LABQUALITY

External Quality Assessment Scheme

Haemoglobin 3-level samples, Cell counters Round 1, 2022

Specimens

Please find enclosed 3 human blood samples S001, S002 and S003, each 1mL. Samples are ready to use.

Caution

Quality control specimens derived from human blood must be handled with the same care as patient samples, i.e. as potential transmitters of serious diseases. The specimens are found to be HBs-Ag and HIV-Ab negative when tested with licensed reagents, but no known test method can offer complete assurance that the specimens will not transmit these or other infectious diseases.

Examinations

Hb

Storage and use

The sample is stored at $+2 \dots +8$ °C. It is stable until the round closing date. Allow the specimen to stand at room temperature for about 30 minutes. Invert the vial several times, until the suspension appears homogenous. Do not mix too vigorously. Avoid foam forming in the sample. The determination should be carried out in the same way as for patient blood.

Result reporting

Please enter the results and methods via LabScala (www.labscala.com). If you cannot find your instrument or reagent from the registry, please contact the EQA coordinator.

S001



S002



S003



2022-09-06

INSTRUCTIONS

Product no. 2113 LQ74722014-016/DK

If the kit is incomplete or contains damaged specimens, please report immediately to info@labquality.fi.

The results should be reported no later than **September 22**, **2022**.

Inquiries

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Labquality Oy

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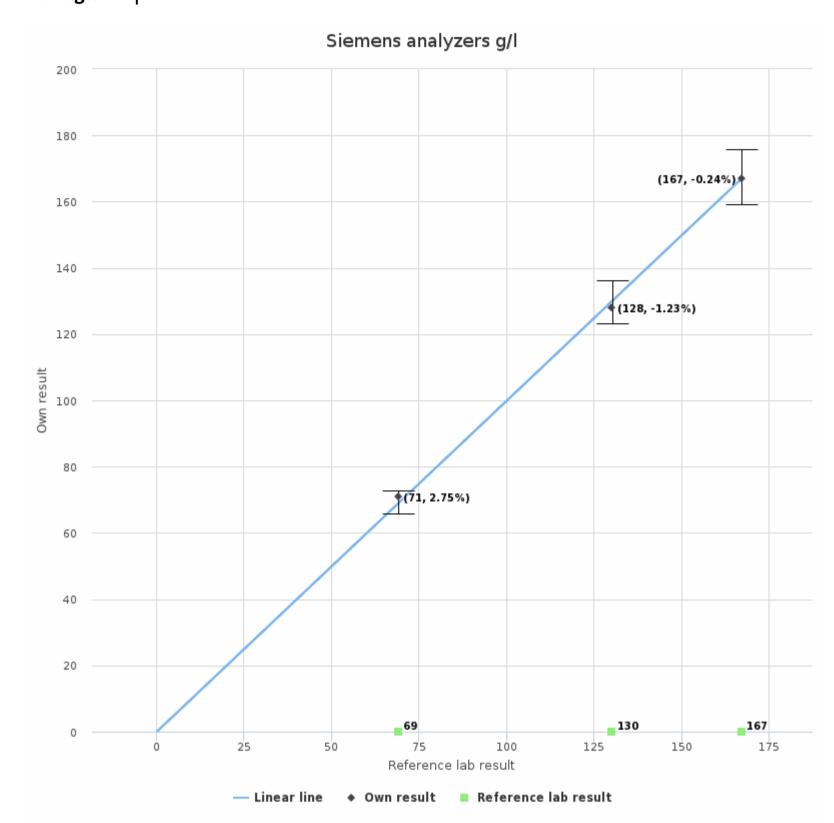
Tel. + 358 9 8566 8200 Fax + 358 9 8566 8280

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Hemoglobin |2120



Sample	Reference values	Target range	Own	diff%
Sample S001	69 g/l	66-73 g/l	71 g/l	2.75%
Sample S002	130 g/l	123-136 g/l	128 g/l	-1.23%
Sample S003	167 g/l	159-176 g/l	167 g/l	-0.24%

