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# New Reports & Interpretation

Annette Thomas

# The Reports – what's different?

- Weqas SDs have been replaced by TAE (Total Allowable Error).
- This provides a better description of the Analytical performance specification as these are not based on the SD of the distribution, (Clinically relevant criteria/ biological variation/ state of the art).

- Performance specification limits = target value ± TAE
- SDI has been replaced by PI (Performance Index)
- $PI = \frac{(\text{your result} - \text{target value})}{(TAE/2)}$

# Poor performance monitoring

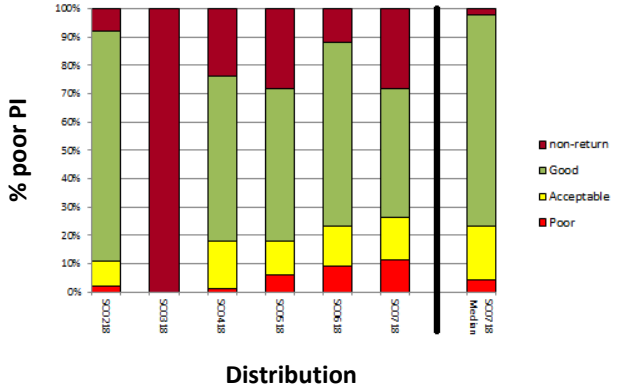
## Interpretation of PI and % poor PI

PI < 1 Good

PI 1-2  Acceptable

PI> 2 Unacceptable (outside TAE)

| P.I. ranges | |
|---|---|
| <1 | Good |
| 1 – 2 | Acceptable |
| >2 | Poor |



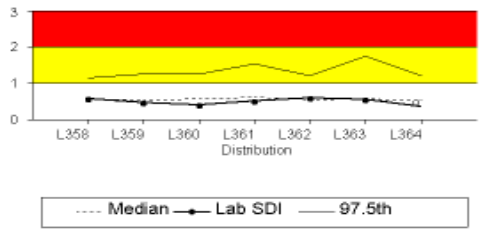

Overall Laboratory SDI has been replaced by % poor PI as the overall performance index. This represents the proportion of tests which obtained a poor score or were not returned

e.g. you measured 30 analytes on 3 samples on 2 instruments (180 tests) and had 5 PI scores > 2, therefore the overall % poor PI =  5/180 = 2.8%. Provides equal weighting for all the samples rather than averaging an SDI score.

# The Reports – Manager's Summary - Quantitative

## Old

| This Distribution | |
|---|---|
| Overall Lab SDI: | 0.36 |
| Median All Laboratory: | 0.52 |
| 97.5th centile: | 1.21 |




| All SDI Ranges | |
|---|---|
| < 1 | Good |
| 1 - 2 | Acceptable |
| > 2 | Poor |

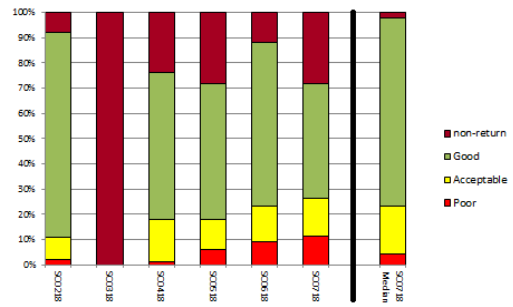
**Section SDI scores for this distribution**

| Section | Harris (700) | Tweed (800) |
|---|---|---|
| **Overall** | **0.41** | **0.31** |
| Cholesterol | 0.46 | 0.30 |
| Triglyceride | 0.42 | 0.35 |
| HDL Cholesterol | 0.22 | 0.20 |
| LDL Cholesterol | 0.55 | 0.39 |

## New

*Quantitative Analyte Data*

| This distribution | |
|---|---|
| Your % Poor P.I. | 12% |
| Median all participant % Poor P.I. | 4% |
| 97.5th Centile % poor P.I. | 14% |




| P.I. ranges | |
|---|---|
| <1 | Good |
| 1 – 2 | Acceptable |
| >2 | Poor |

| P.I. Scores | | | | | |
|---|---|---|---|---|---|
| Location | Location Name 1 | Location Name 2 | | Location Name 3 | |
| Instrument Name | 15Character Name | 15Character Name | 15Character Name | 15Character Name | 15Character Name |
| Instrument Serial # | Serial#00001 | Serial#00002 | Serial#00003 | Serial#00004 | Serial#00005 |
| analyte Name 1 | NRR | NRR | 0.78 | N/A | 5.28 |
| analyte Name 2 | NRR | NRR | 0.69 | 1.18 | 5.01 |
| analyte Name 3 | NRR | NRR | 0.58 | 1.29 | 4.95 |
| analyte Name 4 | NRR | NRR | 0.92 | 1.02 | 4.82 |
| analyte Name 5 | NRR | NRR | 0.38 | 1.38 | 5.29 |
| analyte Name 6 | NRR | NRR | 0.14 | 1.01 | 6.01 |
| analyte Name 7 | NRR | NRR | 0.68 | 0.84 | 4.92 |
| analyte Name 8 | NRR | NRR | 0.25 | 0.78 | 5.12 |
| analyte Name 9 | NRR | NRR | 0.31 | N/A | 4.98 |
| analyte Name 10 | NRR | NRR | 0.42 | N/A | 5.34 |
| **Overall % poor P.I.** | NRR | NRR | **3.3%** | **9.5%** | **66.6%** |

# The Reports – Manager's Summary - Quantitative

## Group Version:

- Group report
  - Your % poor PI should be calculated based on all the tests for all the instruments in the group
  - Include a preference option for a group level user to choose whether or not to include the % poor P.I. for each of the participants within their group on this report

Version 1: user chooses not to include individual participant breakdown

| This distribution | |
|---|---|
| Your Group % Poor P.I. | 3% |
| Median all participant % Poor P.I. | 4% |
| 97.5th Centile % poor P.I. | 14% |

Version 2: users chooses to include individual participant breakdown, small number of participants in the group

| This distribution | | |
|---|---|---|
| Your % Poor P.I. | Overall group | 3% |
| | FGA0001 | 2% |
| | FGC0001 | 5.2% |
| | FHA0001 | 3.1% |
| Median all participant % Poor P.I. | | 4% |
| 97.5th Centile % poor P.I. | | 14% |

| Participant code | Location | Instrument Serial # | Instrument Name | Analyte name 1 | Analyte name 2 | Analyte name 3 | Analyte name 4 | Analyte name 5 | Analyte name 6 | Analyte name 7 | Analyte name 8 | Analyte name 9 | Analyte name 10 | Analyte name 11 | Analyte name 12 | Analyte name 13 | Analyte name 14 | Overall % Poor P.I.. |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| XYZ0001 | A1 | AB123456789C | Link | 0.98 | ##.## | ##.## | ##.## | ##.## | ##.## | 1.02 | ##.## | ##.## | ##.## | N/A | N/A | N/A | 0.98 | 6.1% |
| | | BC123456789D | North | 1.52 | | | | | | 1.68 | | | | N/A | N/A | N/A | 0.98 | 12.1 % |
| | | | South | 0.45 | | | | | | 0.52 | ##.## | ##.## | ##.## | N/A | N/A | N/A | 0.98 | 18.1 % |
| | A2 North | CD123456789E | | 2.58 | | | | | | N/A | ##.## | ##.## | ##.## | N/A | N/A | N/A | 0.98 | 33.3 % |
| | A2 South | DE123456789F | | ? | | | | | | ? | ##.## | ##.## | ##.## | N/A | N/A | N/A | 0.98 | 81.8 % |
| XXZ0001 | A3 Link Trauma | | Bed 1 | ? | | | | | | N/A | ##.## | ##.## | ##.## | N/A | N/A | N/A | 0.98 | 33.3 % |
| | | | Bed 2 | ? | | | | | | N/A | ##.## | ##.## | ##.## | N/A | N/A | N/A | 0.98 | 33.3 % |
| | A4 North | EF123456789G | | ? | | | | | | ? | ##.## | ##.## | ##.## | N/A | N/A | N/A | ? | 100 % |
| | A4 South | FG123456789H | | 0.87 | | | | | | 1.21 | ##.## | ##.## | ##.## | N/A | N/A | N/A | 0.98 | 21.2 % |
| | A5 North (H&N/ENT) | GH123456789I | | 0.25 | 28.45 | | | | | 0.28 | ##.## | ##.## | ##.## | N/A | N/A | N/A | 2.98 | 15.1 % |
| ZZZ0001 | Outpatients department | | Clinic 1 | ##.## | ##.## | ##.## | ##.## | ##.## | ##.## | ##.## | ##.## | ##.## | ##.## | ##.## | ##.## | ##.## | ##.## | 18.2 % |

