Iron Deficiency?
The Iron Deficiency? IP Message is determined by calculation and size comparison of certain RBC items (MCV, RDW-CV).

NOTE: This flag is not used in the North American market.

Suspect, HGB Defect?
The HGB Defect? IP Message is determined by calculation and size comparison of certain RBC items (MCV and RDW-CV).

NOTE: This flag is not used in the North American market.
**Suspect, Fragments?**

The Fragments? IP Message is determined from calculation and size comparison of certain RBC and PLT items (MCV, RDW-SD, MCHC, RBC Lower Discriminator [RL]*, PLT Upper Discriminator [PU]*, PLT Upper Discriminator % [PU%]*) or from the RET scattergram.

*The RBC lower discriminator, PLT upper discriminator, % of the PLT upper discriminator are not reportable parameters and are used only in the algorithm for the Suspect, Fragments flag.

NOTE: Availability of RET analysis depends on system configuration.

**XN-L Series Results**

<table>
<thead>
<tr>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>WBC</td>
<td>17.44+</td>
<td>10^3/uL</td>
<td>NEUT#</td>
<td>13.48+</td>
<td>10^3/uL</td>
</tr>
<tr>
<td>RBC</td>
<td>3.01</td>
<td>10^6/uL</td>
<td>LYMPH#</td>
<td>1.74</td>
<td>10^3/uL</td>
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<tr>
<td>HGB</td>
<td>7.5</td>
<td>g/dL</td>
<td>MONO#</td>
<td>1.64</td>
<td>10^3/uL</td>
</tr>
<tr>
<td>HCT</td>
<td>25.3</td>
<td>%</td>
<td>EO#</td>
<td>0.20</td>
<td>10^3/uL</td>
</tr>
<tr>
<td>MCV</td>
<td>84.1</td>
<td>fl</td>
<td>BASO#</td>
<td>0.19</td>
<td>10^3/uL</td>
</tr>
<tr>
<td>MCH</td>
<td>24.9</td>
<td>pg</td>
<td>RET-%</td>
<td>77.3</td>
<td>%</td>
</tr>
<tr>
<td>MCHC</td>
<td>29.6</td>
<td>g/dL</td>
<td>LYMPH%</td>
<td>10.0</td>
<td>- %</td>
</tr>
<tr>
<td>PLT</td>
<td>693</td>
<td>10^3/uL</td>
<td>MONO%</td>
<td>9.4</td>
<td>%</td>
</tr>
<tr>
<td>RDW-SD</td>
<td>58.9+</td>
<td>fl</td>
<td>EO%</td>
<td>1.1</td>
<td>%</td>
</tr>
<tr>
<td>RDW-CV</td>
<td>19.6+</td>
<td>%</td>
<td>BASO%</td>
<td>1.1</td>
<td>%</td>
</tr>
<tr>
<td>MPV</td>
<td>11.1</td>
<td>fl</td>
<td>IG#</td>
<td>0.19</td>
<td>10^3/uL</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>IG%</td>
<td>1.1</td>
<td>%</td>
</tr>
</tbody>
</table>

Flag(s)

- Mono+
- Hypochromia
- Fragments(170)
Suspect, Fragments? (continued)

Suggested Action Steps:

1. Scan the peripheral smear for the presence of fragmented RBCs and other poikilocytosis according to your local laboratory protocol.

2. Report the presence of any clinically significant RBC morphology according to your local laboratory protocol.
Abnormal, RET Abn Scattergram

The RET Abn Scattergram IP Message can only be generated on the XN-L Series if the reticulocyte parameter is ordered. This IP Message indicates that the analyzer has detected increased activity in the RET-THR (threshold) area of the RET scattergram or increased activity in the RET-UPP (Upper Particle Plateau) area on the RET-EXT scattergram.

RET-EXT Scattergram: The RET-UPP area (green area past reticulocytes) is abnormal due to the possible presence of NRBCs, Howell-Jolly Bodies or parasites. These are not included in the reticulocyte count.

Asterisks (*) appear next to the RET%, RET#, IRF and RET-He parameters. The asterisk (*) indicates these results may be unreliable and should be confirmed according to your laboratory protocol prior to reporting. When the RET Abn Scattergram flag is present and there is no asterisk (*) on the RET%, RET#, IRF and RET-He parameters, they may be reported without further review.

NOTE: Availability of RET analysis function depends on system configuration.

