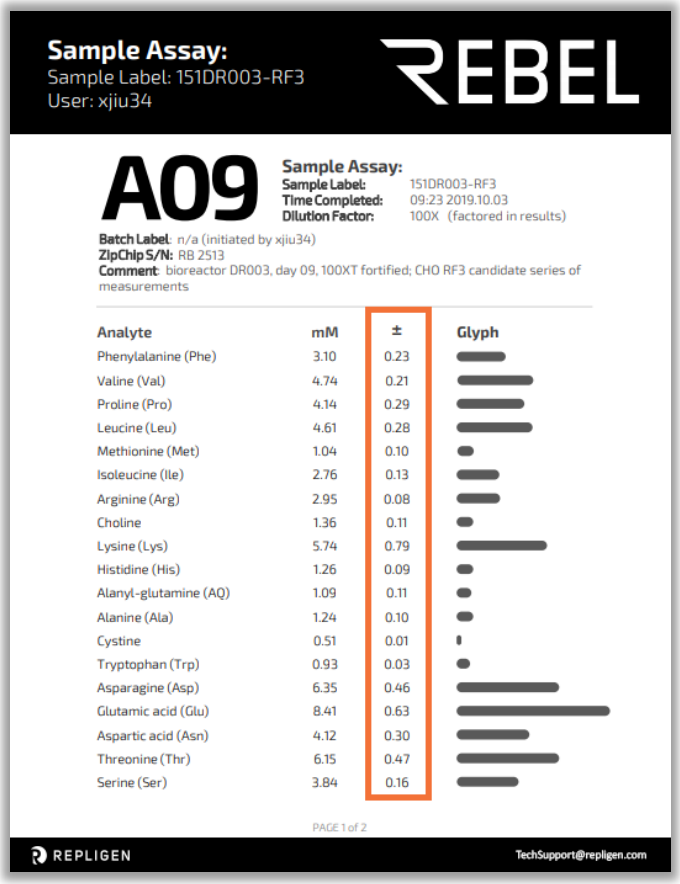
Standard Error in Reports

PATsmart™ REBEL® System

Support Document

PATsmart™ REBEL® System reports all results in mM concentration accompanied by the associated standard error.



Sample Assay:
Sample Label: 151DR003-RF3
User: xjiu34

REBEL

A09

Sample Assay:
Sample Label: 151DR003-RF3
Time Completed: 09:23 2019.10.03
Dilution Factor: 100X (factored in results)

Batch Label: n/a (initiated by xjiu34)
ZipChip S/N: RB 2513
Comment: bioreactor DR003, day 09, 100XT fortified; CHO RF3 candidate series of measurements

Analyte	mM	±	Glyph
Phenylalanine (Phe)	3.10	0.23	
Valine (Val)	4.74	0.21	
Proline (Pro)	4.14	0.29	
Leucine (Leu)	4.61	0.28	
Methionine (Met)	1.04	0.10	
Isoleucine (Ile)	2.76	0.13	
Arginine (Arg)	2.95	0.08	
Choline	1.36	0.11	
Lysine (Lys)	5.74	0.79	
Histidine (His)	1.26	0.09	
Alanyl-glutamine (AQ)	1.09	0.11	
Alanine (Ala)	1.24	0.10	
Cystine	0.51	0.01	
Tryptophan (Trp)	0.93	0.03	
Asparagine (Asp)	6.35	0.46	
Glutamic acid (Glu)	8.41	0.63	
Aspartic acid (Asn)	4.12	0.30	
Threonine (Thr)	6.15	0.47	
Serine (Ser)	3.84	0.16	

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Standard error and relative standard error (RSE) are statistical propagations of error for the system as a whole, based on the QC and individual sample replicate.

*This is **not** to be confused with Coefficient of Variation (%CV) or Standard Deviation.*

The greater the RSE, the greater the uncertainty in the results

- Most common cause for large RSE is extrapolation outside of the calibrated range, or at the extremes of the curve.
- Acceptable RSE are established by each user group, but generally <15% is considered good.

Relative standard error (RSE) can be interpreted as the expected variability in estimated concentrations over many replicates - *samples are recommended to be run in triplicate*.

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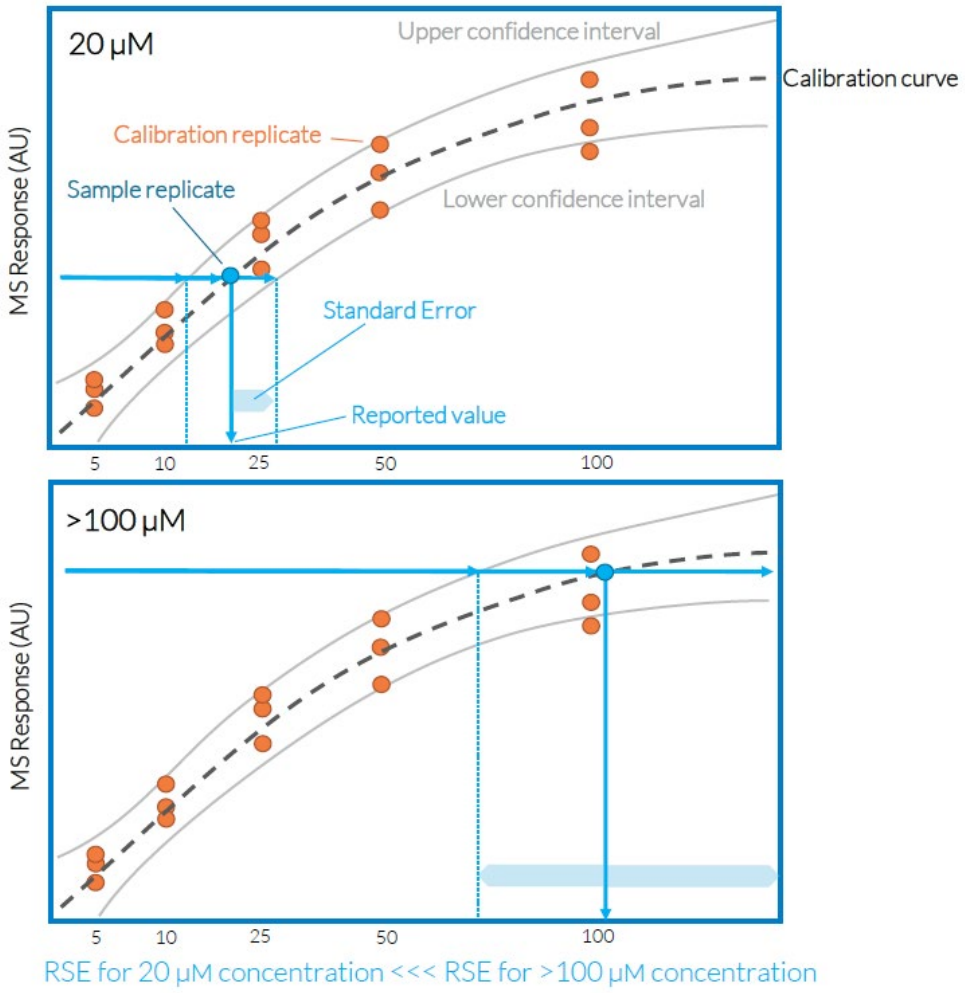

RSE for 20 µM concentration <<< RSE for >100 µM concentration

Customer Service

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