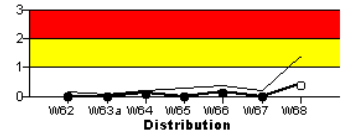
# Manager's Summary - Qualitative

Weqas
Unit 6, Parc Ty Glas
Llanishen, Cardiff
CF14 5DU
office@weqas.com
Scheme Organiser: Annette Thomas

## Old

Lab: AE . Scheme: Urine Pregnancy Testing. Distribution Code: W68.
Final. Report Issued: 5/10/11

| This Distribution | |
|---|---|
| Overall Lab SDI: | 0.40 |
| Median All Laboratory: | 0.00 |
| 97.5th centile: | 1.33 |




| All SDI Ranges | |
|---|---|
| < 1 | Good |
| 1 - 2 | Acceptable |
| > 2 | Poor |

office@weqas.com
Scheme Organiser:
Annette Thomas

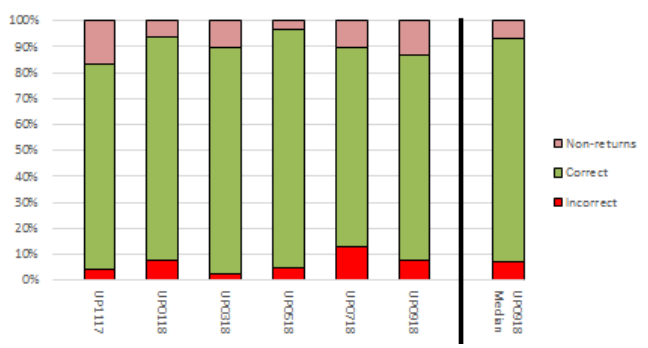
Section SDI scores for this distribution

| Section | 2TB2 | Clinical Research Facility | Dermatology | EAU - Lisa Waters | EAU - Medical A1 Link | EAU - Surgery | Emergency Gynae | FP Broad Street | FP Butetown |
|---|---|---|---|---|---|---|---|---|---|
| Overall | 1.00 | 0.00 | 0.00 | | | | 0.00 | 0.00 | |
| Qualitative HCG (High Sensitivity) | 1.00 (avg) | 0.00 (avg) | 0.00 (avg) | ? | ? | ? | 0.00 (avg) | 0.00 (avg) | ? |
| **Section** | **FP Cardiff Royal** | **FP Gabalfa** | **FP Grangetown** | **FP Heath, C/O ANC** | **FP Llanrumney** | **FP Llantwit** | **FP Park View** | **FP Penarth** | **FP Roath** |
| Overall | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | | 0.00 | 0.00 |
| Qualitative HCG (High Sensitivity) | 0.00 (avg) | 1.00 (avg) | 0.00 (avg) | 0.00 (avg) | 0.00 (avg) | 0.00 (avg) | ? | 0.00 (avg) | 0.00 (avg) |

## New

*Qualitative analyte data*

| This distribution | |
|---|---|
| Your % Incorrect | 12% |
| Median all participant % Incorrect | 4% |
| 97.5th Centile % incorrect | 14% |




How do we calculate the % poor PI?

**% poor PI = % incorrect results**

% of how many samples you misclassified as a total % of all samples assayed.

| Correct Qualitative response | |
|---|---|
| Incorrect Qualitative response | |
| Qualitative Performance not assessed | |
| N/A | Not enrolled for this analyte |
| NRR | Analyte enrolled but no results returned |
| N/S | This quantitative analyte not scored for this distribution |
| NNR | Non-numerical results submitted: P.I. not available |

| | | | | Analyte Name 1 | | | Analyte Name 2 | | | Analyte Name 3 | | | Analyte Name 4 | | | Analyte Name 5 | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Participant** | **Location** | **Instrument Name** | **Serial number** | **Sample 1** | **Sample 2** | **Sample 3** | **Sample 1** | **Sample 2** | **Sample 3** | **Sample 1** | **Sample 2** | **Sample 3** | **Sample 1** | **Sample 2** | **Sample 3** | **Sample 1** | **Sample 2** | **Sample 3** |
| AAA001 | Location Name 1 | | SN0000001 | Neg | Pos | Pos | Pos | Neg | Pos | Pos | Neg | Pos | Neg | Pos | Pos | Pos | Pos | Neg |
| AAA001 | Location Name 2 | Bay 2A | SN0000002 | Neg | Pos | Neg | Neg | Pos | Pos | Neg | Neg | Pos | Neg | Pos | Neg | Neg | Pos | Neg |
| AAA001 | Location Name 2 | Bay 2B | SN0000003 | NRR | NRR | NRR | NRR | NRR | NRR | NRR | NRR | NRR | NRR | NRR | NRR | NRR | NRR | NRR |
| AAA001 | Location Name 3 | | SN0000004 | Neg | Pos | Neg | Equ | Equ | Neg | N/A | N/A | N/A | Neg | Pos | Neg | Neg | Pos | Pos |
| AAA001 | Location Name 3 | | SN0000005 | Neg | Pos | Neg | Pos | Neg | Pos | Neg | Pos | Pos | Neg | Pos | Neg | Pos | Pos | Bor |

# The Reports – Analyte Report - Quantitative

## Old

**Scheme: Lipid. Distribution Code: L364.**
**Distribution Date: 26/03/18. Final. Report Issued: 20/04/18**

| Cholesterol (mmol/l) | | 1 | 2 | 3 | 4 | Analyte SDI |
|---|---|---|---|---|---|---|
| Reported Result | | 6.80 | 2.50 | 4.60 | 4.80 | |
| Method Corrected Result | | 6.800 | 2.500 | 4.600 | 4.800 | |
| Cholesterol oxidase | Mean | 7.092 | 2.617 | 4.876 | 4.963 | |
| | SD | 0.225 | 0.093 | 0.183 | 0.169 | |
| | Number | 174 | 174 | 174 | 174 | |
| | Uncert. | 0.0214 | 0.0088 | 0.0174 | 0.0161 | |
| Cobas C Module | Mean | 7.006 | 2.587 | 4.811 | 4.901 | |
| | SD | 0.123 | 0.075 | 0.112 | 0.106 | |
| | Number | 98 | 98 | 98 | 98 | |
| | Uncert. | 0.0155 | 0.0094 | 0.0142 | 0.0134 | |
| Overall | Mean | 7.081 | 2.615 | 4.868 | 4.953 | |
| | SD | 0.233 | 0.090 | 0.189 | 0.174 | |
| | Number | 179 | 181 | 179 | 181 | |
| | Uncert. | 0.0218 | 0.0084 | 0.0176 | 0.0161 | |
| Reference Values CDC | | 7.038 | 2.606 | 4.867 | 4.963 | |
| Ref. Value Uncertainty | | 0.0140 | 0.0000 | 0.0000 | 0.0000 | |
| Non-scoring Reference Values ID-GCMS | | 7.110 | 2.590 | 4.850 | 4.970 | |
| WeQas SD | | 0.301 | 0.111 | 0.207 | 0.210 | |
| SDI | | -0.79 | -0.95 | -1.29 | -0.77 | 0.95 |

| Sigma Metrics | | | |
|---|---|---|---|
| Critical Level 1: 5.0 mmol/l | | | |
| Minimum Acceptable score | 1.67 | Critical Level 1 Sigma score | 3.8 |
| MAPS Allowable TE | 8.5% | | |
| MAPS Allowable bias % | 4.0% | Lab \|bias\| % | 3.9% |
| MAPS Allowable CV % | 2.7% | Lab CV % | 1.2% |

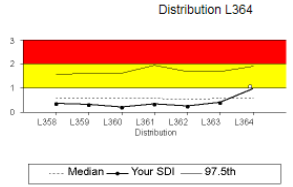
Please note: Linear regression uses CF corrected data.