XN-L Series Results
Abnormal, RET Abn Scattergram (continued)

Suggested Action Steps:

1. Prepare a 1:5 dilution with CELLPACK™ DCL diluent to minimize interference. Run the 1:5 dilution in the manual mode (NOT the Pre-Dilute mode). Dilutions greater than 1:5 should not be used.

   NOTE: Do not use undiluted CELLPACK™ DST for any dilutions.

2. Check that the RBC (x5) on the diluted sample matches the original RBC count to ensure that dilution errors have not occurred. Also, check that the diluted RBC count is not less than 0.50 x 10⁶/μL. In flow cytometry adequate particles must be present for accurate gating to occur. If the diluted sample’s RBC count is <0.50 x 10⁶/μL, make a lower dilution (i.e. 1:2 or 1:3) in order to increase the RBC count.

3. If the RET Abn Scattergram flag is eliminated, multiply the absolute reticulocyte count by the dilution factor and report all results according to your laboratory protocol. The reticulocyte % and IRF do not need to be recalculated with the dilution factor since these percentages/ratios should remain the same regardless of the dilution factor. RET-He also does not need to be recalculated with the dilution factor since it is measured at the cellular level and is unaffected by dilution.

4. If the flag is not eliminated, or the RBC count is <0.50 x 10⁶/μL, follow your local laboratory protocol.

Possible actions include:
- reviewing the peripheral smear for the presence of polychromasia, parasites, NRBCs, Howell-Jolly Bodies or basophilic stippling. If present, report the results with a comment saying that the results may be affected by the presence of interfering substances.
- performing the reticulocyte by an alternate method.

NOTE: Decisions to report with a comment, perform a dilution or perform an alternate method should be based on your local laboratory protocol.
Abnormal, PLT Abn Distribution

The PLT Abn Distribution IP Message is generated by calculation and size comparison of certain PLT items (PDW*, % of PLT lower discriminator [PL%]*, % of upper discriminator [PU%]*, platelet mean-frequent volume [PMFV]*, platelet large cell ratio*, MPV, platelet upper discriminator [PU]*).

*These are all non-reportable parameters that are used as part of the flagging algorithm.

The PLT may be marked with an asterisk (*). Dashes may appear in place of data for the MPV or the MPV may be marked with an asterisk (*). The asterisk (*) indicates these results may be unreliable and should be confirmed according to your local laboratory protocol prior to reporting.

XN-L Series Results

<table>
<thead>
<tr>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>WBC</td>
<td>15.86</td>
<td>10^3/μL</td>
<td>NEUT#</td>
<td>5.26</td>
<td>10^3/μL</td>
<td>RET%</td>
<td>1.08</td>
<td>%</td>
</tr>
<tr>
<td>RBC</td>
<td>5.80</td>
<td>10^6/μL</td>
<td>LYMHP#</td>
<td>8.81</td>
<td>10^3/μL</td>
<td>RET#</td>
<td>0.0626</td>
<td>%</td>
</tr>
<tr>
<td>HGB</td>
<td>10.5</td>
<td>g/dL</td>
<td>MONO#</td>
<td>0.80</td>
<td>10^3/μL</td>
<td>IRF</td>
<td>23.9</td>
<td>%</td>
</tr>
<tr>
<td>HCT</td>
<td>34.2</td>
<td>%</td>
<td>EO#</td>
<td>0.91</td>
<td>10^3/μL</td>
<td>RET-He</td>
<td>19.0</td>
<td>pg</td>
</tr>
<tr>
<td>MCV</td>
<td>59.0</td>
<td>fl</td>
<td>BASO#</td>
<td>0.05</td>
<td>10^3/μL</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MCH</td>
<td>18.1</td>
<td>pg</td>
<td>NEUT%</td>
<td>33.3</td>
<td>%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MCHC</td>
<td>30.7</td>
<td>g/dL</td>
<td>LYMHP%</td>
<td>55.5</td>
<td>%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PLT</td>
<td>427</td>
<td>10^3/μL</td>
<td>MONO%</td>
<td>5.0</td>
<td>%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RDW-SD</td>
<td>38.3</td>
<td>fl</td>
<td>EO%</td>
<td>5.7</td>
<td>%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RDW-CV</td>
<td>19.3</td>
<td>%</td>
<td>BASO%</td>
<td>0.3</td>
<td>%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MPV</td>
<td>10.1</td>
<td>fl</td>
<td>IG#</td>
<td>0.03</td>
<td>10^3/μL</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>IG%</td>
<td>0.2</td>
<td>%</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Platelet Histogram
(Close-Up)