Linearity factor	Neg. pcs (own group)	Pos. pcs (own group)
9.51	0	1

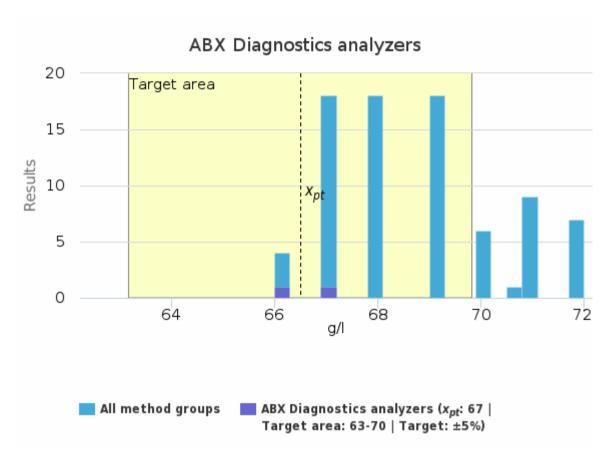
1/1 24.09.2022

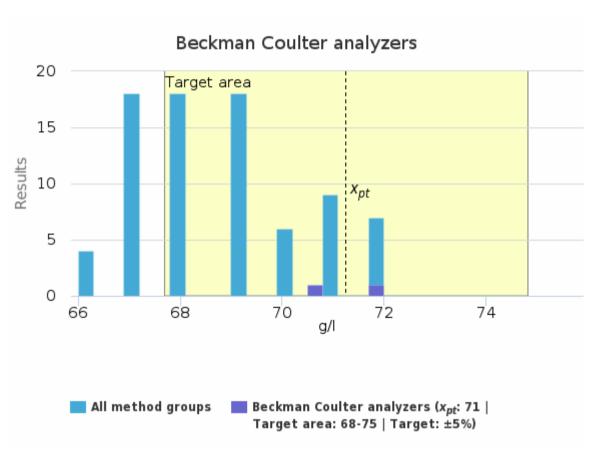


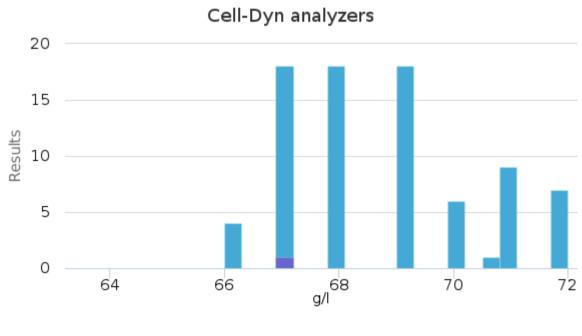
Sample S001 | Hemoglobin, g/l

Methodics	x _{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
ABX Diagnostics analyzers	67	67	<1	1.1	<1	66	67	-	2
Beckman Coulter analyzers	71	71	1	1.5	<1	71	72	-	2
Cell-Dyn analyzers	-	-	-	-	-	67	67	-	1
HemoScreen	-	-	-	-	-	67	67	-	1
Siemens analyzers	-	-	-	-	-	71	71	-	1
Swelab analyzers	-	-	-	-	-	72	72	-	1
Sysmex-analyzers	69	69	2	2.3	<1	66	72	-	73
All	69	69	2	2.5	<1	66	72	-	81

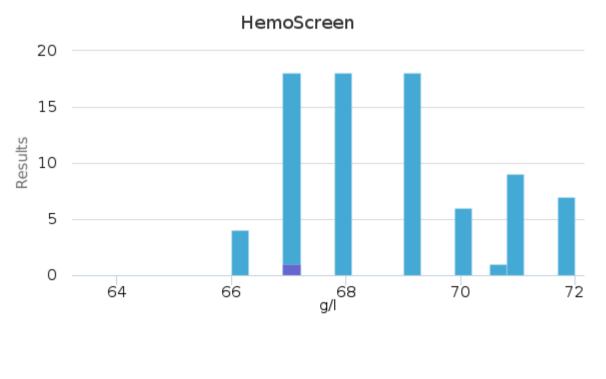
Sample S001 | Hemoglobin, g/l| histogram summaries in LabScala