**Total Error**

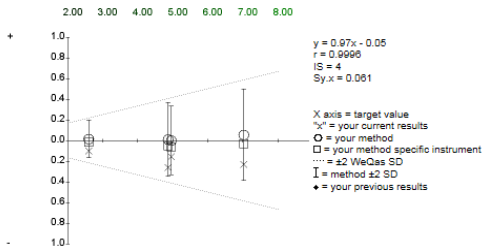
SDI is a measurement of your total error and will include both inaccuracy and imprecision.

| This Distribution L364 |
|---|
| Your average analyte SDI for the 4 samples is 0.95 |

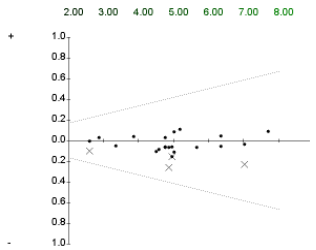
**Previous SDI**




**This Distribution *L364***




**Previous Distributions**



**Precision**

| This Distribution L364 | Previous Distributions | L363 | L362 | L361 | L360 | L359 | L358 |
|---|---|---|---|---|---|---|---|
| Sy.x = 0.061 mmol/l | Sy.x | 0.046 | 0.092 | 0.098 | 0.058 | 0.074 | 0.034 |
| IS = 4 | IS | 6 | 9 | 11 | 6 | 11 | 3 |

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

**Precision Key**

| IS score | Interpretation |
|---|---|
| 0 to 10 | Good |
| 11 to 150 | Acceptable to Warning level |
| > 150 | Unacceptable (including Curvilinear Data) |

**Accuracy**

| This Distribution L364 | Previous Distributions | L363 | L362 | L361 | L360 | L359 | L358 |
|---|---|---|---|---|---|---|---|
| Systematic proportional error (calibration) -2.96% | Proportional (%) | -4.76 | -0.40 | 2.58 | 0.31 | 3.60 | -0.28 |
| Systematic constant error (blank) - 0.049 mmol/l | Constant (mmol/l) | 0.121 | 0.020 | - 0.153 | - 0.005 | - 0.175 | - 0.061 |

Bias includes components of proportional and constant errors. A proportional bias suggests an error of calibration whilst a constant bias suggests a blank error. Mixed errors will include significant components of both.

## New

**Participant Code: BY00001 · Location: <###20 Characters##> Analyser Name: <15 Characters> · Serial #: AB00045237A**
**Scheme: Bilirubin. Distribution Code: B0917. Analyte: Total Bilirubin**
**Distribution start: 04-Sep-17 Distribution End: 18-Sep-2017 Report Issued: 22-Sep-2017 Report Status: final**

Total Bilirubin (µmol/L)

| | Your reported result (µmol/dL) | Your result in standard units (µmol/L) | Your Method Corrected result | | Method: Vanadate Oxidation | Instrument Model: Advia Chemistry | Overall | Scoring Reference Value | Non-Scoring Reference Value |
|---|---|---|---|---|---|---|---|---|---|
| Sample 1 | 14.5 | 145 | | Mean | 145.65 | 145.65 | 141.27 | #.## | |
| | | | | sd | 5.36 | 5.36 | 10.59 | | |
| | | | | uncertainty | 1.537 | 1.537 | 0.738 | #.### | |
| | | | | n | 19 | 19 | 322 | | |
| Sample 2 | 0.4 | 4 | | Mean | 4.03 | 4.03 | 4.35 | #.## | |
| | | | | sd | 0.08 | 0.08 | 1.46 | | |
| | | | | uncertainty | 0.024 | 0.024 | 0.108 | #.### | |
| | | | | n | 19 | 19 | 284 | | |
| Sample 3 | 19.8 | 198 | | Mean | 198.02 | 198.02 | 190.67 | #.## | |
| | | | | sd | 6.53 | 6.53 | 13.50 | | |
| | | | | uncertainty | 1.873 | 1.873 | 0.939 | #.### | |
| | | | | n | 19 | 19 | 323 | | |
| Sample 4 | 35.4 | 354 | | Mean | 357.83 | 357.83 | 339.69 | #.## | |
| | | | | sd | 13.57 | 13.57 | 24.08 | | |
| | | | | uncertainty | 3.891 | 3.891 | 1.685 | #.### | |
| | | | | n | 19 | 19 | 319 | | |

**Running P.I.**

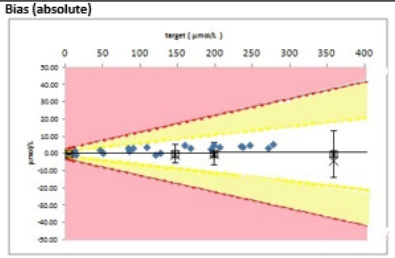
**scoring for B0917:**

| Sample | 1 | 2 | 3 | 4 | average |
|---|---|---|---|---|---|
| scored against: method mean | 145.65 | 4.03 | 198.02 | 357.83 | |
| TAE Weqas | 16.70 | 3.52 | 21.48 | 35.84 | |
| P.I. | -0.08 | -0.02 | 0 | -0.21 | 0.08 |
| Critical level 150.00 µmol/L – Sigma Score | | | | | 3.75 |

**Method Summary Table**

| B0917 | sample 1 | | sample 2 | | sample 3 | | sample 4 | |
|---|---|---|---|---|---|---|---|---|
| Method Name | mean | cv% | mean | cv% | mean | cv% | mean | cv% |
| Abaxis Piccolo (n=5) | 131.2 | 3.4 | 6.4 | 9.7 | 177.0 | 2.4 | 312.2 | 2.0 |
| Beckman LX/CX/DX (n=5) | 140.8 | 2.5 | 4.0 | 51.9 | 188.7 | 2.7 | 341.5 | 1.4 |
| Diazo (n=62) | 141.3 | 4.4 | 4.8 | 13.6 | 190.0 | 4.1 | 334.2 | 3.8 |
| IL Gas Analysers (n=44) | 155.4 | 4.9 | 5.9 | 19.3 | 208.8 | 4.7 | 371.4 | 4.2 |
| Radiometer Gas Analysers (n=44) | 149.7 | 5.5 | 5.7 | 26.4 | 202.1 | 4.6 | 359.6 | 3.7 |
| Randox 500 (n=6) | 149.0 | 2.4 | 3.3 | 85.2 | 194.3 | 2.7 | 362.5 | 5.7 |
| Roche Diazo (n=127) | 133.3 | 3.1 | 3.1 | 9.5 | 180.3 | 2.5 | 322.0 | 2.6 |
| Siemens Gas Analysers (n=4) | 148.3 | 2.3 | 3.3 | 87.2 | 199.3 | 3.1 | 374.0 | 3.6 |
| Vanadate Oxidation (n=19) | 145.7 | 3.7 | 4.0 | 2.1 | 198.0 | 3.3 | 357.8 | 3.8 |
| Vitros (T Bil) (n=3) | 164.7 | 0.4 | 5.3 | 12.3 | 217.0 | 1.4 | 366.0 | 1.9 |

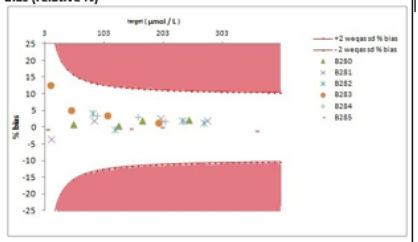
**Bias (absolute)**




Linear regression
y = 1.04 – 1.26
r = 1.0000
IS = 0
$S_{y.x}$ = 1.09

bias key
x axis = target value
'x' = your current results
◊ = your previous results
* = your method mean
□ = your instrument model mean

**Bias (relative %)**




**Precision**

| | B0417 | B0517 | B0617 | B0717 | B0817 | This distribution: B0917 |
|---|---|---|---|---|---|---|
| $S_{y.x}$ | 1.68 | 1.98 | 2.97 | 1.87 | 2.19 | 1.09 |
| IS | 1 | 1 | 4 | 2 | 4 | 0 |

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

# The Reports – what's different?

| Total Bilirubin (µmol/L) | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | Your reported result (µmol/dL) | Your result in standard units (µmol/L) | Your Method Corrected result | | Method: Vanadate Oxidation | Instrument Model: Advia Chemistry | Overall | Scoring Reference Value | Non-Scoring Reference Value |
| Sample 1 | 14.5 | 145 | | Mean | 145.65 | 145.65 | 141.27 | #.## | |
| | | | | sd | 5.36 | 5.36 | 10.59 | | |
| | | | | U | 1.537 | 1.537 | 0.738 | #.### | |
| | | | | n | 19 | 19 | 322 | | |
| Sample 2 | 0.4 | 4 | | Mean | 4.03 | 4.03 | 4.35 | #.## | |
| | | | | sd | 0.08 | 0.08 | 1.46 | | |
| | | | | U | 0.024 | 0.024 | 0.108 | #.### | |
| | | | | n | 19 | 19 | 284 | | |
| Sample 3 | 19.8 | 198 | | Mean | 198.02 | 198.02 | 190.67 | #.## | |
| | | | | sd | 6.53 | 6.53 | 13.50 | | |
| | | | | U | 1.873 | 1.873 | 0.939 | #.### | |
| | | | | n | 19 | 19 | 323 | | |
| Sample 4 | 35.4 | 354 | | Mean | 357.83 | 357.83 | 339.69 | #.## | |
| | | | | sd | 13.57 | 13.57 | 24.08 | | |
| | | | | U | 3.891 | 3.891 | 1.685 | #.### | |
| | | | | n | 19 | 19 | 319 | | |

Results displayed in your units, can directly compare results across the columns for lab, method, instrument, overall and reference method.

