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## Lab EQA Case Studies

### Weqas Connect

Samantha Jones

Operations Manager, Weqas

# Case Study Checklist

## Summary Report

PI Scores:

Running PI analyte –sample scores:

## Standard Report

Analyte results table:

Scoring Table:

Running PI scores:

Bias Chart (Absolute):

Bias Chart (Relative):

Precision Scores:

Sample Histograms:

Method Summary Data:

Error Identification:

**Discuss potential cause and troubleshooting actions.**

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## Case Study - example



## Summary Report

### Programme: Lipids

**PI scores:** overall % poor PI = 19%, attributed to Poor **HDL** performance, other analytes acceptable or good.

**Running PI analyte –sample scores:** approx. 50% good, with consistent mix of acceptable and poor. Worse than median.

**Outcome:** Review HDL performance

Participant Code: [REDACTED] • Location: [REDACTED] • Analyser Name: [REDACTED] • Serial #: [REDACTED]

Date Samples received: 23-Jan-2024 • Date of Analysis: 23-Jan-2024 • Operator Details: YW • Storage Conditions: Ambient Temperature (18 - 30 °C)

Analyte: HDL Cholesterol • Method: [REDACTED] • Kit: [REDACTED]

| HDL Cholesterol mmol/L |                               |             |                    |                              |         |                             |
|------------------------|-------------------------------|-------------|--------------------|------------------------------|---------|-----------------------------|
|                        | Your reported result (mmol/L) |             | Method: [REDACTED] | Instrument Model: [REDACTED] | Overall | Non-Scoring Reference Value |
| Sample 1               | 1.1                           | Mean        | 0.911              | 0.990                        | 0.950   | 1                           |
|                        |                               | SD          | 0.024              | 0.109                        | 0.070   |                             |
|                        |                               | Uncertainty | 0.0039             | 0.0789                       | 0.0094  | n/a                         |
|                        |                               | n           | 60                 | 3                            | 86      |                             |
| Sample 2               | 1.2                           | Mean        | 1.000              | 1.087                        | 1.065   | 1.12                        |
|                        |                               | SD          | 0.008              | 0.116                        | 0.106   |                             |
|                        |                               | Uncertainty | 0.0013             | 0.0840                       | 0.0143  | n/a                         |
|                        |                               | n           | 60                 | 3                            | 86      |                             |
| Sample 3               | 1.8                           | Mean        | 1.553              | 1.630                        | 1.565   | 1.61                        |
|                        |                               | SD          | 0.059              | 0.172                        | 0.069   |                             |
|                        |                               | Uncertainty | 0.0096             | 0.1238                       | 0.0093  | n/a                         |
|                        |                               | n           | 60                 | 3                            | 86      |                             |
| Sample 4               | 2.6                           | Mean        | 2.197              | 2.333                        | 2.217   | 2.29                        |
|                        |                               | SD          | 0.068              | 0.268                        | 0.083   |                             |
|                        |                               | Uncertainty | 0.0110             | 0.1934                       | 0.0112  | n/a                         |
|                        |                               | n           | 60                 | 3                            | 86      |                             |

### Summary Report

**PI scores:** overall % poor PI = 19%, attributed to Poor **HDL** performance, other analytes acceptable or good

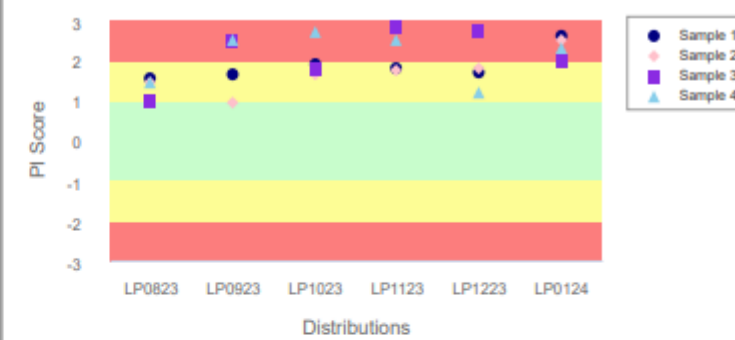
### Standard Report for HDL

**Analyte results table:** your results higher than method mean, instrument mean and non scoring ref value

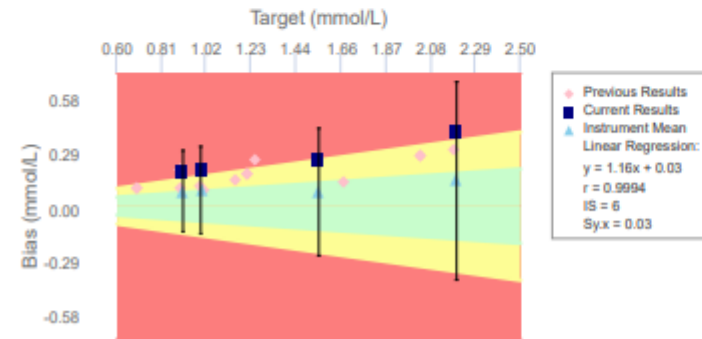
### Scoring

| Sample                | 1     | 2    | 3     | 4     | Overall Performance |
|-----------------------|-------|------|-------|-------|---------------------|
| Target: (Method Mean) | 0.911 | 1    | 1.553 | 2.197 |                     |
| Weqas TAE             | 0.146 | 0.16 | 0.248 | 0.352 |                     |
| PI                    | 2.6   | 2.5  | 1.99  | 2.29  | Poor                |

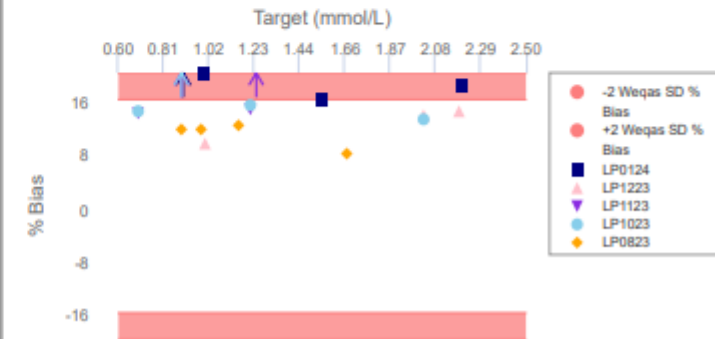
### Running PI



### Bias (Absolute)



### Bias (Relative %)



### Precision

|      | LP0823 | LP0923 | LP1023 | LP1123 | LP1223 | This distribution: LP0124 |
|------|--------|--------|--------|--------|--------|---------------------------|
| Sy.x | 0.02   | 0.05   | 0.04   | 0.05   | 0.06   | 0.03                      |
| IS   | 7      | 11     | 12     | 80     | 20     | 6                         |

*Sy.x is the average deviation from the best fit line and is an index of scatter.*

| IS Score  | Interpretation                        |
|-----------|---------------------------------------|
| 0 to 10   | Good                                  |
| 11 to 150 | Acceptable to Warning level           |
| > 150     | Unacceptable (incl. Curvilinear Data) |

### Summary Report

PI scores: overall % poor PI = 19%, attributed to Poor HDL performance, other analytes acceptable or good

### Standard Report for HDL

Analyte results table: your results higher than method mean, instrument mean and non scoring ref value

**Scoring Table:** 3 samples poor PI, 1 sample acceptable but PI 1.99.

**Running PI scores:** LP0823 acceptable, from LP0923 consistently poor performance for > 25% of samples, 75% poor for LP0124

### **Bias Chart (Absolute):**

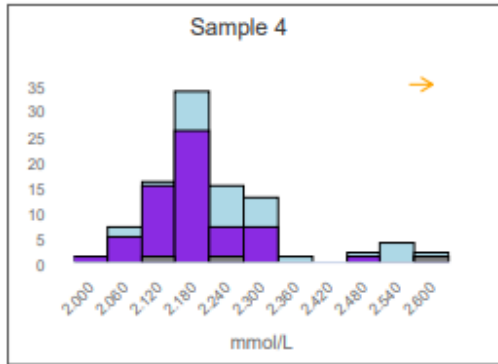
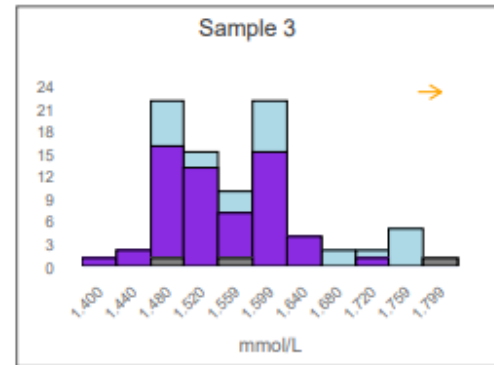
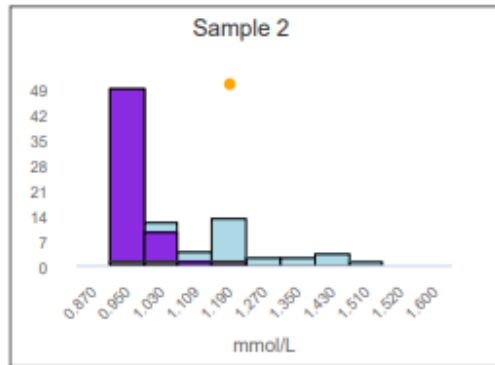
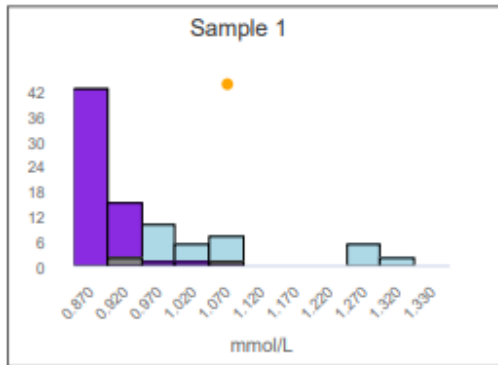
**Current results:** instrument mean close to method mean (target), instrument SDs wide but n = 3.