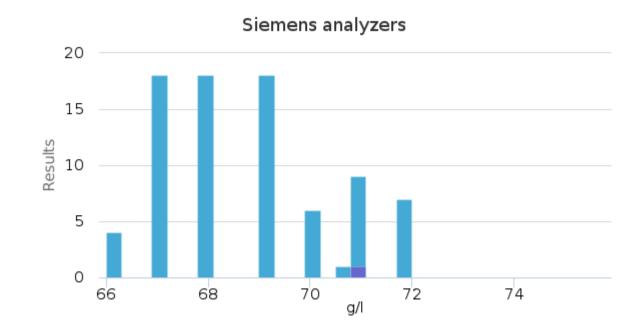


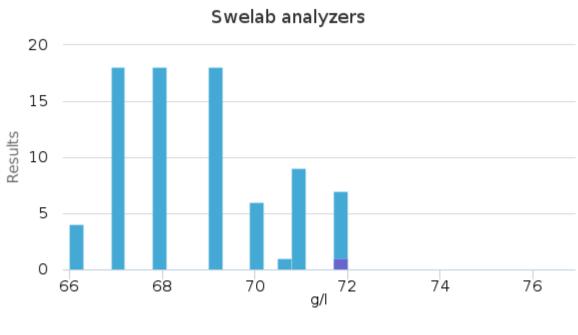
All method groups Cell-Dyn analyzers



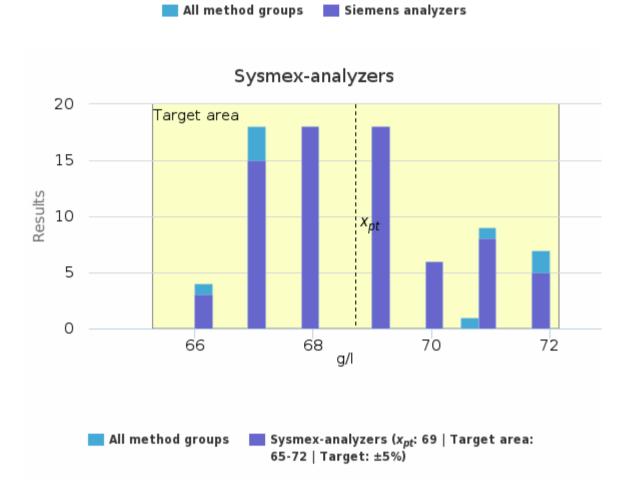
All method groups HemoScreen

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All method groups Swelab analyzers