## Method Summary Table – top 10 methods displayed

| B0917 | sample 1 | | sample 2 | | sample 3 | | sample 4 | |
|---|---|---|---|---|---|---|---|---|
| **Method Name** | **mean** | **cv%** | **mean** | **cv%** | **mean** | **cv%** | **mean** | **cv%** |
| Abaxis Piccolo (n=5) | 131.2 | 3.4 | 6.4 | 9.7 | 177.0 | 2.4 | 312.2 | 2.0 |
| Beckman LX/CX/DX (n=5) | 140.8 | 2.5 | 4.0 | 51.9 | 188.7 | 2.7 | 341.5 | 1.4 |
| Diazo (n=62) | 141.3 | 4.4 | 4.8 | 13.6 | 190.0 | 4.1 | 334.2 | 3.8 |
| IL Gas Analysers (n=44) | 155.4 | 4.9 | 5.9 | 19.3 | 208.8 | 4.7 | 371.4 | 4.2 |
| Radiometer Gas Analysers (n=44) | 149.7 | 5.5 | 5.7 | 26.4 | 202.1 | 4.6 | 359.6 | 3.7 |
| Rapidpoint 500 (n=6) | 149.0 | 2.4 | 3.3 | 85.2 | 194.3 | 2.7 | 362.5 | 5.7 |
| Roche Diazo (n=127) | 133.3 | 3.1 | 3.1 | 9.5 | 180.3 | 2.5 | 322.0 | 2.6 |
| Siemens Gas Analysers (n=4) | 148.3 | 2.3 | 3.3 | 87.2 | 199.3 | 3.1 | 374.0 | 3.6 |
| **Vanadate Oxidation (n=19)** | **145.7** | **3.7** | **4.0** | **2.1** | **198.0** | **3.3** | **357.8** | **3.8** |
| Vitros (T Bil) (n=3) | 164.7 | 0.4 | 5.3 | 12.3 | 217.0 | 1.4 | 366.0 | 1.9 |

- top 10 method groups ordered in terms of decreasing values of n=#
- Hyperlink allows the user to access the full method summary table listing data for all the method groups for that analyte

# The Reports – what's different?

Running PI

PI

Distribution

PI Scores for this Distribution B0917

| Sample | 1 | 2 | 3 | 4 | average |
|---|---|---|---|---|---|
| scored against: method mean | 145.65 | 4.03 | 198.02 | 357.83 | |
| TAE Weqas | 16.70 | 3.52 | 21.48 | 35.84 | |
| P.I. | -0.08 | -0.02 | 0 | -0.21 | 0.08 |
| Critical level 150.00 µmol/L – Sigma Score | | | | | 3.75 |

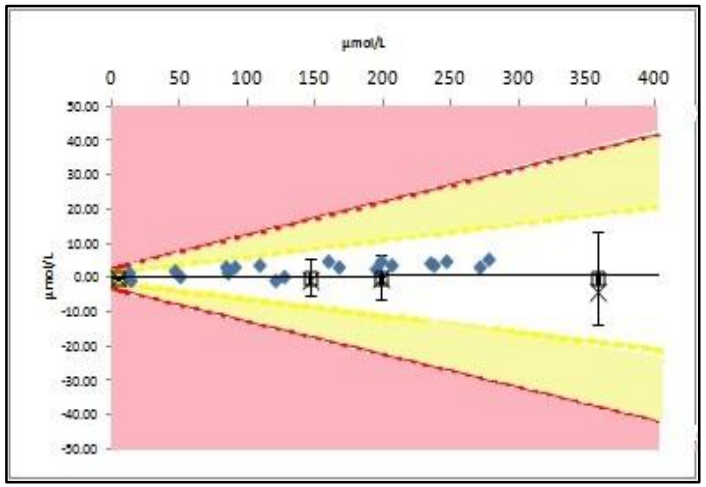
**This plot shows the current distribution and the previous 5 distributions in which this instrument was included, in date order from left (earliest distribution) to right (most recent distribution**

**All the Samples are now plotted rather than just the Avg SDI**

**Both negative and positive PIs are displayed**

**States what is being used at the target value**
**States the performance specification limits (TAE)**
**PI score for each sample (+ or - )**
**Sigma score**

## Absolute –Bias plot



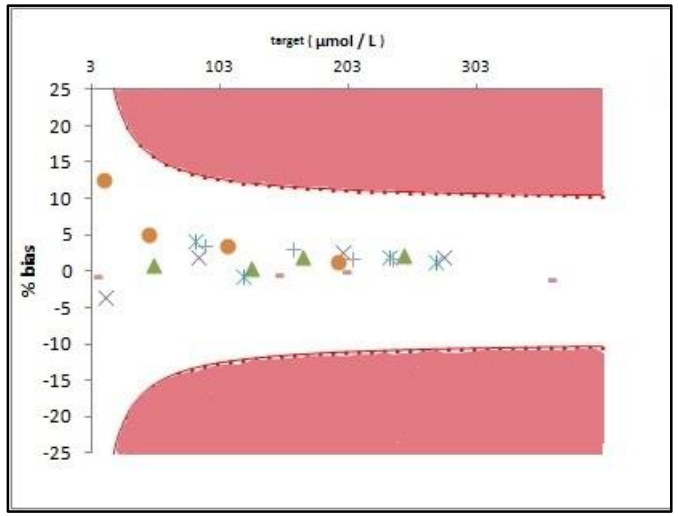

Your result - target

Target value

Linear regression
y = 1.04 – 1.26
r = 1.0000
IS = 0
$S_{y.x}$ = 1.09

bias key
x axis = target value
'x' = your current results
◊ = your previous results
° = your method mean
□ = your instrument model mean

## Relative –Bias plot



Target value

Red line represents target ± TAE, yellow line represents target ± 0.5 TAE .

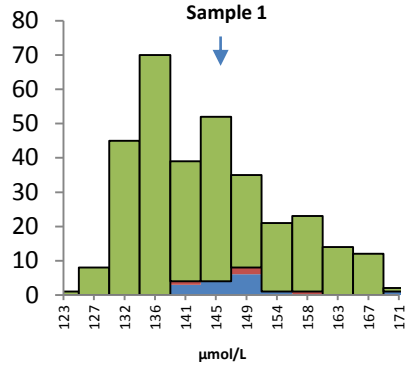
Red area represents unacceptable results, PI >2
Yellow area represents acceptable results, PI = 1-2
White area represents good results, PI <1

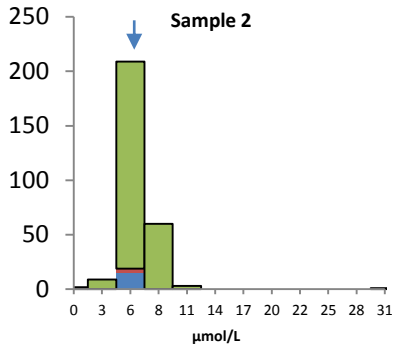
Graph now includes previous results

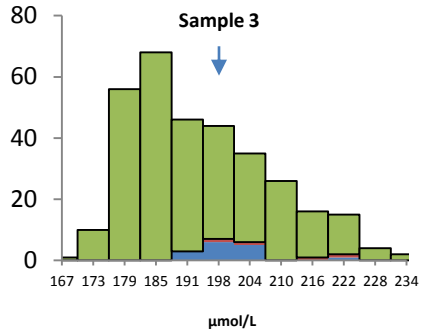
Red line represents target ± TAE

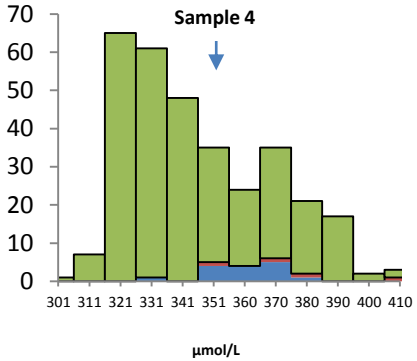
Previous Distributions are highlighted as separate series

