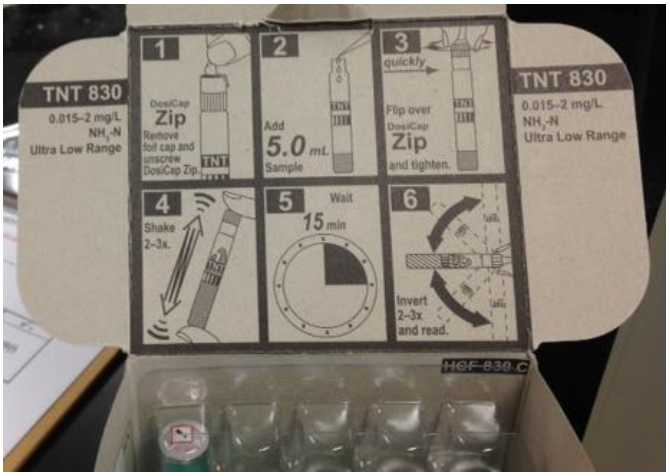
Ammonia TNT830 QA/QC



	Sample	True value	Actual reading	% Recovery for LFB (std)	LFM (Spike) %Recovery ± 20%	RPD ≤ 20%	ICV or CCV % Recovery ± 10%
1	**Blank** (< detection limit)		0.0				
2	**ICV** - 1.0 mg/L NH_3-N	1.0	0.98				0.98 *100 / 1.0 =98%
3	**LFB** - 0.5 mg/L NH_3-N	0.5	0.51	0.51 *100 / 0.50 =102%			
4	Influent, Composite – 25 x dilution		0.96 (x 25 = 24.00)				
5	**LFM** Influent, Composite – 25 x dilution *1.0 mg/L NH_3-N		1.95		1.95-0.96 *100 / 1.0 = 99%	1.98-1.95 *100 / (1.98+1.95) / 2 = 1.5%	
6	**LFMD** - Influent, Composite – 25 x dilution *1.0 mg/L NH_3-N		1.98		= 102%		
7	Sample, mg/L		0.05				
8	**LFM** - Sample Spike *1.0 mg/L NH_3-N added to Samples		1.13		= 108%	= 7.7%	
9	**LFMD** - Sample Spike Dup * 1.0 mg/L NH_3-N added to Samples		1.22		= 117%		
10	**CCV -** 1.0 mg/L NH_3-N	1.0	0.99				0.99 *100 / 1.0 =99%

* For spike – Put 1.0 mL of 100 mg/L standard in 100 mL of sample (A or B). Use 100 mL volumetric flask. That will give you 101 mL of sample and spike. Then, take 5 mL of this to run test. This should raise the sample + spike value by 1.0 mg/L (ppm). Spike volume should be <1% of total volume.

(unspiked sample conc. * unspiked sample vol.) + (std conc for spike * vol of spike) / (total sample vol. + spike vol) = (? sample conc * 100 mL) + (100 mg/L * 1.0 mL) / (100 mL + 1.0 mL) = mg/L

Calculations

- % Recovery for LFB
  - = LFB Result / Expected Concentration X 100%
- RPD – relative percent differences for duplicates and LFM/LFMD
  - = Difference between sample and duplicate / Average of the sample and duplicate X 100%
- % Recovery for LFM – when using less than or equal to 1% spike volume compared to sample volume
  - = LFM Result – Sample Result / Actual Concentration of spike X 100%

Example Calculations:

Blanks < MDL (example 0.004 mg/L)

% Recovery LFB $\frac{0.51}{0.50} * 100 = 102\ \%$

ICV/CCV ± 10% $\frac{0.98}{0.99} * 100 = 98\%$

LFM/LFMD ± 10% Recovery

$\frac{(1.22 - 0.051)\ mg/L}{1\ mg/L} = \frac{1.17}{1} = 1.17 * 100 = 117\%$

$\frac{(1.13 - 0.051)\ mg/L}{1\ mg/L} = \frac{1.08}{1} = 1.08 * 100 = 108\%$

Reporting Limit = MDL

RPD < 20% (for LFM/LFMD) = $\frac{1.22 - 1.13}{\frac{(1.22 + 1.13)}{2}} = \frac{0.09}{1.175} = 0.0766 * 100 = 7.66\%$