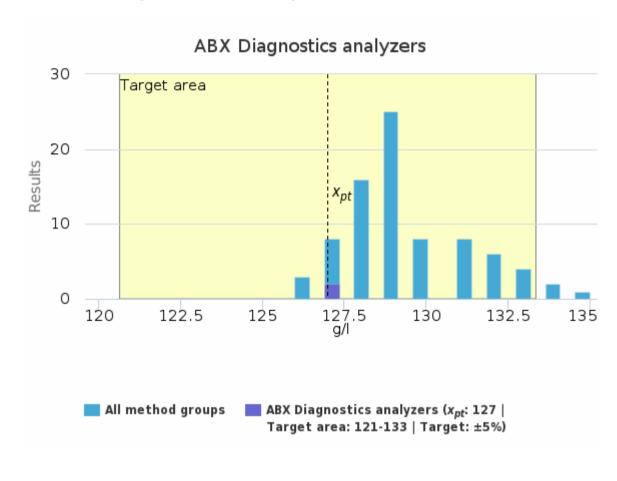


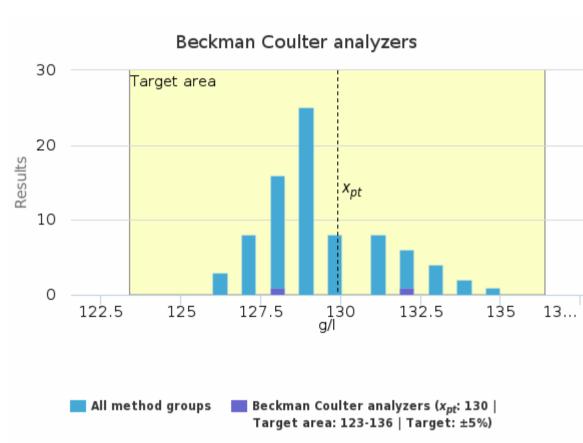


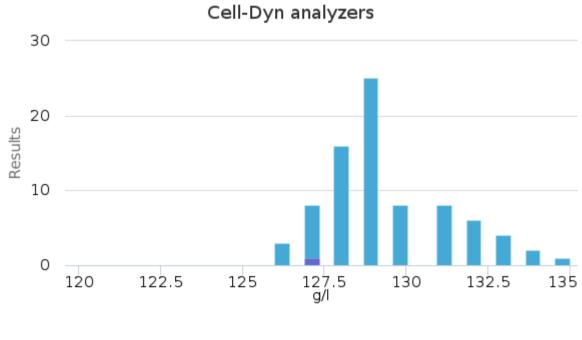
Sample S002 | Hemoglobin, g/l

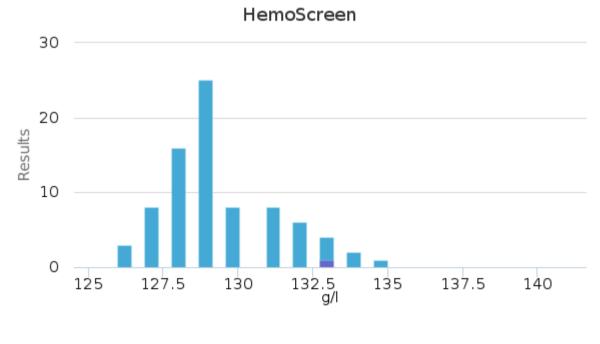
Methodics	x _{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
ABX Diagnostics analyzers	127	127	<1	<0.1	<1	127	127	-	2
Beckman Coulter analyzers	130	130	3	2.3	2	128	132	-	2
Cell-Dyn analyzers	-	-	-	-	-	127	127	-	1
HemoScreen	-	-	-	-	-	133	133	-	1
Siemens analyzers	-	-	-	-	-	128	128	-	1
Swelab analyzers	-	-	-	-	-	132	132	-	1
Sysmex-analyzers	129	129	2	1.4	<1	126	134	1	73
All	129	129	2	1.4	<1	126	134	1	81

Sample S002 | Hemoglobin, g/l| histogram summaries in LabScala

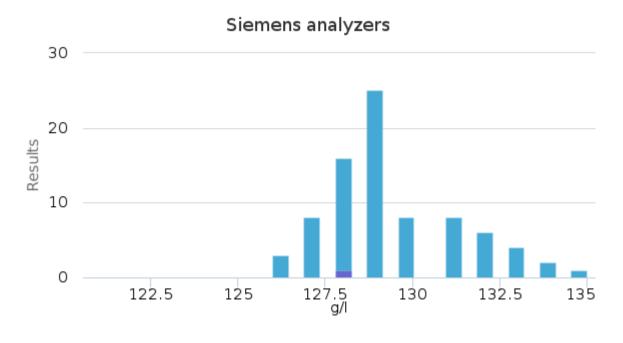


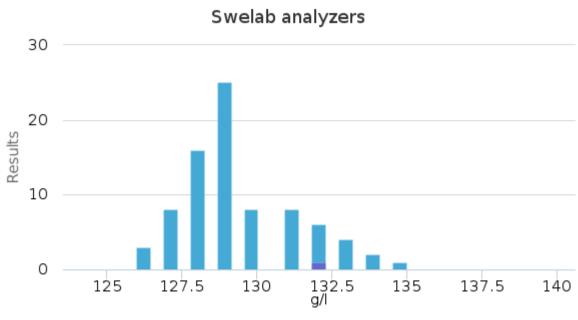




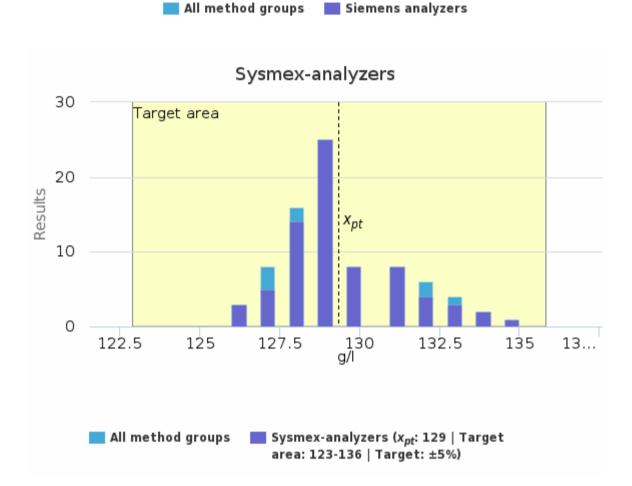


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All method groups Swelab analyzers