**Linear regression analysis:**  $y = 1.16 * x + 0.03$ , 16% positive systematic proportional bias

**Previous results:** longstanding positive systematic proportional bias, this dist worse than previous,

**Bias Chart (Relative):** longstanding positive systematic proportional bias of approx. 12-18%

**Precision Scores: *this distribution*:** precision good, previously good or acceptable



■ All Results ■ My Method ■ My Instrument ● My Result

### Method Summary

| LP0124                            | Sample 1     |            | Sample 2     |            | Sample 3     |            | Sample 4     |            |
|-----------------------------------|--------------|------------|--------------|------------|--------------|------------|--------------|------------|
| Method Name                       | Mean         | CV%        | Mean         | CV%        | Mean         | CV%        | Mean         | CV%        |
| Elimination (n=8)                 | 1.225        | 13.0       | 1.381        | 10.9       | 1.754        | 1.5        | 2.475        | 7.8        |
| Enzymatic Immunoinhibition (n=14) | 1.046        | 4.8        | 1.193        | 4.3        | 1.564        | 3.7        | 2.217        | 3.4        |
| NMR Spectroscopy (n=1)            | 1.280        | 0.0        | 1.290        | 0.0        | 1.590        | 0.0        | 2.280        | 0.0        |
| <b>[REDACTED] (n=60)</b>          | <b>0.911</b> | <b>2.6</b> | <b>1.000</b> | <b>0.8</b> | <b>1.553</b> | <b>3.8</b> | <b>2.197</b> | <b>3.1</b> |
| Vitros (n=3)                      | 1.033        | 6.3        | 1.200        | 0.0        | 1.633        | 4.0        | 2.333        | 2.8        |

There are no Weqas or Participant supplied comments for HDL Cholesterol for this distribution.

## Summary Report

PI scores: overall % poor PI = 19%, attributed to Poor HDL performance, other analytes acceptable or good

## Standard Report for HDL

Analyte results table: your results higher than method mean, instrument mean and non scoring ref value

**Scoring Table:** 3 samples poor PI, 1 sample acceptable but PI 1.99.

**Running PI scores:** LP0823 acceptable, from LP0923 consistently poor performance for > 25% of samples, 75% poor for LP0124

### **Bias Chart (Absolute):**

**Current results:** instrument mean close to method mean (target), instrument SDs wide but  $n = 3$ .

**Linear regression analysis:**  $y = 1.16 * x + 0.03$ , 16% positive systematic proportional bias

**Previous results:** longstanding positive systematic proportional bias, this dist worse than previous,

**Bias Chart (Relative):** longstanding positive systematic proportional bias of approx. 12-18%

**Precision Scores:** *this distribution:* precision good, previously good or acceptable

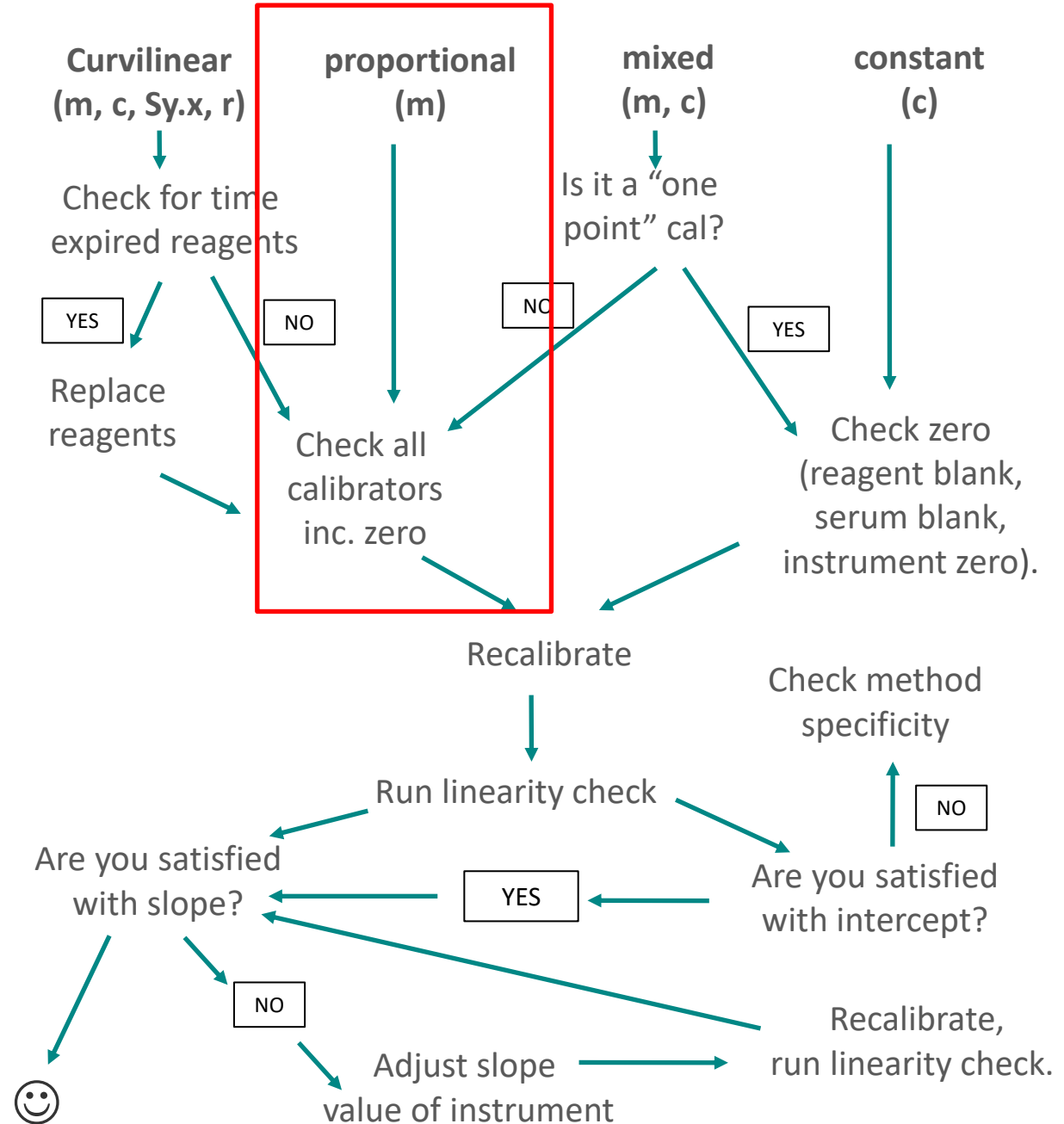
**Sample Histograms:** samples 3 and 4 off the scale, samples 1 and 2 non gaussian distributions but lab result over to the right of the majority.