Normal Platelet Histogram
(Reference)
Abnormal, PLT Abn Distribution
(continued)

Suggested Action Steps:

1. Review results according to your local laboratory protocol. Possible actions include:
   a. Scan the peripheral smear to estimate the platelet count and review for the presence of abnormal RBC or PLT morphology such as:
      - large or giant platelets
      - small platelets
      - platelet clumps
      - fragmented RBCs
      - microcytic RBCs
      - parasites
   b. If abnormal RBC, PLT or other morphology is noted, report according to your local laboratory protocol.

   NOTE: Reviewing the feathered edge and sides of the peripheral smear is suggested as platelet clumps and fibrin strands may migrate to this area during smear preparation.

2. If no abnormalities are found when reviewing the smear and analyzer platelet result is consistent with smear review findings, the results with asterisks (*) may be reported.

3. If platelet estimate does not confirm accuracy of analyzer count, confirm with an alternate method such as a manual platelet count according to your local laboratory protocol. Depending on the source of the interference, the analyzer PLT count may be falsely increased or decreased. Report any clinically significant RBC and/or PLT morphology according to your local laboratory protocol.

4. If platelet clumps have interfered, perform one of the alternate procedures recommended in the section Suggested Actions for "PLT Clumps?" IP Message.

   NOTE: When dashes (—) appear in place of data for the MPV, follow your laboratory protocol for reporting results that cannot be measured or calculated. In most laboratory information systems, this is done by using a code for "do not report" or "not measured" in place of the MPV result.
Suspect, PLT Clumps?

The PLT Clumps? IP Message is determined by abnormal clustering in the WDF scattergram.

Asterisks (*) will appear next to the PLT result. Dashes may appear in place of data for the MPV or the MPV may be marked with an asterisk (*). The asterisk (*) indicates these results may be unreliable and should be confirmed according to your laboratory protocol prior to reporting.

XN-L Series Results

<table>
<thead>
<tr>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
<th>Item</th>
<th>Data</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>WBC</td>
<td>8.44</td>
<td>10^3/μL</td>
<td>NEUT#</td>
<td>4.60</td>
<td>10^3/μL</td>
<td>RET%</td>
<td>2.11</td>
<td>%</td>
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<tr>
<td>RBC</td>
<td>4.14</td>
<td>10^6/μL</td>
<td>LYMPH#</td>
<td>2.69</td>
<td>10^3/μL</td>
<td>RET#</td>
<td>0.0874</td>
<td>10^6/μL</td>
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<tr>
<td>HGB</td>
<td>12.6</td>
<td>g/dL</td>
<td>MONO#</td>
<td>0.89</td>
<td>10^3/μL</td>
<td>IRF</td>
<td>14.9</td>
<td>%</td>
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<tr>
<td>HCT</td>
<td>37.4</td>
<td>%</td>
<td>ED#</td>
<td>0.11</td>
<td>10^3/μL</td>
<td>RET-He</td>
<td>32.4</td>
<td>pg</td>
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<tr>
<td>MCV</td>
<td>90.3</td>
<td>FL</td>
<td>BASO#</td>
<td>0.06</td>
<td>10^3/μL</td>
<td></td>
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<td>MCH</td>
<td>30.4</td>
<td>pg</td>
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<tr>
<td>MCHC</td>
<td>33.7</td>
<td>g/dL</td>
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<tr>
<td>PLT</td>
<td>167 *</td>
<td>10^3/μL</td>
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<td>RDW-SD</td>
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<tr>
<td>RDW-CV</td>
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<td>%</td>
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<td>FL</td>
<td></td>
<td></td>
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<td></td>
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</tr>
</tbody>
</table>

Flag(s)

| PLT Clumps? (300) |

WDF Scatter (Close-Up)  
Normal WDF Scatter (Reference)
Suspect, PLT Clumps?
(continued)

Suggested Action Steps:
1. Follow your local laboratory protocol. Possible actions may include:
   a. Checking the sample for the presence of clots
   b. Scanning the peripheral smear, especially the feathered edge, for the presence of abnormal morphology including:
      • fibrin strands
      • platelet clumps
      i. If any of the above are present, verify the WBC and PLT by a manual slide estimate.
      ii. If the WBC and PLT estimates are consistent with the analyzer counts, report the results according to your local laboratory protocol.
      iii. If the estimates do not match the analyzer counts, refer to the next step to obtain an accurate count.