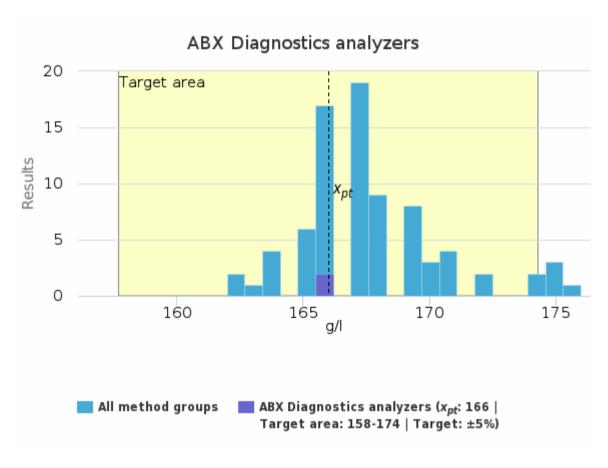
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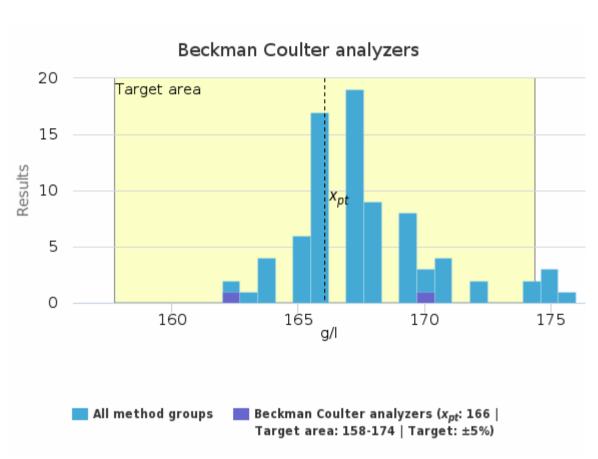


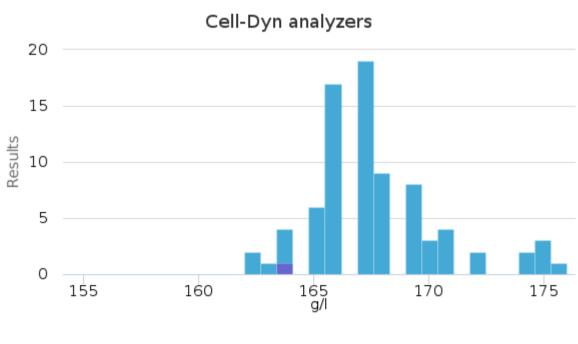
Sample S003 | Hemoglobin, g/l

Methodics	x _{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
ABX Diagnostics analyzers	166	166	<1	<0.1	<1	166	166	-	2
Beckman Coulter analyzers	166	166	6	3.4	4	162	170	-	2
Cell-Dyn analyzers	-	-	-	-	-	164	164	-	1
HemoScreen	-	-	-	-	-	175	175	-	1
Siemens analyzers	-	-	-	-	-	167	167	-	1
Swelab analyzers	-	-	-	-	-	169	169	-	1
Sysmex-analyzers	168	167	3	1.6	<1	162	175	1	73
All	168	167	3	1.6	<1	162	175	1	81