**Method Summary Data:** Method negative bias to other methods

**Error identified:** 16% positive systematic proportional bias

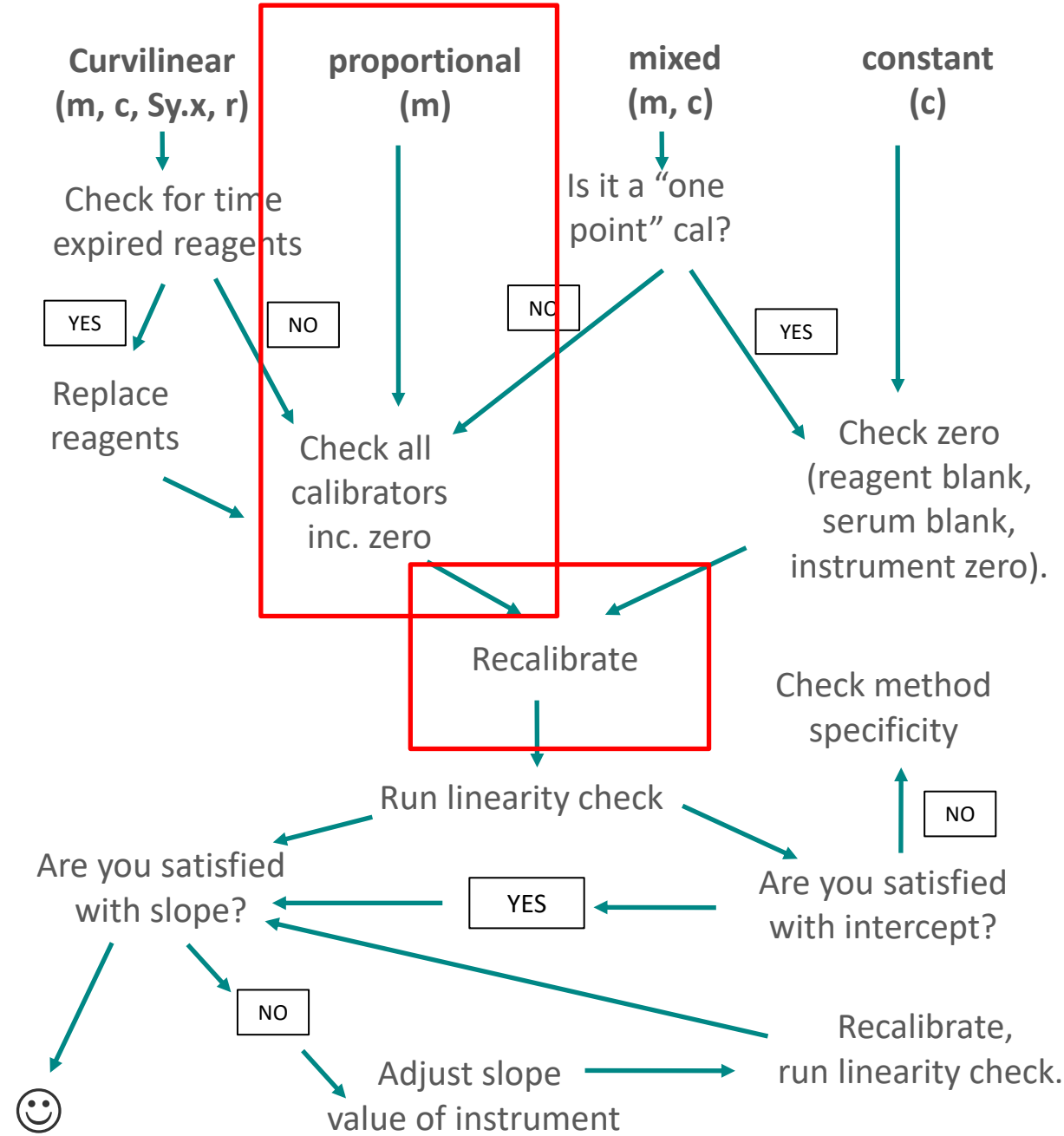
# Problem Solving Flow Chart

## INACCURACY



# Problem Solving Flow Chart

## INACCURACY



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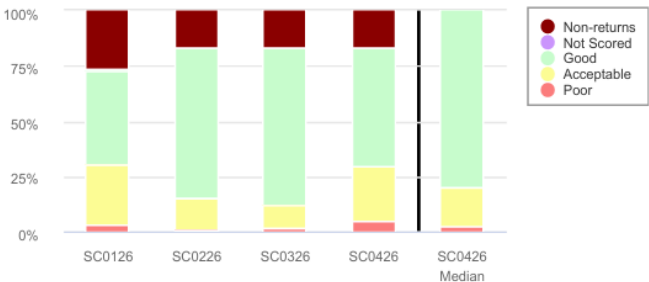
## Case 1 – Serum Chemistry – Total Protein

# Summary Report

Programme: **Serum Chemistry** • Distribution Code: **SC0426**  
 Distribution Start: 30-Mar-2026 • Distribution End: 14-Apr-2026 • Report Issued: 20-May-2026 • Report Status: Final  
 Requested By: #####

| This Distribution                    |     |
|--------------------------------------|-----|
| Your % Poor PI                       | 5%  |
| Median All Participant % Poor PI     | 2%  |
| 97.5 <sup>th</sup> Centile % Poor PI | 25% |

Running PI analyte-sample Scores



| PI Ranges |            |
|-----------|------------|
| <1        | Good       |
| 1-2       | Acceptable |
| >2        | Poor       |

| PI Code | Meaning                                                    |
|---------|------------------------------------------------------------|
| N/A     | Not enrolled for this analyte                              |
| NRR     | Analyte enrolled but no results returned                   |
| N/S     | This quantitative analyte not scored for this distribution |

\*\*\*\*\* **Please note** \*\*\*\*\*  
 Weqas are a UKAS ISO 17043 accredited EQA provider. Our accredited programmes are described on our UKAS schedule of accreditation which is available here: [WEQAS 17043 Schedule of Accreditation](#)

**Distribution Specific Comment**  
 There is no specific comment for this distribution.

No participant comments have been submitted for any instruments for this distribution.

| PI Scores            |              |
|----------------------|--------------|
| Location             | Location 1   |
| Instrument Name      | Instrument 1 |
| Instrument Serial #  | #####        |
| Sodium               | Acceptable   |
| Potassium            | Good         |
| Chloride             | Good         |
| Bicarbonate          | NRR          |
| Urea                 | Good         |
| Creatinine           | Acceptable   |
| Glucose              | Warning      |
| Calcium              | Acceptable   |
| Phosphate            | Good         |
| Total Protein        | Poor         |
| Albumin              | Good         |
| Magnesium            | Acceptable   |
| Urate                | Warning      |
| Lithium              | NRR          |
| AST                  | Good         |
| ALT                  | Good         |
| ALP                  | Acceptable   |
| CK                   | Good         |
| Gamma GT             | Good         |
| Amylase              | Acceptable   |
| LDH                  | Acceptable   |
| Gentamicin           | NRR          |
| Lipase               | NRR          |
| Overall % poor PI    | 5%           |
| Overall % Non-return | 17%          |

**Programme:** Serum Chemistry • **Distribution Code:** SC0426  
Distribution Start: 30-Mar-2026 • Distribution End: 14-Apr-2026 • Report Issued: 20-May-2026 • Report Status: Final

**Participant Code:** WQ##### • **Location:** Location 1 • **Analysed Name:** Instrument 1 • **Serial #:** #####  
Date Samples received: 31-Mar-2026 • Date of Analysis: 31-Mar-2026 • Operator Details: ## • Storage Conditions: Analysed on receipt

**Analyte:** Total Protein • **Method:** Roche Biuret End-Point • **Kit:** TP2 (Total Protein Gen. 2) (3183734190)

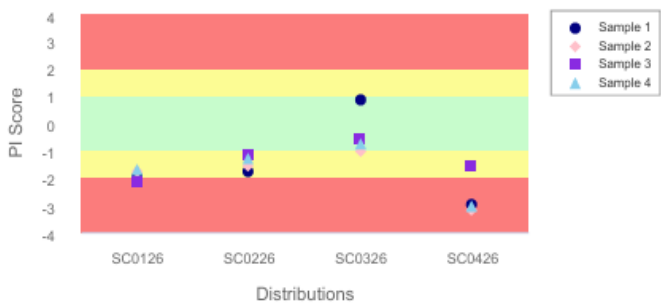
| Total Protein g/L |                            |             |                                   |                                  |         |
|-------------------|----------------------------|-------------|-----------------------------------|----------------------------------|---------|
|                   | Your reported result (g/L) |             | Method:<br>Roche Biuret End-Point | Instrument Model:<br>cobas c 501 | Overall |
| Sample 1          | 57                         | Mean        | 60.4                              | 61.2                             | 61.0    |
|                   |                            | SD          | 1.1                               | 1.7                              | 1.4     |
|                   |                            | Uncertainty | 0.16                              | 0.66                             | 0.16    |
|                   |                            | n           | 71                                | 10                               | 118     |
| Sample 2          | 61                         | Mean        | 64.8                              | 65.4                             | 65.3    |
|                   |                            | SD          | 1.3                               | 1.7                              | 1.4     |
|                   |                            | Uncertainty | 0.19                              | 0.67                             | 0.16    |
|                   |                            | n           | 71                                | 10                               | 117     |
| Sample 3          | 50                         | Mean        | 51.6                              | 52.5                             | 52.0    |
|                   |                            | SD          | 1.0                               | 1.5                              | 1.1     |
|                   |                            | Uncertainty | 0.15                              | 0.61                             | 0.13    |
|                   |                            | n           | 71                                | 10                               | 117     |
| Sample 4          | 74                         | Mean        | 78.0                              | 79.1                             | 78.9    |
|                   |                            | SD          | 1.3                               | 2.1                              | 1.6     |
|                   |                            | Uncertainty | 0.19                              | 0.83                             | 0.18    |
|                   |                            | n           | 71                                | 10                               | 118     |

# Analyte Standard Report

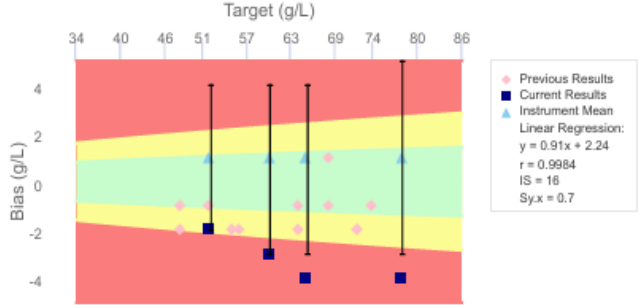
## Scoring

| Sample                | 1     | 2    | 3     | 4     | Overall Performance |
|-----------------------|-------|------|-------|-------|---------------------|
| Target: (Method Mean) | 60.4  | 64.8 | 51.6  | 78    |                     |
| Weqas TAE             | 2.3   | 2.4  | 2.1   | 2.7   |                     |
| PI                    | -3.02 | -3.2 | -1.55 | -3.03 | Poor                |