# Histogram of results




Green – all results
Blue – Method
Pink - Instrument

# Comments box

| Weqas supplied comment for Total Bilirubin: | Participant supplied comment for Total Bilirubin: |
|---|---|
| *There is no comment for Total Bilirubin for this distribution* | Calibrator Lot # BB128974.<br>Awaiting engineer callout for scheduled maintenance |

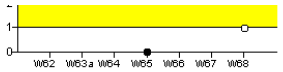
# The Reports – Analyte Report - Qualitative

## Old

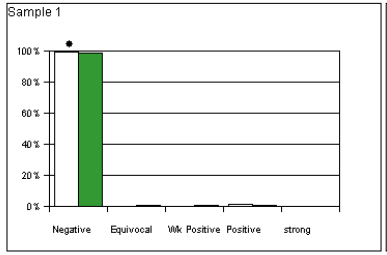
Qualitative Report

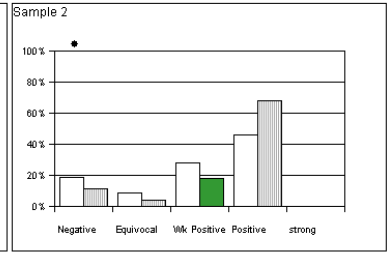
Lab Code: AE Section: 2TB2

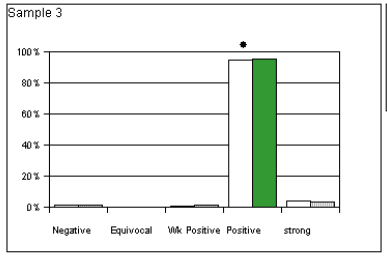
Qualitative HCG (High Sensitivity) Results




| Lab Code | Section | Method | Instrument | Sample Number | | | Sample Score | | | Average Score |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | 1 | 2 | 3 | 1 | 2 | 3 | (Average) |
| AE | 2TB2 | Unipath | Clearview HCG (3min) | Negative | Negative | Positive | 0 | 2 | 0 | 1.00 |
| | | | | | | | | | | |
| Interpretation | | | | Negative | Wk Positive | Positive | | | | |
| Spiked Value | | | | Urine from non pregnant donor | Pregnant donor urine diluted to approx 29iu | Pregnant donor urine diluted to approx 336iu | | | | |



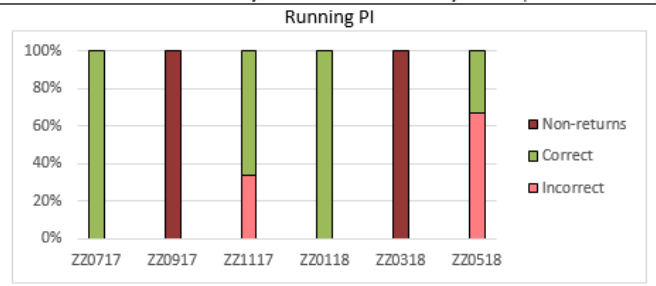



## New

Participant Code: **BY00001** · Location: **<###20 Characters##>** Analyser Name: **<15 Characters>** · Serial #: **AB00045237A**

Scheme: **SchemeName.** Distribution Code: **ZZ0518.** **Analyte: AnalyteName**

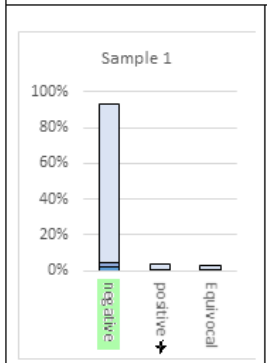
Distribution start: **04-May-18** Distribution End: **14-May-2018** Report Issued: **21-May-2018** Report Status: **final**

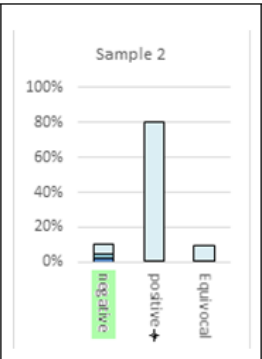


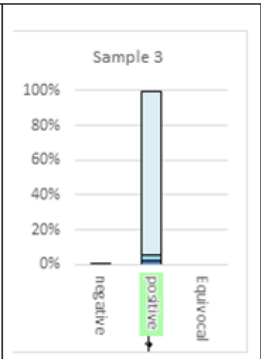

P.I. Key

- Incorrect Response
- Correct Response
- Sample Un-scored
- NRR – no response reported

| Method | Instrument | Sample 1 | Sample 2 | Sample 3 |
|---|---|---|---|---|
| MethodName 2 | InstrumentName | Positive | Positive | Positive |
| | | | | |
| Correct Interpretation** | | Negative | Negative | Positive |
| Preparation information | | Non spiked | Spiked to xx | Spiked with xx from positive donor |
| | | | | |
| From <Associated Quantitative Analyte> results | | | | |
| Mean | | 5.1 | 7.3 | 23.1 |
| sd | | 0.8 | 1.2 | 2.1 |
| CV % | | 15.7 | 16.4 | 9.1% |



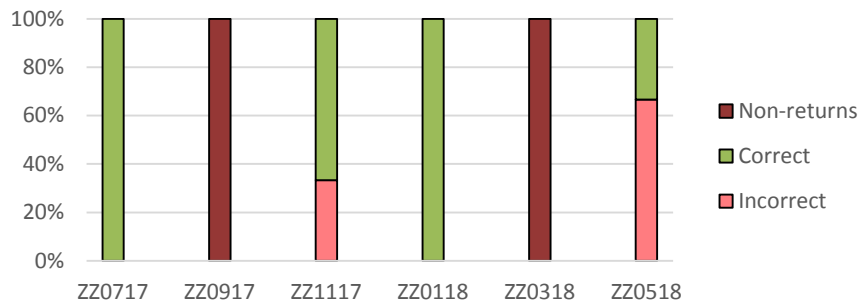




- other methods
- other instruments your method
- Your instrument, your method
- + Your response
- Correct response

# The Reports – what's different?

Running PI




Similar to the manager's summary for qualitative analytes, this plot is a stacked % plot based on the performance interpretation of individual test responses for the given analyte-instrument combination across all samples.

Data Table

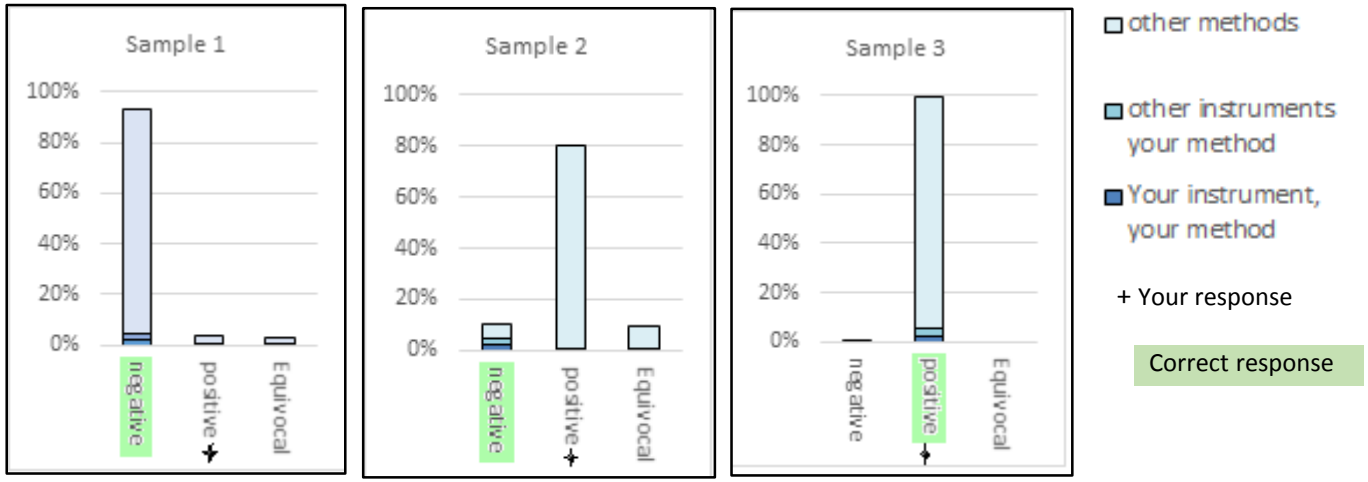
| **Method** | **Instrument** | **Sample 1** | **Sample 2** | **Sample 3** |
|---|---|---|---|---|
| MethodName 2 | InstrumentName | Positive | Positive | Positive |
| | | | | |
| Interpretation** | | Negative | Negative | Positive |
| Sample Description | | Non spiked | Spiked to xx | Spiked with xx from positive donor |
| | | | | |
| From <Associated Quantitative Analyte> results | | | | |
| Mean | | 5.1 | 7.3 | 23.1 |
| SD | | 0.8 | 1.2 | 2.1 |
| CV % | | 15.7 | 16.4 | 9.1% |