NOTE: Reviewing the feathered edge and sides of the peripheral smear is suggested as platelet clumps and fibrin strands may migrate to this area during smear preparation.

NOTES:
1. There are different methods for handling samples with platelet clumps. These may include vortexing of the original sample, recollection of the specimen, use of a different anticoagulant, introduction of additives to the primary tube, or other next steps. Each laboratory should review reference documents that contain recommendations for resolving problematic specimens or spurious values and adopt protocols based on available medical equipment, resources, and approval of their medical director.

2. Some samples with severe platelet clumping may not be resolved (or only be partially resolved) using any method. In such samples, the only option is to not report the numeric platelet result and instead report a platelet estimate from a review of a stained smear.

3. The incidence of completely unflagged instances of pseudothrombocytopenia is very low. However, to identify samples with pseudothrombocytopenia due to platelet clumping, multiple approaches must be employed together. Approaches for detecting platelet clumping may include:
   a. Smear review based on analyzer generated or user defined flags such as “Thrombocytopenia” or “Platelet Abnormal Distribution”, etc.
   b. Use of delta checks comparing the current result against previous results
   c. Review of smears based on both PLT and Mean Platelet Volume (MPV) results. (Low PLT with high MPV may indicate the presence of platelet clumps.)
   d. Use of review criteria for results that fall between the “thrombocytopenia” threshold and a critical low value that might warrant transfusion support.
**Abnormal, PLT Abn Scattergram**

This IP Message occurs when clustering in the platelet area of the RET Scattergram is abnormal. This flag is not related to the PLT measured in the RBC/PLT channel. In the absence of other flags on the PLT count, results may be reported with no further review.

**NOTE:** This flag is not used in the North American market.

**NOTE:** Availability of RET analysis function depends on system configuration.
**Body Fluid IP Messages**

**Abnormal, WBC Abn Scattergram**

The WBC Abn Scattergram IP message is generated during body fluid analysis whenever clustering in the WDF scattergram is abnormal. This flag can also be generated when the HF-BF#* or HF-BF%* result exceeds the HF-BF user defined limits in the WBC Abnormal Flag (Body Fluid Analysis) setting.

*These parameters are not reportable and are used only in the algorithm for the WBC Abn Scattergram flag during body fluid analysis.

Dashes may appear in place of data that was not calculated.

NOTE: Availability of Body Fluid analysis function depends on system configuration.

---

**XN-L Series Results**

![XN-L Series Results](image-url)
Abnormal, WBC Abn Scattergram (continued)

WDF Scatter (Close-Up)  Normal WDF Scatter (Reference)

Suggested Action Steps:
1. Dashes (— —) in place of numeric data:
   - Verify WBC-BF, TNC-BF and differential results according to your laboratory’s policy.
     Possible actions may include:
     o repeating the sample
     o diluting the sample with CELLPACK DCL diluent to minimize interference
     o performing a manual cell count
     o performing a manual differential and review for potential interferences such as bacteria or other debris

2. Asterisk (*) next to result:
   - Verify WBC-BF, TNC-BF and differential results according to your laboratory’s policy.
     Possible actions may include:
     o performing a manual cell count
     o performing a manual differential
   - If the WBC ABN Scattergram IP Message is present due to HF-BF results exceeding the HF-BF user defined limits—scan the slide for the presence of mesothelial and/or abnormal cells or cell clusters . Report results according to your laboratory protocol.
   - If no abnormalities are found when reviewing the smear and the WBC and TNC estimates are consistent with analyzer reported WBC-BF and TNC-BF, the results with asterisks (*) may be reported.

NOTES:
1. Decisions to report with a comment, perform a dilution or perform an alternate method should be based on your local laboratory protocol.
2. Body fluid dilutions should be made with CELLPACK DCL diluent. Correct results for dilution factor prior to reporting. Differential percent results are unaffected by dilution and do not require correction.
3. The viscosity of some synovial fluids may interfere with sample aspiration. Adding hyaluronidase to an aliquot of the original sample prior to analysis may reduce the viscosity of synovial fluid.1,2

---

Action and Error Messages

NOTE: Not all Action messages will trigger the POSITIVE sample judgement.

Insufficient blood volume (short sample)
This error message is generated by the sample aspiration sensor based on the absorbance of the diluted sample. Results are suppressed when this error message is generated.