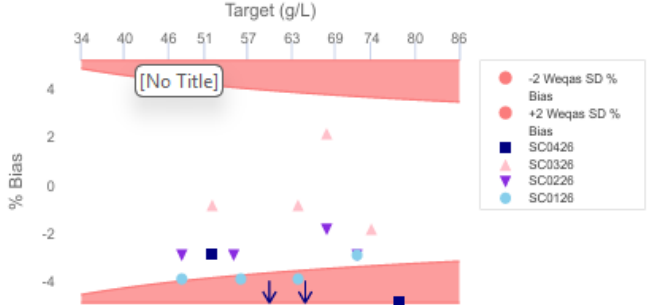
## Running PI



## Bias (Absolute)



## Bias (Relative %)

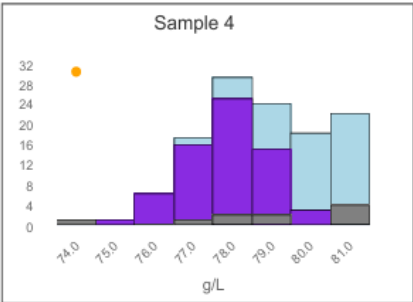
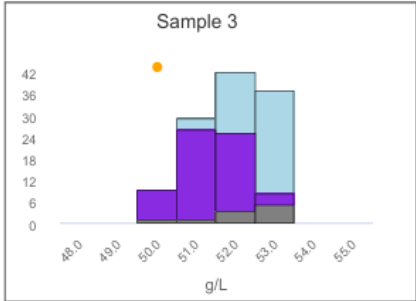
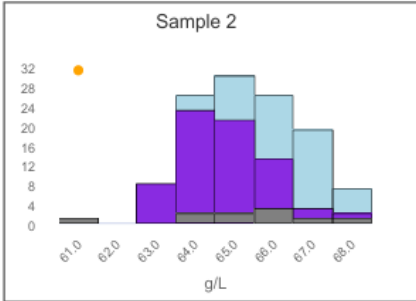
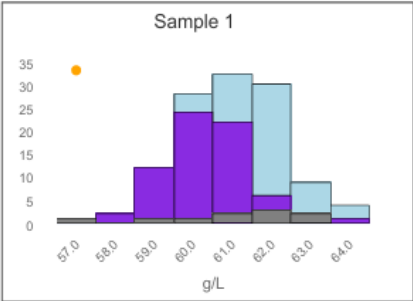


# Precision

|      | SC0126 | SC0226 | SC0326 | This distribution:<br>SC0426 |
|------|--------|--------|--------|------------------------------|
| Sy.x | 0.27   | 0.38   | 1.29   | 0.7                          |
| IS   | 2      | 4      | 60     | 16                           |

Sy.x is the average deviation from the best fit line and is an index of scatter.

| IS Score  | Interpretation                        |
|-----------|---------------------------------------|
| 0 to 10   | Good                                  |
| 11 to 150 | Acceptable to Warning level           |
| > 150     | Unacceptable (incl. Curvilinear Data) |



■ All Results
 ■ My Method
 ■ My Instrument
 ● My Result

# Method Summary

| SC0426                               | Sample 1    |            | Sample 2    |            | Sample 3    |            | Sample 4    |            |
|--------------------------------------|-------------|------------|-------------|------------|-------------|------------|-------------|------------|
| Method Name                          | Mean        | CV%        | Mean        | CV%        | Mean        | CV%        | Mean        | CV%        |
| Abaxis Piccolo (n=16)                | 61.4        | 1.8        | 65.9        | 2.3        | 52.5        | 2.0        | 79.9        | 1.8        |
| Beckman Biuret End-Point (n=10)      | 62.2        | 1.2        | 66.9        | 1.0        | 52.7        | 1.5        | 80.7        | 1.3        |
| <b>Roche Biuret End-Point (n=71)</b> | <b>60.4</b> | <b>1.8</b> | <b>64.8</b> | <b>2.0</b> | <b>51.6</b> | <b>2.0</b> | <b>78.0</b> | <b>1.7</b> |
| Siemens Biuret End-Point (n=21)      | 62.0        | 1.2        | 66.3        | 1.5        | 52.6        | 1.3        | 80.0        | 1.4        |

There are no Weqas or Participant supplied comments for Total Protein for this distribution.

# Analyte Standard Report

# Case 1

## Summary Report

**Overall PI:** Poor for Total Protein

Mostly good and acceptable scores for other analytes, a few non returns and one warning score for glucose and urate.  
No distribution specific comments.

## Standard Report for Total Protein

**Analyte results table:** Shows lower results for all samples compared to the method, instrument and overall means. Instrument Model SDs are wider for each sample than both the method mean and the overall mean, indicating wide variation within the instrument group data.

**Scoring Table:** Samples 1, 2 and 4 have PI scores >3 (negative PIs), with sample 3 having a PI of -1.55 (acceptable).

**Running PI scores:** Good scores for SC0326. SC0126 and SC0226 show similar scores to this distribution. SC0426 worse than previous 3 months.

**Bias Chart (Absolute):** Imprecision Score = 16 (acceptable). Accuracy: Linear regression shows - 9% proportional bias and 2.24 g/L constant bias ( $Y=0.91x + 2.24$ ). Bias between approximately -2 and -4 g/L across the 4 samples. Wide SD for the instrument mean. However Lab results outside instrument +2SD.

**Bias Chart (Relative):** Majority of samples over the last 4 months show negative % bias with this distribution showing the largest % negative bias. 2 samples from this distribution are off the chart (shown as arrows).

**Precision Scores table:** IS score acceptable for this distribution and SC0326, and good for distributions SC0126 and SC0226.

**Sample Histograms:** Lab results at the far left of the histogram for samples 1, 2 and 4 showing lower results against the method mean. Lab is likely the only results causing the instrument tail at the lower end. Sample 3 histogram shows sample result at the tail end of the method and instrument mean.

**Method Summary Data:** Lab method is highlighted in bold text. 71 instruments enrolled for this method. Method mean lower than other methods on the programme. Comparatively high CV%. If you click on the 'method' name in the analyte results table this would bring you up the instrument breakdown for the programme.

**Error Identification:** Mixed systematic error with predominant negative bias across the analytical range 30 – 80g/L

**Troubleshooting performed by the lab:** Calibrator, reagent & QC reviewed from initial analysis - all within normal parameters. Reagent and calibrator also within stability window. Repeat analysis performed – no poor performance on repeat (manually calculated the PI scores for each sample). SC0526 performance is good.

| Total Protein g/L |                            |             |         |                   |         |
|-------------------|----------------------------|-------------|---------|-------------------|---------|
|                   | Your reported result (g/L) |             | Method: | Instrument Model: | Overall |
| Sample 1          | 57                         | Mean        | 60.4    | 61.2              | 61.0    |
|                   |                            | SD          | 1.1     | 1.7               | 1.4     |
|                   |                            | Uncertainty | 0.16    | 0.66              | 0.16    |
|                   |                            | n           | 71      | 10                | 118     |
| Sample 2          | 61                         | Mean        | 64.8    | 65.4              | 65.5    |
|                   |                            | SD          | 1.3     | 1.7               | 1.4     |
|                   |                            | Uncertainty | 0.19    | 0.67              | 0.16    |
|                   |                            | n           | 71      | 10                | 117     |
| Sample 3          | 50                         | Mean        | 51.6    | 52.5              | 52.0    |
|                   |                            | SD          | 1.0     | 1.5               | 1.1     |
|                   |                            | Uncertainty | 0.15    | 0.61              | 0.13    |
|                   |                            | n           | 71      | 10                | 117     |
| Sample 4          | 74                         | Mean        | 78.0    | 79.1              | 78.9    |
|                   |                            | SD          | 1.3     | 2.1               | 1.6     |
|                   |                            | Uncertainty | 0.19    | 0.83              | 0.18    |
|                   |                            | n           | 71      | 10                | 118     |

Instrument  
Summary Report

| Participant Code | Location Name | Instrument Name | Instrument Serial Number | 1    | 2    | 3    | 4    |
|------------------|---------------|-----------------|--------------------------|------|------|------|------|
| WQ0              |               |                 |                          | 57 * | 61 * | 50   | 74 * |
| WQ0              |               |                 |                          | 63 * | 65   | 54 * | 81 * |
| WQ0              |               |                 |                          | 62   | 68 * | 54 * | 81 * |
| WQ0              |               |                 |                          | 61   | 66   | 54 * | 79   |
| WQ0              |               |                 |                          | 63 * | 66   | 53   | 79   |
| WQ0              |               |                 |                          | 61   | 67   | 53   | 81 * |
| WQ0              |               |                 |                          | 59   | 64   | 51   | 77   |
| WQ0              |               |                 |                          | 60   | 64   | 52   | 78   |
| WQ0              |               |                 |                          | 62   | 66   | 52   | 78   |
| WQ0              |               |                 |                          | 62   | 65   | 52   | 81 * |

# Repeat Analysis Performance

| Sample      | 1     | 2     | 3     | 4     |
|-------------|-------|-------|-------|-------|
| Result      | 59.1  | 63.3  | 50.4  | 77.2  |
| Method Mean | 60.4  | 64.8  | 51.6  | 78    |
| Weqas TAE   | 2.3   | 2.4   | 2.1   | 2.7   |
| PI          | -1.13 | -1.25 | -1.14 | -0.59 |

## SC0526 Performance

### Scoring

| Sample                | 1     | 2     | 3     | 4     | Overall<br>Performance |
|-----------------------|-------|-------|-------|-------|------------------------|
| Target: (Method Mean) | 47.1  | 73.6  | 56.1  | 69.2  |                        |
| Weqas TAE             | 1.9   | 2.6   | 2.2   | 2.5   |                        |
| PI                    | -0.41 | -0.65 | -0.91 | -0.03 | Good                   |