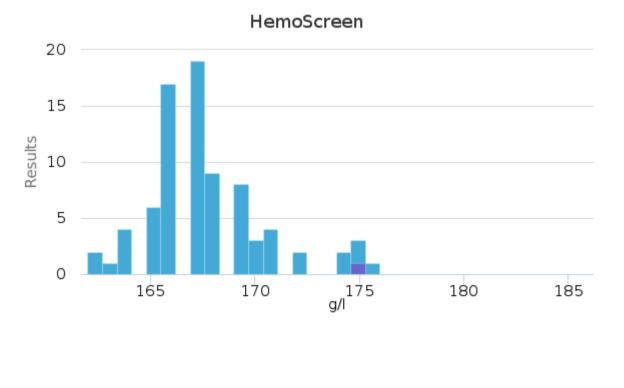
Sample S003 | Hemoglobin, g/l| histogram summaries in LabScala





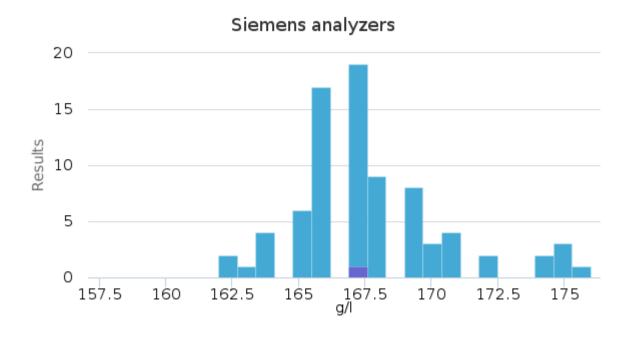


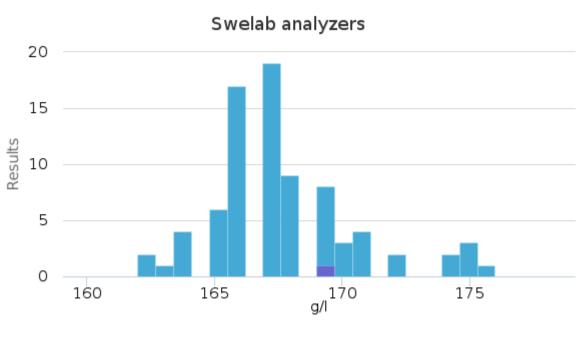
All method groups Cell-Dyn analyzers



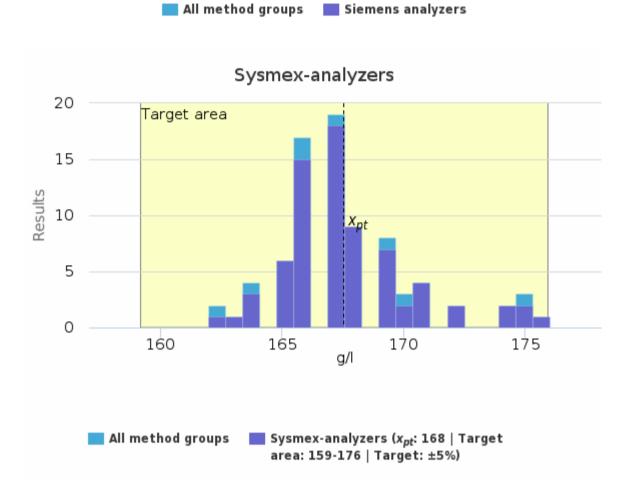
All method groups HemoScreen

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All method groups Swelab analyzers



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Report info

Participants

50 participants from 4 countries.

Report info

Your own result should be compared to others using the same method. Assigned values (x_{pt}, target values) are means of the results where results deviating more than +/- 3*standard deviation from the median are removed. The standard uncertainty (u) of

the assigned value is reported as standard error of the mean (SEM). Additionally, if the measurement uncertainty of the target value is large an automatic text is printed on the report: "The uncertainty of the assigned value is not negligible, and evaluations could be affected."
In case the client's result is the only one in the method group, no assigned value will be calculated, no target area shown, and no statistics calculated. In case there are only a few results in the client's own method group, the result can be compared to all method mean or to a group that is similar to the own method. Results reported with < or > -signs cannot be included in the statistics.

For information on report interpretation and performance evaluation, please see the "EQAS Interpretation guidelines" LabScala User instructions (top right corner? Help link).

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LABQUALITY

External Quality Assessment Scheme

Haemoglobin, 3-level samples, cell counters Round 1, 2022

Specimens

Samples S001 (LQ747222014), S002 (LQ747222015) and S003 (LQ747222016) were human whole blood preparations.