Row 1: the responses reported by the User, colour coded according to the performance classification assigned for that response.

Where no result has been submitted, NRR would be indicated and coloured red
Where no performance classification has been assigned (flagged to not score) the response would appear with no coloured background applied

Row 2: The correct interpretation for that sample. Cut off for interpretation based on clinical use / outcomes
Row 3: Description of the concentration / nature of the sample

Row 4 – 7: If the qualitative analyte has been associated with a quantitative analyte in the same scheme, the table would include summary information for that analyte.



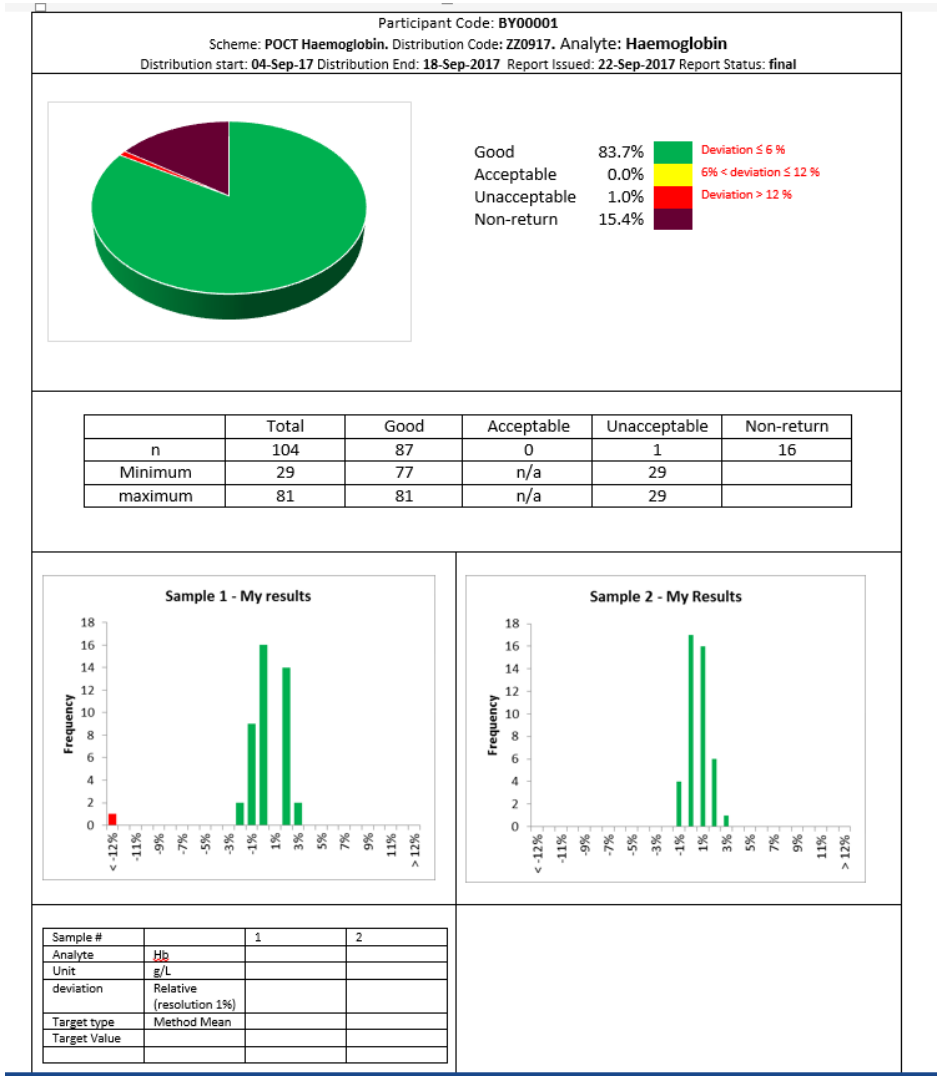

Simpler and clearer than previous graphs

## Method Summary Table – top 10 methods displayed

| | | sample 1 | | | sample 2 | | | sample 3 | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Detection limit | Negative | Positive | Equivocal | Negative | Positive | Equivocal | Negative | Positive | Equivocal |
| Method 1 (n=51) | 7 | 48 | 2 | 1 | 8 | 27 | 15 | 0 | 51 | 0 |
| **†Method 2 (n=16)** | **9** | **14** | **1** | **1** | **13** | **1** | **2** | **0** | **15** | **0** |
| Method 3 (n=25) | 7 | 25 | 0 | 0 | 0 | 24 | 1 | 0 | 25 | 0 |
| Method 4 (n=30) | 6 | 26 | 1 | 3 | 1 | 29 | 0 | 1 | 29 | 0 |
| Method 5 (n=97) | 7 | 92 | 3 | 2 | 2 | 90 | 5 | 0 | 97 | 0 |
| Method 6 (n=12) | 7 | 12 | 0 | 0 | 0 | 12 | 0 | 0 | 12 | 0 |
| Method 7 (n=20) | 7 | 18 | 2 | 0 | 0 | 19 | 1 | 0 | 20 | 0 |
| Method 8 (n=4) | 7 | 4 | 0 | 0 | 1 | 3 | 0 | 0 | 4 | 0 |
| Method 9 (n=34) | 7 | 31 | 1 | 2 | 5 | 26 | 3 | 1 | 33 | 0 |

method group for the instrument to which this report relates is highlighted in bold.

# POCT Manager's overview report



Participant Code: **BY00001**
Scheme: **POCT Haemoglobin.** Distribution Code: **ZZ0917.** Analyte: **Haemoglobin**
Distribution start: **04-Sep-17** Distribution End: **18-Sep-2017** Report Issued: **22-Sep-2017** Report Status: **final**

| | | |
|---|---|---|
| Good | 83.7% | Deviation ≤ 6 % |
| Acceptable | 0.0% | 6% < deviation ≤ 12 % |
| Unacceptable | 1.0% | Deviation > 12 % |
| Non-return | 15.4% | |

| | Total | Good | Acceptable | Unacceptable | Non-return |
|---|---|---|---|---|---|
| n | 104 | 87 | 0 | 1 | 16 |
| Minimum | 29 | 77 | n/a | 29 | |
| maximum | 81 | 81 | n/a | 29 | |





| Sample # | | 1 | 2 |
|---|---|---|---|
| Analyte | Hb | | |
| Unit | g/L | | |
| deviation | Relative (resolution 1%) | | |
| Target type | Method Mean | | |
| Target Value | | | |
| | | | |

All the existing reports from Cuesee website will be available but with improved formatting:

Overview report with link to reagent lot no.
Simplified report
No-results booked
Poor-performance report

Standard letters will also be made available:

Distribution letters
No results booked letter
Poor performance letter

# Other improved reports

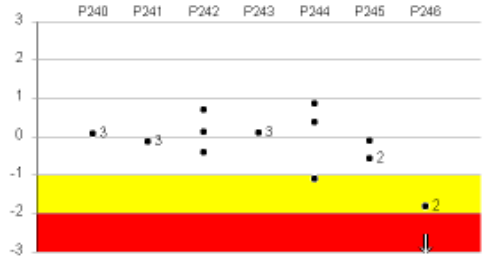
# Simplified Reports – PI scores and % poor PI added