SC0526 results:  
46.7, 71.8, 55.1, 69.2

# Audience Poll

**Is there any further troubleshooting that you would do?**

**What other actions would you take?**

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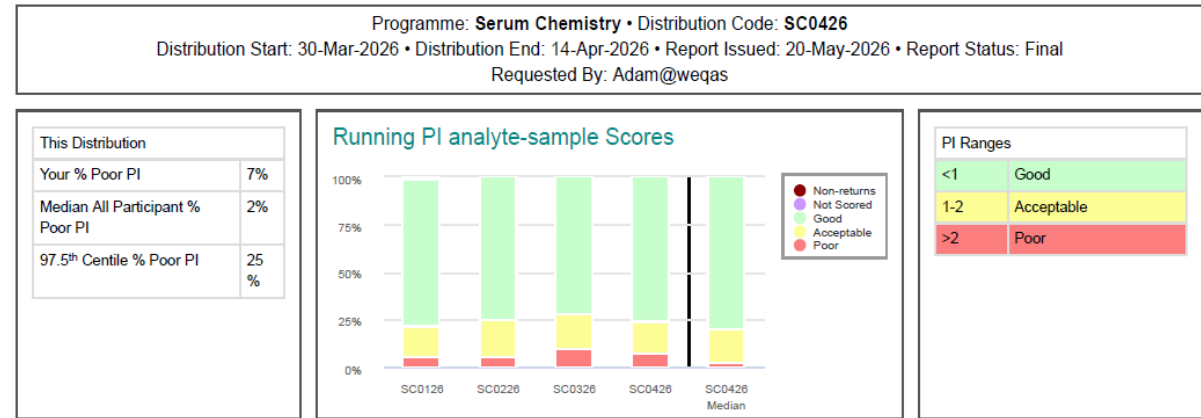
REFERENCE  
MEASUREMENT  
SERVICES



EDUCATION &  
TRAINING

## Case 2 – Serum Chemistry - Glucose

| PI Scores              |              |              |              |              |              |
|------------------------|--------------|--------------|--------------|--------------|--------------|
| Location               | Location 1   |              |              |              |              |
| Instrument Name        | Instrument 1 | Instrument 2 | Instrument 3 | Instrument 4 | Instrument 5 |
| Instrument Serial #    | #####        | #####        | #####        | #####        | #####        |
| Sodium                 | N/A          | Warning      | Poor         | Warning      | Poor         |
| Potassium              | N/A          | Good         | Good         | Good         | Good         |
| Chloride               | N/A          | Acceptable   | Good         | Good         | Acceptable   |
| Urea                   | N/A          | Good         | Good         | Acceptable   | Acceptable   |
| Creatinine             | N/A          | Good         | Good         | Good         | Good         |
| eGFR                   | N/A          | Good         | Good         | Good         | Good         |
| Glucose                | N/A          | Poor         | Poor         | Acceptable   | Acceptable   |
| Calcium                | N/A          | Acceptable   | Good         | Warning      | Good         |
| Adjusted Calcium       | N/A          | Good         | Good         | Acceptable   | Good         |
| Phosphate              | N/A          | Good         | Acceptable   | Good         | Acceptable   |
| Total Protein          | N/A          | Good         | Good         | Good         | Good         |
| Albumin                | N/A          | Good         | Good         | Good         | Good         |
| Calculated Globulin    | N/A          | Acceptable   | Acceptable   | Poor         | Poor         |
| Magnesium              | N/A          | N/A          | Acceptable   | N/A          | Acceptable   |
| Urate                  | N/A          | N/A          | Good         | N/A          | Good         |
| Lithium                | N/A          | N/A          | N/A          | N/A          | Acceptable   |
| Osmolality             | Poor         | N/A          | N/A          | N/A          | N/A          |
| AST                    | N/A          | N/A          | Acceptable   | N/A          | Acceptable   |
| ALT                    | N/A          | Good         | Good         | Good         | Good         |
| ALP                    | N/A          | Good         | Good         | Good         | Good         |
| CK                     | N/A          | N/A          | Good         | N/A          | Good         |
| Gamma GT               | N/A          | N/A          | Good         | N/A          | Good         |
| Amylase                | N/A          | N/A          | Good         | N/A          | Good         |
| LDH                    | N/A          | N/A          | Warning      | N/A          | Warning      |
| Iron                   | N/A          | N/A          | Good         | N/A          | Good         |
| Transferrin            | N/A          | N/A          | Acceptable   | N/A          | Acceptable   |
| Transferrin Saturation | N/A          | N/A          | Good         | N/A          | Good         |
| Gentamicin             | N/A          | N/A          | N/A          | N/A          | Good         |
| Overall % poor PI      | 75%          | 5%           | 6%           | 7%           | 6%           |
| Overall % Non-return   | 0%           | 0%           | 0%           | 0%           | 0%           |



## Summary Report

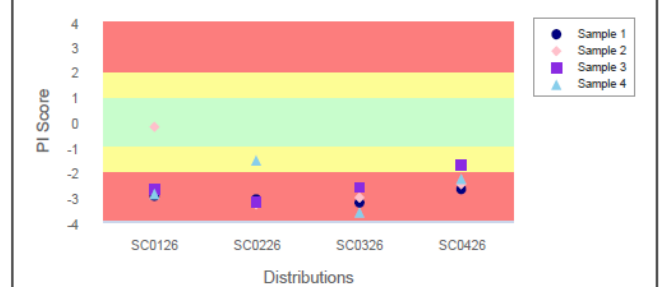
# Analyte Standard Report

| Glucose mmol/L |                               |             |                            |                                   |         |                         |
|----------------|-------------------------------|-------------|----------------------------|-----------------------------------|---------|-------------------------|
|                | Your reported result (mmol/L) |             | Method: Siemens Hexokinase | Instrument Model: Atellica CH 930 | Overall | Scoring Reference Value |
| Sample 1       | 10.8                          | Mean        | 11.30                      | 11.30                             | 11.49   | 11.45                   |
|                |                               | SD          | 0.24                       | 0.24                              | 0.22    |                         |
|                |                               | Uncertainty | 0.051                      | 0.051                             | 0.021   | 0.12                    |
|                |                               | n           | 22                         | 22                                | 113     |                         |
| Sample 2       | 13.9                          | Mean        | 14.43                      | 14.43                             | 14.66   | 14.67                   |
|                |                               | SD          | 0.27                       | 0.27                              | 0.28    |                         |
|                |                               | Uncertainty | 0.057                      | 0.057                             | 0.027   | 0.15                    |
|                |                               | n           | 22                         | 22                                | 113     |                         |
| Sample 3       | 4.8                           | Mean        | 5.01                       | 5.01                              | 5.06    | 5.02                    |
|                |                               | SD          | 0.12                       | 0.12                              | 0.12    |                         |
|                |                               | Uncertainty | 0.025                      | 0.025                             | 0.011   | 0.05                    |
|                |                               | n           | 22                         | 22                                | 113     |                         |
| Sample 4       | 23.1                          | Mean        | 23.98                      | 23.98                             | 24.29   | 24.34                   |
|                |                               | SD          | 0.48                       | 0.48                              | 0.50    |                         |
|                |                               | Uncertainty | 0.102                      | 0.102                             | 0.047   | 0.25                    |
|                |                               | n           | 22                         | 22                                | 114     |                         |

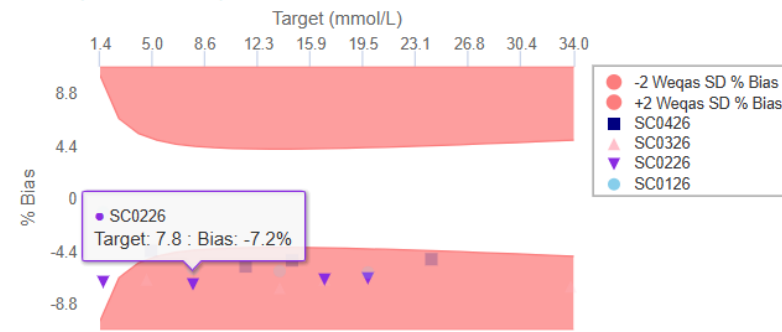
## Scoring

| Sample                    | 1     | 2     | 3     | 4     | Overall Performance |
|---------------------------|-------|-------|-------|-------|---------------------|
| Target: (Reference Value) | 11.45 | 14.67 | 5.02  | 24.34 |                     |
| Weqas TAE                 | 0.47  | 0.6   | 0.25  | 1.07  |                     |
| PI                        | -2.75 | -2.55 | -1.77 | -2.32 | Poor                |

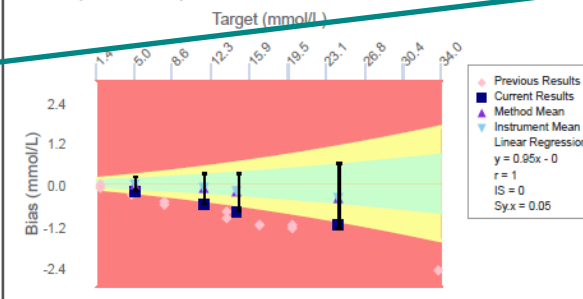
## Running PI



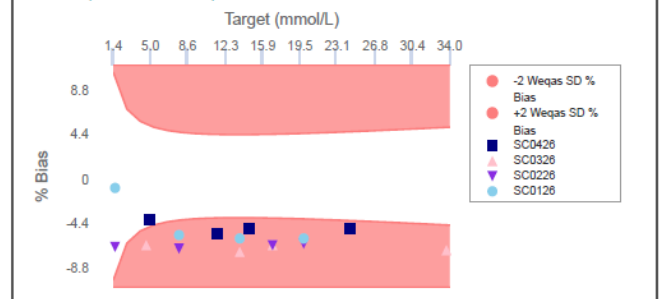
## Bias (Relative %)