Suggested Action Steps:
1. Check the sample for clots and ensure that the minimum volume requirements have been met; remix and rerun the sample.
2. If the message is not eliminated, follow your laboratory protocol.
   a. If a sample is suspected of having low hemoglobin, turn off the aspiration sensor in the Manual Analysis dialog box, remix and rerun the sample in the manual mode.
   b. If this error message is occurring on multiple samples, refer to the analyzer Instructions for Use for troubleshooting information.

NOTE: Enable the aspiration sensor prior to testing subsequent samples.
Action Messages (continued)

Difference between RBC and RET. Check the results
This message is generated based on the ratio of the RBC result from the RET channel (RBC-O) and the RBC result from the impedance channel. The ratio is calculated as: (RBC-O / RBC). The message is generated when the ratio is > 1.2 or < 0.8.

NOTE: Availability of RET analysis function depends on system configuration.

Suggested Action Steps:
1. Rerun the sample
2. If the message is not eliminated, follow your laboratory protocol. Possible actions may include:
   a. Scanning the peripheral smear for the presence of abnormal RBC morphology such as rouleaux or RBC agglutination (refer to suggested action for Suspect, “RBC Agglutination?” flag if present), polychromasia, parasites, NRBCs, Howell-Jolly Bodies. Report any abnormal RBC morphology according to your laboratory protocol.
   b. Verifying the reticulocyte using an alternate method.

PLT test result may have low reliability
Refer to the Suggested Action Steps for the Suspect, “PLT Clumps?” flag.
Interfering Substances
Some abnormal samples may interfere with automated cell counting methods. The following is a list from the Sysmex XN-L Series Instructions for Use of possible substances that may interfere with these parameters.

NOTE: Compromised samples, such as those not properly collected, stored, transported, or containing clots may cause misleading results. Always use good laboratory practices for inspecting specimens for acceptability and verifying results.

WBC
If any of the following conditions are present, the system may erroneously report a low white blood cell count.
- White blood cell aggregation

If any of the following conditions are present, the system may erroneously report a high white blood cell count.
- Platelet aggregation
- Poor lysing of red blood cells during analysis
- Erythroblasts
- Red blood cell aggregation (cold agglutinin)
- Chylemia
- Cryoprotein
- Cryoglobulin
- Fibrin
- Giant platelets

RBC
If any of the following conditions are present, the system may erroneously report a low red blood cell count.
- Red blood cell aggregation (cold agglutinin)
- Microcytic red blood cells
- Fragmented red blood cells

If any of the following conditions are present, the system may erroneously report a high red blood cell count.
- Leukocytosis (>100,000/μL)
- Giant platelets

HGB
If any of the following conditions are present, the system may erroneously report a high hemoglobin value.
- Leukocytosis (>100,000/μL)
- Lipemia
- Abnormal protein
Interfering Substances
(continued)

HCT
If any of the following conditions are present, the system may erroneously report a low hematocrit value.
- Red blood cell aggregation (cold agglutinin)
- Microcytic red blood cells
- Fragmented red blood cells

If any of the following conditions are present, the system may erroneously report a high hematocrit value.
- Leukocytosis (> 100,000/μL)
- Hyperglycemia
- Uremia
- Spherocytes

PLT
If any of the following conditions are present, the system may erroneously report a low platelet count.
- Platelet aggregation
- Pseudothrombocytopenia
- Giant platelets

If any of the following conditions are present, the system may erroneously report a high platelet count.
- Microcytic red blood cells
- Fragmented red blood cells
- Fragmented white blood cells
- Cryoprotein
- Cryoglobulin

RET
If any of the following conditions are present, the system may erroneously report a high reticulocyte count.
- Red blood cell aggregation (cold agglutinin)
- Giant platelets
- Platelet aggregation
- Fragmented white blood cells
- Malaria
- Howell-Jolly bodies
Interfering Substances
(continued)

Body Fluid
• Excessive mixing of samples
• Debris
• Fat globules
• Crystals
• Highly viscous synovial fluids
• Bacteria
• Fungi

NOTE: The Sysmex XN-L Series Analyzer is designed to flag abnormal samples that may contain interfering substances. These results should be reviewed carefully and may require further examination in accordance with your local laboratory protocol.

NOTE: Availability of RET and Body Fluid analysis functions depends on system configuration.
References


XN-530/XN-430/XN-330 Troubleshooting Instructions for Use (North American Edition), June 2017
