

## Changes between RDML v1.1 to v 1.2 (2014-10-02)

### sampleType

annotation: New element occurring 0 to unlimited times  
This element has two subelements, property and value, both strings.  
It should be used to annotate the properties of samples.

templateRNAQuality: Element was removed  
Use the annotation element instead.

templateDNAQuality: Element was removed  
Use the annotation element instead.

templateRNAQuantity: Element was removed  
Use the templateQuantity element instead.

templateDNAQuantity: Element was removed  
Use the templateQuantity element instead.

templateQuantity: New optional element  
Use this element to define the nucleotide concentration of the template.  
It has the subelements:

- conc: Concentration of the template in nanogram per microliter in the final reaction mix.
- nucleotide: The type of nucleotide used as template. Possible values are genomic DNA, cDNA, DNA, RNA.

### targetType

amplificationEfficiencySE: New optional element  
The standard error of the value provided in "amplificationEfficiency" should be given.

### dataType

bgFluorSlp: New optional element  
This element contains the slope of the baseline function.  
Background fluorescence slope - The slope of the baseline trend based on the estimated background fluorescence. The element should be absent to indicate a slope of 0.0; If this element is present without the bgFluor element it should be ignored.

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*Clarifications of existing elements without functional changes:*

sampleType

quantity:

Quantity - The reference quantity of this sample. It should be only used if the sample is part of a standard curve. The provided value will be used to quantify unknown samples in absolute quantification assays.

Only the use of true numbers is valid like 1, 10, 100, 1000 or 1, 0.1, 0.01, 0.001. The use of exponents is not valid like 1, 2, 3, 4 or -1, -2, -3, -4 because it will not be interpreted as 10E1, 10E2, 10E3, 10E4 or 10E-1, 10E-2, 10E-3, 10E-4.

targetType

A target is a defined PCR reaction. PCR reactions for the same gene which differ in primer sequences are considered different targets.

dataType

bgFluor: Clarification of the documentation:

Background fluorescence - The y-intercept of the baseline trend based on the estimated background fluorescence.

excl: Clarification of the documentation:

Excluded - If present, this entry should not be evaluated. Do not set this element to false if this entry is valid, leave the entire element out instead.

It may contain a string with reason for exclusion. Several reasons for exclusion should be separated by semicolons ";".

dpAmpCurveType / dpMeltingCurveType // fluor: Clarification of the documentation:

Fluorescence - The fluorescence intensity measured without any correction. The fluorescence intensity must not be baseline corrected.

idType

Clarification of the documentation: A ID must be at least one character and unique. The id should be a human readable short name as it was provided by the user.

targetType

amplificationEfficiency: Clarification of the documentation:

Amplification efficiency should be given as the fold-increase of DNA per cycle (the base of the exponential function), for example 1.95 for 95% efficiency.