## Bias (Absolute)



## Bias (Relative %)



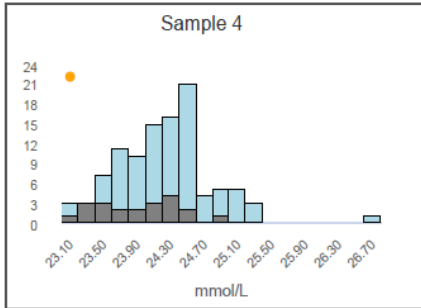
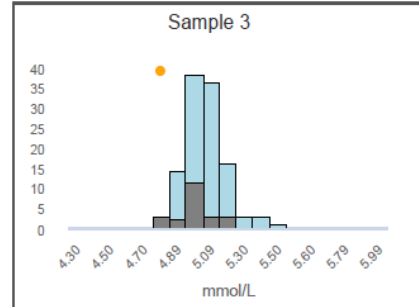
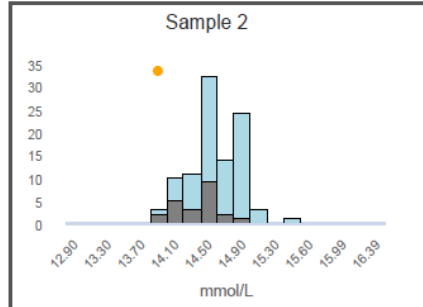
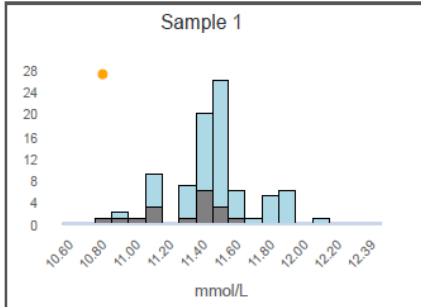
## Precision

|      | SC0126 | SC0226 | SC0326 | This distribution:<br>SC0426 |
|------|--------|--------|--------|------------------------------|
| Sy.x | 0.02   | 0.02   | 0.06   | 0.05                         |
| IS   | 0      | 0      | 0      | 0                            |

Sy.x is the average deviation from the best fit line and is an index of scatter.

| IS Score  | Interpretation                        |
|-----------|---------------------------------------|
| 0 to 10   | Good                                  |
| 11 to 150 | Acceptable to Warning level           |
| > 150     | Unacceptable (incl. Curvilinear Data) |

# Analyte Standard Report



■ All Results
 ■ My Method
 ■ My Instrument
 ● My Result

## Method Summary

| SC0426                    | Sample 1 |     | Sample 2 |     | Sample 3 |     | Sample 4 |     |
|---------------------------|----------|-----|----------|-----|----------|-----|----------|-----|
| Method Name               | Mean     | CV% | Mean     | CV% | Mean     | CV% | Mean     | CV% |
| Abaxis Piccolo (n=9)      | 11.56    | 1.4 | 14.66    | 1.4 | 5.34     | 2.0 | 23.97    | 0.9 |
| Abbott Hexokinase (n=3)   | 11.37    | 0.5 | 14.63    | 0.4 | 4.93     | 1.2 | 25.30    | 5.1 |
| Beckman Hexokinase (n=10) | 11.39    | 2.5 | 14.42    | 1.5 | 5.01     | 2.4 | 23.81    | 1.5 |
| NMR Spectroscopy (n=6)    | 11.72    | 1.5 | 14.90    | 2.3 | 5.11     | 1.8 | 24.68    | 2.0 |
| Roche Hexokinase (n=63)   | 11.52    | 1.5 | 14.77    | 1.5 | 5.07     | 1.7 | 24.47    | 1.8 |
| Siemens Hexokinase (n=22) | 11.30    | 2.1 | 14.43    | 1.8 | 5.01     | 2.3 | 23.98    | 2.0 |

There are no Weqas or Participant supplied comments for Glucose for this distribution.

## Summary Report

Analyte: Glucose

Overall PI for glucose: Poor.

**Note:** 5 instruments are enrolled with 4 submitting glucose results. All 4 instruments are the same manufacturer. Model, kit number.

## Standard Report

**Analyte results table:** Analyte is scored against the Reference Value. Reported results are low compared to Reference Value, Method, Instrument and Overall means.

**Scoring Table:** 3 samples with PI scores  $>2$  (negative PIs). Sample 3 PI -1.77. Overall performance category is poor.

**Running PI scores:** graph shows pattern of negative PI scores around 2 and 3 for a few months. SC0126 is the only distribution where there is a good PI score (for one sample only).

**Bias Chart (Absolute):** IS = O,  $r = 1$ . Imprecision scores are very good. Accuracy: Linear regression shows -5% systematic negative proportional bias ( $y = 0.95x - 0$ ), This concentration dependent proportional bias is mirrored for previous distributions.

**Bias Chart (Relative):** Fairly consistent relative bias of around -5% (range -4.4% to -7.2%).

**Precision Scores table:** Excellent precision scores for all distributions displayed on this report.

**Sample Histograms:** Lab results at the extreme lower end of the instrument (and all results) bars.

**Method Summary Data:** N=22. Method CV% approx 2%.

**Error Identification:** Negative systematic proportional error.

**Note:** Persistent poor performance notice issued to the participant recently.

**Open floor for discussion of potential troubleshooting and causes of this error.**

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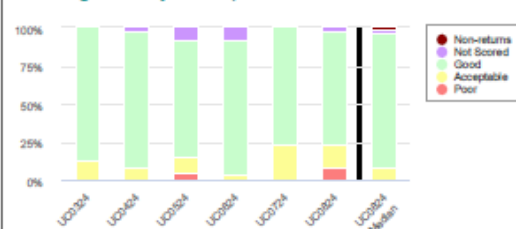


EDUCATION &  
TRAINING

## Case 3 – Urine Chemistry - Sodium

| This Distribution                    |     |
|--------------------------------------|-----|
| Your % Poor PI                       | 5%  |
| Median All Participant % Poor PI     | 0%  |
| 97.5 <sup>th</sup> Centile % Poor PI | 38% |

Running PI analyte-sample Scores



| PI Ranges |            |
|-----------|------------|
| <1        | Good       |
| 1-2       | Acceptable |
| >2        | Poor       |

## Summary Report

| PI Scores            |            |
|----------------------|------------|
| Location             | Main Lab   |
| Instrument Name      | c501       |
| Instrument Serial #  | AA16       |
| Sodium               | Poor       |
| Potassium            | Acceptable |
| Chloride             | Acceptable |
| Urea                 | Good       |
| Creatinine           | Acceptable |
| Glucose              | Warning    |
| Calcium              | Good       |
| Phosphate            | Good       |
| Protein              | Warning    |
| Albumin              | Acceptable |
| Magnesium            | Good       |
| Urate                | Good       |
| Amylase              | Acceptable |
| Overall % poor PI    | 5%         |
| Overall % Non-return | 0%         |

| PI Code | Meaning                                                    |
|---------|------------------------------------------------------------|
| N/A     | Not enrolled for this analyte                              |
| NRR     | Analyte enrolled but no results returned                   |
| N/S     | This quantitative analyte not scored for this distribution |

\*\*\*\*\* Please note\*\*\*\*\*

The NQAAP expects 100% compliance on EQA returns. If you are enrolled for an analyte and have not returned a result (denoted by NRR in your PI table), this will be treated as a poor performance score. Please let us know as soon as possible if you are no longer providing this analyte as part of your diagnostic service.

Distribution Specific Comment

There is no specific comment for this distribution.