**Scheme: Blood Gas. Distribution Code: P246.**
**Distribution Date: 21/09/15. Final. Report Issued: 14/10/15**

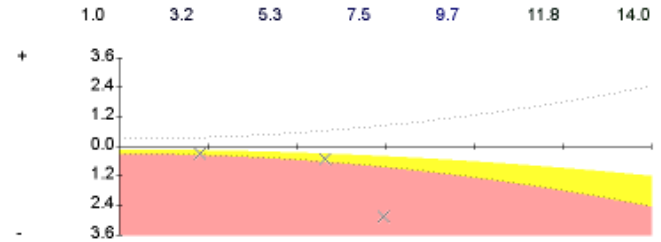
| pCO2 (kPa) | Sample 1 | Sample 2 | Sample 3 | Sample 4 |
|---|---|---|---|---|
| Reported Result | 4.58 | 5.49 | 2.66 | |
| Overall Mean | 7.42 | 5.98 | 2.89 | 8.52 |
| Method Mean: Cobas b123 | 7.46 | 6.03 | 2.98 | 8.38 |
| Instrument Mean: Cobas b123 | 7.46 | 6.03 | 2.98 | 8.38 |
| Your results are compared against | 7.46 | 6.03 | 2.98 | |

| |
|---|
| Good |
| Acceptable |
| Unacceptable |
| Discuss with QC officer |

**Running scores**




**Cumulative Bias Plot**




Previous: ~~P245~~ , ~~P244~~ , ~~P243~~ , ~~P242~~ , ~~P241~~ , ~~P240~~

**Cumulative Submitted results**

| | P240 | P241 | P242 | P243 | P244 | P245 | P246 |
|---|---|---|---|---|---|---|---|
| **Sample 1** | 5.98 | 5.9 | 8.68 | 6.0 | 5.31 | 7.43 | 4.58 |
| **Sample 2** | 3.94 | 7.29 | 2.77 | 8.35 | 2.7 | 3.91 | 5.49 |
| **Sample 3** | 7.43 | 5.14 | 3.98 | 4.0 | 7.82 | ? | 2.66 |
| **Sample 4** | N/A | ? | N/A | N/A | N/A | 2.85 | ? |

| Key | |
|---|---|
| ? | Analyte enrolled but no results returned |
| N/A | Not enrolled for this analyte |

**⚠ Performance Alert**

Your results show a significant consistent bias. Please discuss your results with your EQA Officer

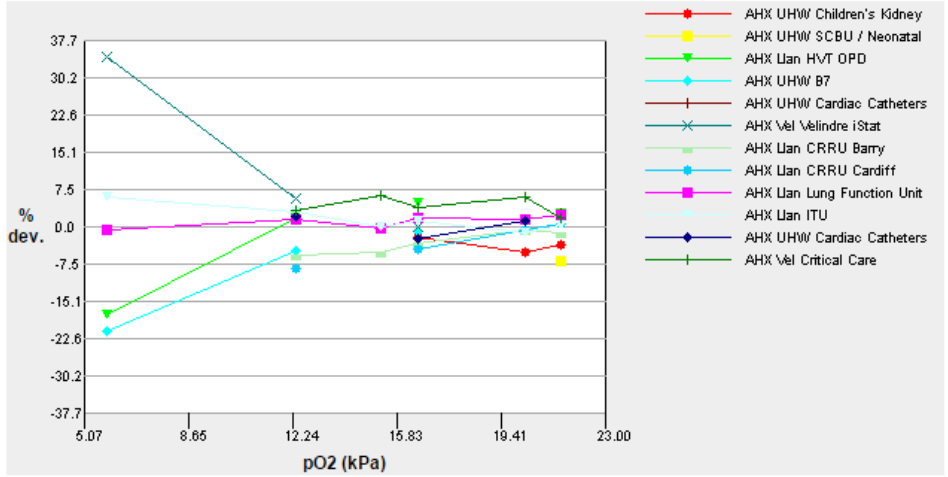
# Regional report – improved graphics.

Analyte: pO2. Region: Cardiff and Vale POC. Scheme: Blood Gas. Distributions: P247 - P252. Distribution Dates: 19-Oct-15 - 18-Apr-16.

**% Deviation from Regional Means**

| | | 224-1-B540 | 224-2-B540 | 224-3-B540 | 224-4-B540 | 224-5-B540 | 224-6-B540 |
|---|---|---|---|---|---|---|---|
| AHX | UHW Children's Kidney Centre | 29.89 * | 2.56 | - | -2.17 | -5.40 | -3.74 |
| AHX | UHW SCBU / Neonatal Unit | 76.04 * | 4.45 * | -5.73 * | 1.45 * | -14.04 * | -6.99 |
| AHX | Llan HVT OPD | -17.96 | 1.62 | -3.76 * | 4.78 | -1.20 * | 2.46 |
| AHX | UHW B7 | -21.38 | -4.86 | 0.82 * | -0.96 | -2.19 * | 2.62 |
| AHX | UHW Cardiac Catheters Lab B | 1.35 * | 9.72 * | 1.47 * | 2.66 | 0.28 * | 2.54 |
| AHX | Vel Velindre iStat | 34.25 | 5.67 | 0.16 * | -0.05 | -29.56 * | -9.32 * |
| AHX | Llan CRRU Barry | -24.80 * | -5.80 | -5.40 | -3.58 | -0.71 | -1.41 |
| AHX | Llan CRRU Cardiff | -28.22 * | -8.50 | -6.38 * | -4.79 | -0.87 | 0.45 |
| AHX | Llan Lung Function Unit | -0.87 | 1.21 | -0.49 | 1.66 | 1.43 | 2.15 |
| AHX | Llan ITU | 5.96 | 2.83 | -0.16 | 1.05 | -1.36 | 0.29 |
| AHX | UHW Cardiac Catheters Lab C | 9.38 * | 2.02 | 1.47 * | -2.47 | 1.02 | 0.91 * |
| AHX | Vel Critical Care | 20.21 * | 3.24 | 6.06 | 3.87 | 5.88 | 1.61 |

* - not included in group mean

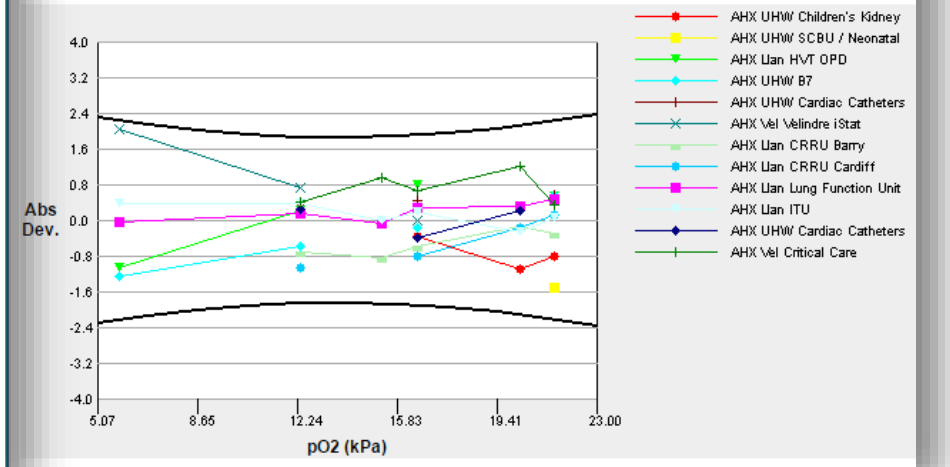



Analyte: pO2. Region: Cardiff and Vale POC. Scheme: Blood Gas. Distributions: P247 - P252. Distribution Dates: 19-Oct-15 - 18-Apr-16.