Based on the previous tests and the results of this round, the samples are homogeneous, stable and suitable for the external quality assessment scheme.

The materials were sent without temperature control packaging.

Report info

Please see the description of the data analysis on the last page of the laboratory-specific histogram and numerical summary report. It is important to read the Final report first, because it contains important information of the samples and results in each round.

Assigned values

Assigned values are the values of a reference method.1

Table 1

Haemoglobin concentrations by the reference method							
	Hb 2 x SEM						
concentration							
	g/L						
Sample 1	69.1	0.58	3				
Sample 2	129.6	0.064	3				
Sample 3	167.4	0.13	3				

Results

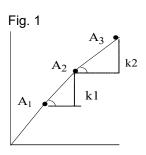
The reports were generated in LabScala. The results are given in a graphical presentation. The name of your own method group is printed on top of the y-axis. The assigned values are given on the x-axis in the graph, the laboratory's own results on the y-axis. The straight line in the graph represents x=y. The laboratory's own haemoglobin results are shown as black squares, with the haemoglobin concentration and deviation from the reference values (Diff %) in brackets. The vertical lines show the target limits.

Trueness

The assigned values \pm -5% are used to estimate the trueness of own results. Own result should lie within the target limits which means that the Diff% should be less than 5%.

Linearity

The deviation from linearity (linearity coefficient, %), is calculated from the relative difference of two slopes (k2-k1)/k1, see Fig 1.



2022-10-06

FINAL REPORT

Product no. 2113

 Samples sent
 2022-09-06

 Round closed
 2022-09-22

 Final report
 2022-10-06

Request for correction

Typing errors in laboratory's result forms are on laboratory's responsibility. Labquality accepts responsibility only for result processing. Requests must be notified by writing within three weeks from the date of this letter.

Authorized by

EQA Coordinator Päivi Ranta paivi.ranta@labquality.fi

Expert

M. Sc. Chemist, Ulla-Riitta Nordberg

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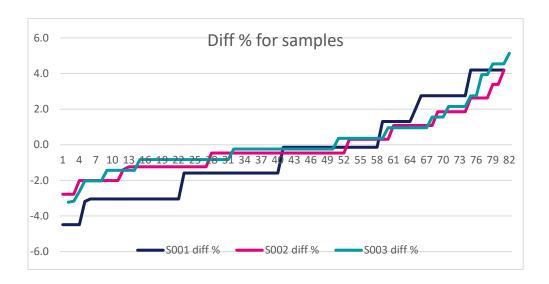
Below the graphical presentation there is a table showing laboratory's own linearity coefficient, and the number of negative and positive linearity coefficients in the own method group.

Comments - EQA Coordinator

Most of the results of the round (73/81) were measured with Sysmex instruments. Those customers who did not report results for all samples will receive the trueness value (difference% compared to the target value) for samples, but the linearity factor will not be reported. At the bottom of the device-specific graph is the device linearity factor. If the coefficient of linearity is greater than 10%, the linearity of the haemoglobin results should be questioned. There were 76/81 linearity coefficients within the acceptable limits. The biggest deviation of linearity coefficients was 16.17.

In addition to the coefficient of linearity, the customer should also look at the trueness of each sample. The graph below (Fig 2) shows the difference % of the samples from the target value. On this round only one S003 result was not in the target area.

Fig. 2



The condition and calibration of the instrument should be checked if there is a large deviation in either linearity or trueness (or both). The client should also check if the deviation is due to too low volume of sample or another sample handling problem.

Comments - Expert

The trueness (accuracy) of the cell counters that participated in the round is good (assigned value +/- 5%). The results correlate well with the results measured by the reference method.

The linearity of the hemoglobin results is good, too. Only a few devices show a clear non-linearity. The linearity factor of these devices is greater than 10%. Their condition and the processing of the samples should be checked.

References

¹ Recommendations for reference method for haemoglobinometry in human blood (ICSH standard 1995) and specifications for international haemoglobinometry standard (4th edition), J Clin Pathol, 1996; 49:271-274, International Council for Standardisation in Haematology: Expert Panel on Haemoglobinometry.

End of report

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