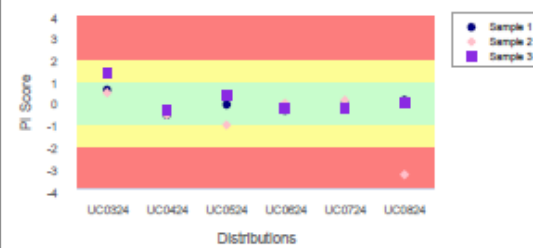
# Analyte Standard Report

| Sodium mmol/L |                               |             |                         |                                  |         |
|---------------|-------------------------------|-------------|-------------------------|----------------------------------|---------|
|               | Your reported result (mmol/L) |             | Method:<br>Indirect ISE | Instrument Model:<br>cobas c 501 | Overall |
| Sample 1      | 115                           | Mean        | 114.53                  | 114.11                           | 114.53  |
|               |                               | SD          | 1.55                    | 0.49                             | 1.55    |
|               |                               | Uncertainty | 0.271                   | 0.230                            | 0.271   |
|               |                               | n           | 51                      | 7                                | 51      |
| Sample 2      | 143                           | Mean        | 157.41                  | 156.63                           | 157.41  |
|               |                               | SD          | 2.05                    | 1.11                             | 2.05    |
|               |                               | Uncertainty | 0.363                   | 0.569                            | 0.363   |
|               |                               | n           | 50                      | 6                                | 50      |
| Sample 3      | 53                            | Mean        | 53.03                   | 53.06                            | 53.03   |
|               |                               | SD          | 0.96                    | 1.02                             | 0.96    |
|               |                               | Uncertainty | 0.170                   | 0.482                            | 0.170   |
|               |                               | n           | 50                      | 7                                | 50      |

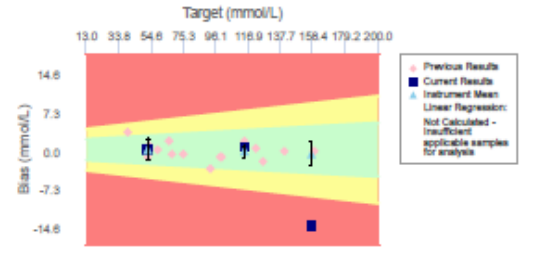
## Scoring

| Sample                | 1      | 2      | 3     | Overall Performance |
|-----------------------|--------|--------|-------|---------------------|
| Target: (Method Mean) | 114.53 | 157.41 | 53.03 |                     |
| Weqas TAE             | 7.26   | 8.69   | 5.22  |                     |
| PI                    | 0.13   | -3.32  | -0.01 | Poor                |

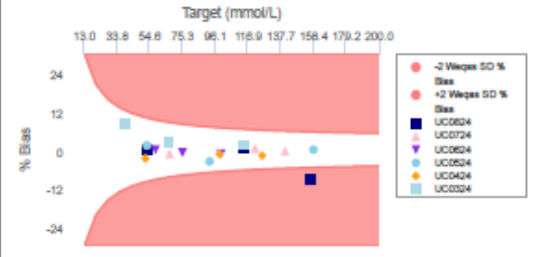
## Running PI



## Bias (Absolute)



## Bias (Relative %)

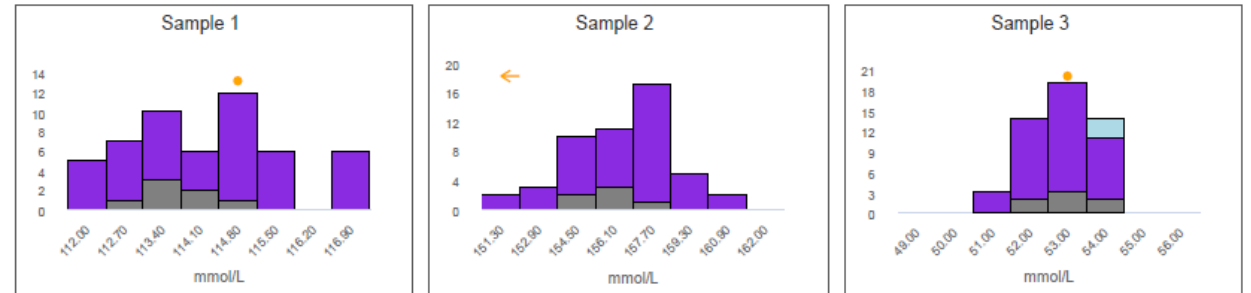


## Precision

|      | UC0324 | UC0424 | UC0524 | UC0624 | UC0724 | This distribution:<br>UC0824 |
|------|--------|--------|--------|--------|--------|------------------------------|
| Sy.x | 0.87   | 0.46   | 3.09   | 0.23   | 0.64   | 7.29                         |
| IS   | 1      | 0      | 8      | 0      | 1      | 63                           |

Sy.x is the average deviation from the best fit line and is an index of scatter.

| IS Score  | Interpretation                        |
|-----------|---------------------------------------|
| 0 to 10   | Good                                  |
| 11 to 150 | Acceptable to Warning level           |
| > 150     | Unacceptable (Incl. Curvilinear Data) |



## Method Summary

| UC0824              | Sample 1 |     | Sample 2 |     | Sample 3 |     |
|---------------------|----------|-----|----------|-----|----------|-----|
| Method Name         | Mean     | CV% | Mean     | CV% | Mean     | CV% |
| Indirect ISE (n=51) | 114.53   | 1.4 | 157.41   | 1.3 | 53.03    | 1.8 |

There are no Weqas or Participant supplied comments for Sodium for this distribution.

### Summary Report

**Overall Performance Category:** poor for Urine Sodium

**Running PI analyte:** Generally good performance scores over the 6 months. This month 5% poor PI.

**PI scores table:** shows high % of acceptable and warning scores across all analytes. Only 5 analytes show good overall performance scores.

### Standard Report

**Analyte results table:** Shows significantly lower results for sample 2 compared to the method, instrument and overall means.

**Scoring Table:** Samples 1 and 3 have good PI scores. Sample 3 is poor, PI = -3.32.

**Running PI scores:** Predominantly good from 0424, with only the one sample from this distribution in the red category.

**Bias Chart (Absolute):** Anomaly for this distribution's sample at a concentration of around 158 mmol/L. Narrow SD bars for the method. Linear regression – not calculated therefore suggests that error is one of imprecision. All previous results acceptable.

**Bias Chart (Relative):** All previous results acceptable bias (in the white area).

**Precision Scores:** Previous imprecision score excellent. IS of 63 is suggestive of imprecision attributed to sample 2.

**Sample Histograms:** Sample 2 result off the scale compared to all results, your method and your instrument.

**Method Summary Data:** all participants in same method group. If you click on the 'method' name in the analyte results table this would bring you up the instrument breakdown for the programme.

**Error Identification:** Imprecision for sample 2, check other results for sample 2. Potential sample issue as sample 2 shows a negative bias for several other analytes (out of consensus with samples 1 and 2 scores).

### **Troubleshooting performed by the lab:**

Repeat sample 2 requested and re-assayed for analytes with acceptable/poor performance. Samples assayed by a different technician. Performance calculated by the lab and found to show vastly improved scores (PI scores between -0.03 and 1.74 (most <0.6)).

Following discussion with the staff member, it transpired that this is likely a pre-analytical error. Potentially insufficient mixing of the sample prior to analysis. Root cause and troubleshooting discussed with the staff member as a re-training exercise.

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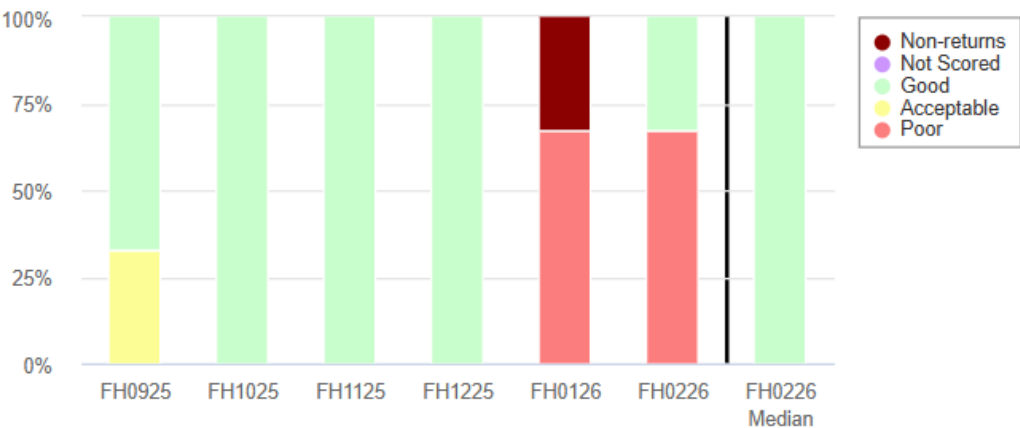
## Case 4 – Quantitative FHb

# Summary Report

Programme: **Quantitative Faecal Hb** • Distribution Code: **FH0226**  
Distribution Start: 25-Feb-2026 • Distribution End: 11-Mar-2026 • Report Issued: 20-Mar-2026 • Report Status: Final  
Requested By: sam@weqas.com

| This Distribution                    |      |
|--------------------------------------|------|
| Your % Poor PI                       | 67%  |
| Median All Participant % Poor PI     | 0%   |
| 97.5 <sup>th</sup> Centile % Poor PI | 53 % |

Running PI analyte-sample Scores



| PI Ranges |            |
|-----------|------------|
| <1        | Good       |
| 1-2       | Acceptable |
| >2        | Poor       |

| PI Scores            |      |
|----------------------|------|
| Location             |      |
| Instrument Name      |      |
| Instrument Serial #  |      |
| Quantitative FHb     | Poor |
| Overall % poor PI    | 67%  |
| Overall % Non-return | 0%   |