**Absolute Deviation from Regional Means**

| | | 224-1-B540 | 224-2-B540 | 224-3-B540 | 224-4-B540 | 224-5-B540 | 224-6-B540 |
|---|---|---|---|---|---|---|---|
| AHX | UHW Children's Kidney Centre | 1.75 * | 0.32 | - | -0.36 | -1.09 | -0.80 |
| AHX | UHW SCBU / Neonatal Unit | 4.45 * | 0.55 * | -0.87 * | 0.24 * | -2.84 * | -1.50 |
| AHX | Llan HVT OPD | -1.05 | 0.20 | -0.57 * | 0.79 | -0.24 * | 0.53 |
| AHX | UHW B7 | -1.25 | -0.60 | 0.13 * | -0.16 | -0.44 * | 0.56 |
| AHX | UHW Cardiac Catheters Lab B | 0.08 * | 1.20 * | 0.23 * | 0.44 | 0.06 * | 0.55 |
| AHX | Vel Velindre iStat | 2.00 | 0.70 | 0.03 * | -0.01 | -5.98 * | -2.00 * |
| AHX | Llan CRRU Barry | -1.45 * | -0.72 | -0.82 | -0.59 | -0.14 | -0.30 |
| AHX | Llan CRRU Cardiff | -1.65 * | -1.05 | -0.97 * | -0.79 | -0.18 | 0.10 |
| AHX | Llan Lung Function Unit | -0.05 | 0.15 | -0.07 | 0.27 | 0.29 | 0.46 |
| AHX | Llan ITU | 0.35 | 0.35 | -0.02 | 0.17 | -0.28 | 0.06 |
| AHX | UHW Cardiac Catheters Lab C | 0.55 * | 0.25 | 0.23 * | -0.41 | 0.21 | 0.20 * |
| AHX | Vel Critical Care | 1.18 * | 0.40 | 0.93 | 0.64 | 1.19 | 0.35 |
| | | | | | | | |
| | Weqas SD | 1.11 | 0.93 | 0.93 | 0.95 | 1.05 | 1.11 |

* - not included in group mean



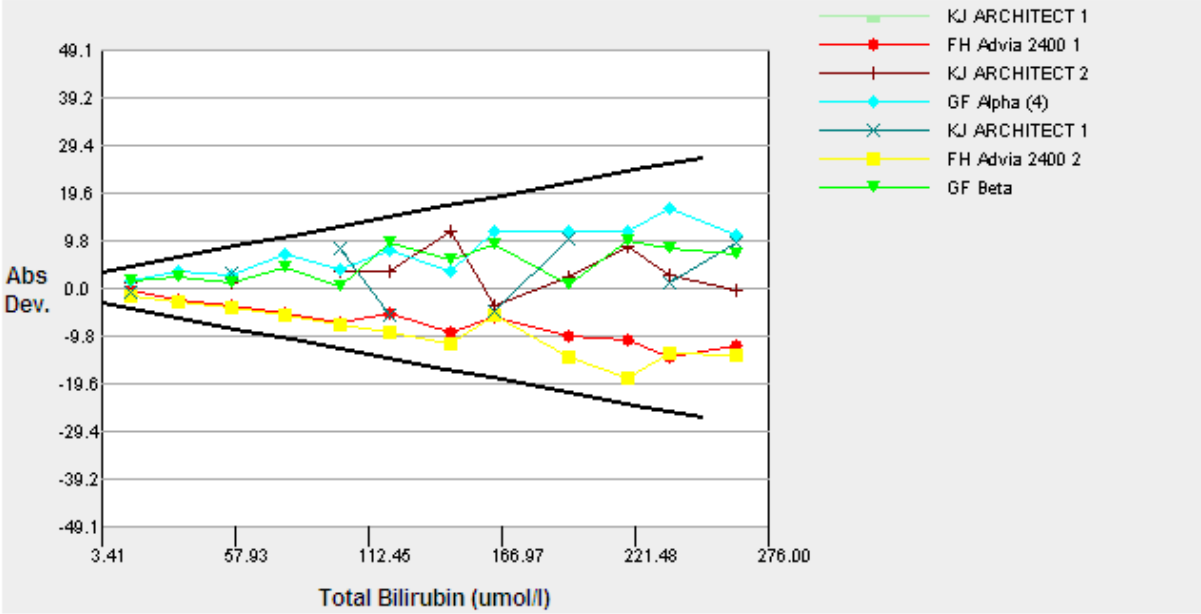

for all instruments in the group, deviation reports provide absolute and % deviation from the group mean on a per analyte basis

Available to print from your browser, or in PDF format to your email address

# Regional report – available as a region/ group/ participant

| Absolute Deviation from Regional Means | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | B291 | B297 | B300 | B296 | B301 | B292 | B293 | B294 | B295 | B298 | B299 | B302 |
| FH | Advia 2400 1 | -0.59 | -9.31 | -10.89 | -5.39 | -14.48 | -2.56 | -3.67 | -5.22 | -7.38 | -6.15 | -10.04 | -11.82 |
| FH | Advia 2400 2 | -1.92 | -11.48 | -18.52 | -9.36 | -13.35 | -2.92 | -4.20 | -5.86 | -7.84 | -5.65 | -14.51 | -14.05 |
| GF | Beta | 1.21 | 5.82 | 9.58 | 9.14 | 8.08 | 2.24 | 1.13 | 4.21 | 0.06 | 8.95 | 0.72 | 6.72 |
| GF | Alpha (4) | 1.21 | 3.49 | 11.58 | 7.81 | 16.42 | 3.24 | 2.47 | 6.88 | 3.72 | 11.62 | 11.72 | 10.72 |
| KJ | ARCHITECT 2 | 0.88 | 11.49 | 8.25 | 3.48 | 2.42 | 1.91 * | 1.13 | 4.21 * | 3.39 | -3.88 | 2.06 | -0.62 |
| KJ | ARCHITECT 1 | -0.79 | 6.49 * | 1.25 * | -5.69 | 0.92 | 0.91 * | 3.13 | 1.21 * | 8.06 | -4.88 | 10.06 | 9.05 |
| KJ | ARCHITECT 1 | 3.21 * | 16.49 * | 9.25 * | 16.81 * | - | - | - | - | - | - | - | - |
| | | | | | | | | | | | | | |
| | Weqas SD | 2.31 | 8.61 | 12.09 | 7.39 | 12.90 | 3.24 | 4.27 | 5.34 | 6.41 | 9.47 | 10.93 | 14.24 |

* - not included in group mean




A group can be set up as an individual lab code with multiple sections or with different lab codes and sections.

# 15189 Compliance Report

To include:

Measurement uncertainty – Between batch SD over length of batch.

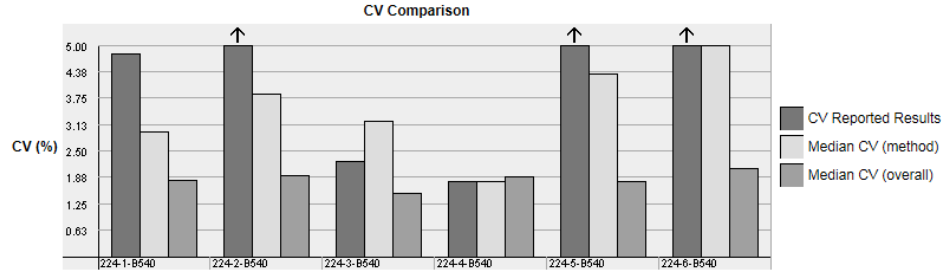
Accuracy - average bias over length of batch against reference method or peer group

Traceability to high order reference method (if available)

Sigma Score where:
δ = (TAE – Average Bias) / between batch CV%

Provides between batch imprecision over length of batch – 6 to 12 months for all sections.

Lab Code: **AHX** . Section Name: **Llan CRRU Barry**. Scheme: **Blood Gas**. Distribution Range: **P247 - P252**

**Analyte: pCO2 (kPa)**

| Method: **ABL 80** | **224-1-B540** | **224-2-B540** | **224-3-B540** | **224-4-B540** | **224-5-B540** | **224-6-B540** |
|---|---|---|---|---|---|---|
| **Section Stats** | | | | | | |
| Mean reported results | 8.62 | 7.58 | 5.96 | 5.16 | 3.99 | 2.77 |
| SD reported results | 0.41 | 0.43 | 0.13 | 0.09 | 0.34 | 0.25 |
| CV(%) reported results | 4.79 | 5.67 | 2.26 | 1.78 | 8.55 | 8.94 |
| Number of results | 3 | 3 | 2 | 3 | 3 | 3 |
| **Method Result Stats** | | | | | | |
| Mean method mean | 8.75 | 7.59 | 6.32 | 5.18 | 4.22 | 2.92 |
| Median CV | 2.95 | 3.83 | 3.21 | 1.78 | 4.32 | 4.97 |
| **Overall Result Stats** | | | | | | |
| Median CV | 1.80 | 1.90 | 1.48 | 1.90 | 1.78 | 2.09 |