Method Detection Limit

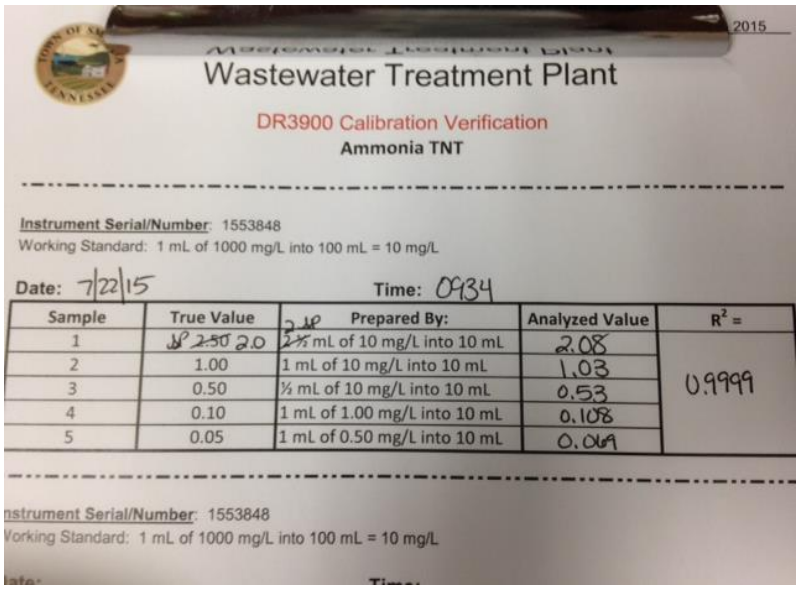
The MDL must be greater than 1/10 the concentration of each spike.
Example: if the spike was 0.05, the MDL cannot be lower than 0.005 (0.05 divided by 10)

Date	Analyst	Number	True Value	Value Read	% Recovery (50-150%)
6/22/2015	SEP	1	0.05	0.066	132.00
6/22/2015	SEP	2	0.05	0.080	160.00
6/23/2015	SEP	3	0.05	0.056	112.00
6/23/2015	SEP	4	0.05	0.055	110.00
6/23/2015	SEP	5	0.05	0.054	108.00
6/24/2015	SEP	6	0.05	0.056	112.00
6/24/2015	SEP	7	0.05	0.056	112.00
			Standard Deviation	0.009519404	
			Average	0.06	
			Relative Standard Deviation (RSD)	15.75315	(Needs to be ≤ 20%)
			MDL	0.0298909	

This information is found in 22nd Edition of Standard Methods on page 1-8.

Calibration Curve

* The appropriate linear correlation coefficient for standard concentration-to-instrument response should be greater than or equal to 0.995.



2015

Wastewater Treatment Plant

DR3900 Calibration Verification

Ammonia TNT

Instrument Serial/Number: 1553848

Working Standard: 1 mL of 1000 mg/L into 100 mL = 10 mg/L

Date: 7/22/15 Time: 0934

Sample	True Value	Prepared By:	Analyzed Value	R^2 =
1	~~2.50~~ 2.0	~~2.5~~ mL of 10 mg/L into 10 mL	2.08	0.9999
2	1.00	1 mL of 10 mg/L into 10 mL	1.03	
3	0.50	½ mL of 10 mg/L into 10 mL	0.53	
4	0.10	1 mL of 1.00 mg/L into 10 mL	0.108	
5	0.05	1 mL of 0.50 mg/L into 10 mL	0.069	

nstrument Serial/Number: 1553848

Vorking Standard: 1 mL of 1000 mg/L into 100 mL = 10 mg/L

Low Range Calibration

S/N: 1553848

Time: 0934

Date	Subject	true value (x)	value read (y)	(x)(y)	X^2	y^2
22-Jul-2015	1	2.00	2.080	4.1600	4.0000	4.3264
22-Jul-2015	2	1.00	1.030	1.0300	1.0000	1.0609
22-Jul-2015	3	0.50	0.530	0.2650	0.2500	0.2809
22-Jul-2015	4	0.10	0.108	0.0108	0.0100	0.0117
22-Jul-2015	5	0.05	0.069	0.0035	0.0025	0.0048
	Sum (Σ)	3.65	3.817	5.4693	5.2625	5.6846
22-Jul-2015	R^2 =	0.999900144				

1 mg/L is in the middle of the "curve", so it's a good place to spike with. You used 1 mL of 100 mg/L into 100 mL of sample. That should increase your sample value by 1 mg/L.

*C1*V1 = C2*V2*

(1 mL)(100 mg/L) = (100 mL)(x)

1 mg/L = x the spiked value