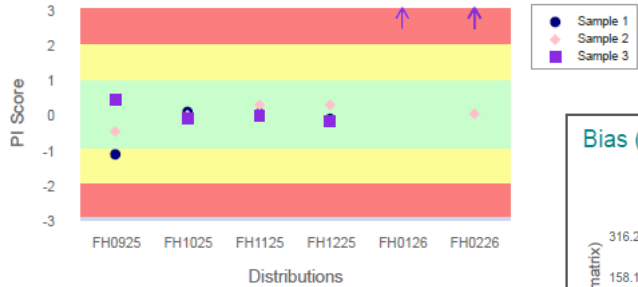
# Analyte Standard Report

| Quantitative FHb µg Hb/g matrix |                                       |             |                      |                                       |         |
|---------------------------------|---------------------------------------|-------------|----------------------|---------------------------------------|---------|
|                                 | Your reported result (µg Hb/g matrix) |             | Method:<br>OC Sensor | Instrument Model:<br>OC Sensor Pledia | Overall |
| Sample 1                        | 305.7                                 | Mean        | 60.42                | 60.74                                 | 64.52   |
|                                 |                                       | SD          | 3.32                 | 3.30                                  | 7.60    |
|                                 |                                       | Uncertainty | 0.523                | 0.561                                 | 0.927   |
|                                 |                                       | n           | 63                   | 54                                    | 105     |
| Sample 2                        | >200.0                                | Mean        | 212.46               | 206.83                                | 247.66  |
|                                 |                                       | SD          | 24.15                | 18.20                                 | 40.14   |
|                                 |                                       | Uncertainty | 6.294                | 5.364                                 | 6.223   |
|                                 |                                       | n           | 23                   | 18                                    | 65      |
| Sample 3                        | 88.3                                  | Mean        | 16.04                | 16.15                                 | 19.08   |
|                                 |                                       | SD          | 1.54                 | 1.36                                  | 5.34    |
|                                 |                                       | Uncertainty | 0.243                | 0.231                                 | 0.655   |
|                                 |                                       | n           | 63                   | 54                                    | 104     |

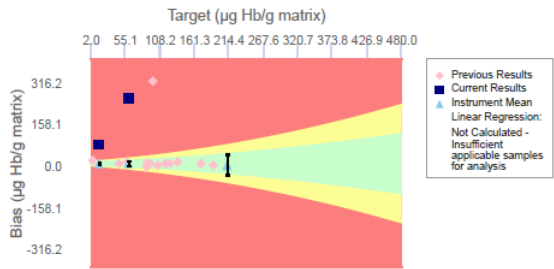
## Scoring

| Sample                | 1     | 2      | 3     | Overall Performance |
|-----------------------|-------|--------|-------|---------------------|
| Target: (Method Mean) | 60.42 | 212.46 | 16.04 |                     |
| Weqas TAE             | 16.93 | 67.69  | 6.98  |                     |
| PI                    | 28.97 | 0      | 20.71 | Poor                |

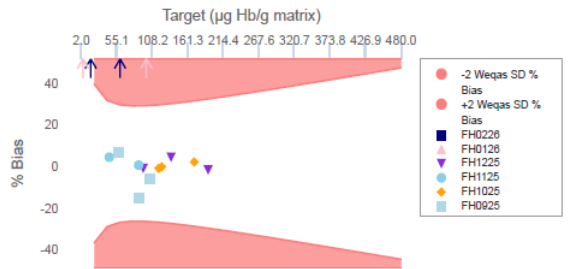
## Running PI



## Bias (Absolute)



## Bias (Relative %)

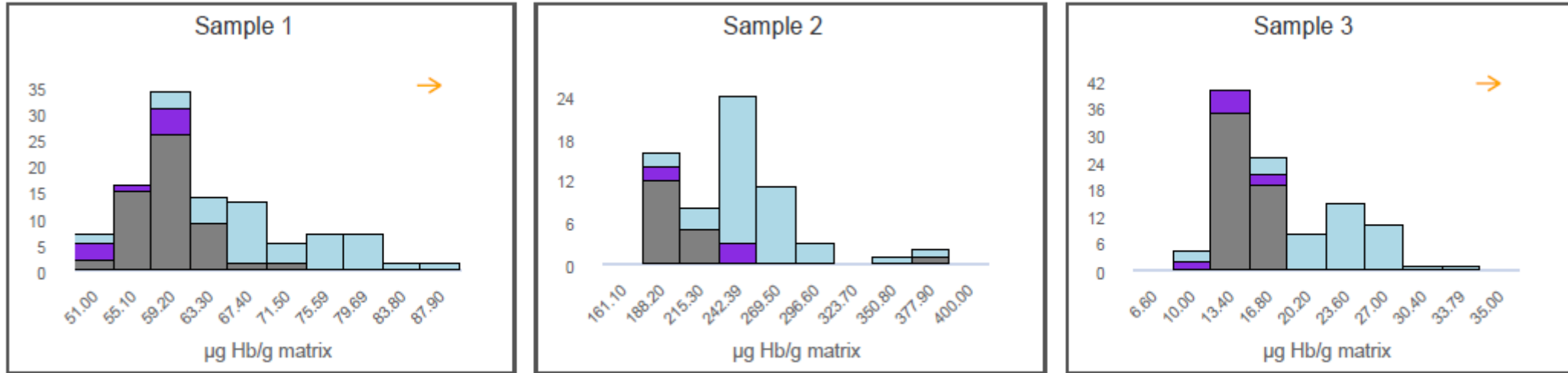


## Precision

|      | FH0925 | FH1025 | FH1125 | FH1225 | FH0126 | This distribution:<br>FH0226 |
|------|--------|--------|--------|--------|--------|------------------------------|
| Sy.x | 8.35   | 0.6    |        | 6.61   |        |                              |
| IS   | 560    | 1      |        | 50     |        |                              |

Sy.x is the average deviation from the best fit line and is an index of scatter.

| IS Score  | Interpretation                        |
|-----------|---------------------------------------|
| 0 to 10   | Good                                  |
| 11 to 150 | Acceptable to Warning level           |
| > 150     | Unacceptable (incl. Curvilinear Data) |



■ All Results
 ■ My Method
 ■ My Instrument
 ● My Result

## Method Summary

| FH0226            | Sample 1 |      | Sample 2 |      | Sample 3 |      |
|-------------------|----------|------|----------|------|----------|------|
| Method Name       | Mean     | CV%  | Mean     | CV%  | Mean     | CV%  |
| FOB Gold (n=3)    | 38.10    | 8.1  | 147.91   | 1.8  | 7.31     | 15.1 |
| HM-JACKarc (n=38) | 73.33    | 11.0 | 266.84   | 9.0  | 25.00    | 13.1 |
| NS-Prime (n=1)    | 51.00    | 0.0  | 206.00   | 0.0  | 17.00    | 0.0  |
| OC Sensor (n=63)  | 60.42    | 5.5  | 212.46   | 11.4 | 16.04    | 9.6  |

There are no Weqas or Participant supplied comments for Quantitative Fhb for this distribution.

## Summary Report

**Overall Performance Category:** poor for Quant FHb

### **Running PI analyte:**

Generally good performance scores up until FH0126. FH0126 – 67% poor PI, 33% non returns. This month 67% poor PI.

**PI scores table:** Only 1 analyte on this programme, overall category poor.

## Standard Report

**Analyte results table:** Reported result 5 x higher compared to the method and instrument.

**Scoring Table:** Samples 1 and 3 have very high PI scores (28.97 and 20.71 respectively). Sample 2 has a good PI score (due to reporting >200).

**Running PI scores:** Predominantly good from FH0925 to FH1225, very poor from at FH0126.

**Bias Chart (Absolute):** Chart shows generally good performance, then a significant shift for FH0126 and FH0226. Narrow SD bars for the method. Linear regression – not calculated as only 2 quant results returned. Both results within the red area, significant positive bias for samples 1 and 3.

**Bias Chart (Relative):** All previous results except FH0126 and FH0226 acceptable bias (in the white area). Off the chart relative bias for FH 0126 and FH 0226

**Precision Scores:** Precision scores not calculated for FH1125, FH0126 and FH0226. Imprecision score excellent at FH1025, acceptable/warning at FH1225.

**Sample Histograms:** Sample 1 and 3 results off the scale compared to all results, your method and your instrument. Sample 2, result not plotted as > result returned.

**Method Summary Data:** N = 63. Low method CV% for samples 1 and 3 compared with other methods.

**Error Identification:** The two results reported in this distribution along with the poor results for FH 0126 suggest a catastrophic error of +500% positive systematic proportional error. It is highly unlikely that this was associated with transcription or transposition as it occurred on 2 successive occasions.

**Root cause of the error:** results were not reported in the correct units. Conversion to µg/g not carried out.

# FH0126

| Quantitative FHb µg Hb/g matrix |                                       |             |                      |                                       |         |
|---------------------------------|---------------------------------------|-------------|----------------------|---------------------------------------|---------|
|                                 | Your reported result (µg Hb/g matrix) |             | Method:<br>OC Sensor | Instrument Model:<br>OC Sensor Pledia | Overall |
| Sample 1                        | NRR                                   | Mean        | 165.40               | 166.64                                | 180.21  |
|                                 |                                       | SD          | 14.70                | 13.88                                 | 29.87   |
|                                 |                                       | Uncertainty | 2.297                | 2.340                                 | 3.662   |
|                                 |                                       | n           | 64                   | 55                                    | 104     |
| Sample 2                        | 410.5                                 | Mean        | 99.01                | 99.85                                 | 102.82  |
|                                 |                                       | SD          | 7.88                 | 7.63                                  | 10.34   |
|                                 |                                       | Uncertainty | 1.213                | 1.287                                 | 1.255   |
|                                 |                                       | n           | 66                   | 55                                    | 106     |
| Sample 3                        | 15.0                                  | Mean        | 4.67                 | 4.69                                  | 6.93    |
|                                 |                                       | SD          | 1.22                 | 1.00                                  | 3.13    |
|                                 |                                       | Uncertainty | 0.250                | 0.227                                 | 0.458   |
|                                 |                                       | n           | 37                   | 30                                    | 73      |