

## ViPER® ANLYTX: Tags for OPC UA Integration

**Abstract:**

This article contains Node IDs and OPC Tags for ViPER® ANLYTX software functions that can be leveraged to interface with Open Platform Communications (OPC) clients.

**Applicability:**

These tags apply in general to OPC UA clients for integration with ViPER ANLYTX Software. Some data types may not be compatible with all platforms.

OPC UA Server Address: `opc.tcp://localhost:4841/VptServer`

*localhost* can be replaced by the IP address of the PC if attempting to connect from another PC.

### Point Source

The Point Source column in the tables below indicates the applicable VPT instrument for each OPC tag. Some OPC tags apply only to the FlowVPX® System or the SoloVPE® PLUS System. “Both” indicates the tag is valid for both the FlowVPX and SoloVPE PLUS Systems.

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## 1. CycleData

Node ID	OPC Tag	Description	Units	Point Source	Data Type
ns=2;s=CycleData/ID	CycleData/ID	ID of specific datapoint cycle within a run	-	Both	Int32
ns=2;s=CycleData/CompletionDateTime	CycleData/CompletionDateTime	Time when the cycle was completed	-	Both	String
ns=2;s=CycleData/SlopeValue	CycleData/SlopeValue	Steepness of the linear regression of the datapoints between absorbance and pathlength	Abs/mm	Both	Float
ns=2;s=CycleData/RSquared	CycleData/RSquared	Statistical measure on how well the data fit the regression model	-	Both	Float
ns=2;s=CycleData/Concentration	CycleData/Concentration	Amount of substance per volume	mg/ml	Both	Float
ns=2;s=CycleData/CalculatedEcValue	CycleData/CalculatedECValue	Molar absorptivity of sample calculated from known concentration and slope measurement	ml/(mg*cm)	Both	Float
ns=2;s=CycleData/Wavelength	CycleData/Wavelength	Distance of identical points between one wave	nm	Both	Float
ns=2;s=CycleData/ExtinctionCoefficient	CycleData/ExtinctionCoefficient	Molar absorptivity of sample at specific wavelength	ml/(mg*cm)	Both	Float
ns=2;s=CycleData/MinutesFromDaqStart	CycleData/MinutesfromDaqStart	Run duration from start of collection.	mins	Both	Float
ns=2;s=CycleData/DeltaConcentration	CycleData/DeltaConcentration	Change in value from previous concentration measurement	mg/ml	Both	Float
ns=2;s=CycleData/IntegralConcentration	CycleData/IntegralConcentration	Area under the concentration curve	(mg/ml)*min	Both	Float
ns=2;s=CycleData/MovingAverageConcentration	CycleData/MovingAverageConcentration	Average of last 5 concentration values	mg/ml	Both	Float
ns=2;s=CycleData/PercentRSDConcentration	CycleData/PercentRSDConcentration	The measurement of the datapoints' average deviation from the mean	%	Both	Float
ns=2;s=CycleData/PercentRelDiffConcentration	CycleData/PercentRelDiffConcentration	Range of the datapoints divided by the mean	%	Both	Float
ns=2;s=CycleData/GetCycleInfo	CycleData/GetCycleInfo	Returns slope, concentration, R <sup>2</sup> , etc. in the cycle data node	-	Both	Methodnodeclass
ns=2;s=CycleData/Aav/Id	CycleData/Aav/Id	AAV Record Id	-	Both	Float
ns=2;s=CycleData/Aav/DaqId	CycleData/Aav/DaqId	AAV DAQ Id	-	Both	Float
ns=2;s=CycleData/Aav/ReplicateId	CycleData/Aav/ReplicateId	AAV Replicate Id	-	Both	Float
ns=2;s=CycleData/Aav/RValue	CycleData/Aav/RValue	AAV Slope Ratio R-Value	-	Both	Float
ns=2;s=CycleData/Aav/PercentFullCapsid	CycleData/Aav/PercentFullCapsid	Percentage of full capsids	-	Both	Float
ns=2;s=CycleData/Aav/CapsidTiter	CycleData/Aav/CapsidTiter	Concentration of capsids per milliliter	cp/ml	Both	Float
ns=2;s=CycleData/Aav/GenomeTiter	CycleData/Aav/GenomeTiter	Concentration of viral genomes per milliliter	vg/ml	Both	Float
ns=2;s=CycleData/Aav/CycleDataAav	CycleData/Aav/CycleDataAav	Json representation of CycleData AAV object	-	Both	String
ns=2;s=CycleData/Adc/Id	CycleData/Adc/Id	ADC Record Id	-	Both	Float
ns=2;s=CycleData/Adc/DaqId	CycleData/Adc/DaqId	ADC DAQ Id	-	Both	Float
ns=2;s=CycleData/Adc/ReplicateId	CycleData/Adc/ReplicateId	ADC Replicate Id	-	Both	Float
ns=2;s=CycleData/Adc/DrugConcentration	CycleData/Adc/DrugConcentration	Drug concentration	mg/mL	Both	Float
ns=2;s=CycleData/Adc/AntibodyConcentration	CycleData/Adc/AntibodyConcentration	Antibody concentration	mg/mL	Both	Float
ns=2;s=CycleData/Adc/DAR	CycleData/Adc/DAR	Drug-to-Antibody Ratio	-	Both	Float
ns=2;s=CycleData/Adc/CycleDataAdc	CycleData/Adc/CycleDataAdc	Json representation of CycleData ADC object	-	Both	String

## 2. Daq

Node ID	OPC Tag	Description	Units	Point Source	Data Type
ns=2;s=Daq/CurrentDaqId	Daq/CurrentDaqId	Current ID of data acquisition run	-	Both	Int32
ns=2;s=Daq/CycleData	Daq/CycleData	Json representation of Cycle Data. Subscribing to the /Daq/CycleData node reports not only the slope data, but also the raw data (the pathlength, wavelength, and the acquired absorbance at each data point) that was used to calculate the slope, as well as when the cycle was run and the user who ran the cycle	-	Both	String
ns=2;s=Daq/IsCollecting	Daq/IsCollecting	Will return true if data is collecting	-	Both	Boolean
ns=2;s=Daq/IsScanning	Daq/IsScanning	Will return true if spectral scans data is collecting	-	Both	Boolean
ns=2;s=Daq/SampleName	Daq/SampleName	Sample name	-	Both	String
ns=2;s=Daq/BaselineDaqId	Daq/BaselineDaqId	Signifies that the method is currently running the baseline before running the actual method	-	Both	Int32
ns=2;s=Daq/SlopeData	Daq/SlopeData	Includes, but not limited to, the slope, concentration, and $R^2$ value	-	Both	String
ns=2;s=Daq/UserResultCollected	Daq/UserResultCollected	Flag OPC Client that a User Result was calculated, dynamic nodes will be filled in later or can be retrieved in the database using the cycle ids	-	Both	String
ns=2;s=Daq/MethodCollected	Daq/MethodCollected	Event triggered to signify that method collection is completed	-	Both	String
ns=2;s=Daq/MethodStopped	Daq/MethodStopped	Event triggered to signify that a method was manually stopped or interrupted.	-	Both	String
ns=2;s=Daq/RepCount	Daq/RepCount	Signifies the current repeat that the instrument is currently collecting	-	Both	String
ns=2;s=Daq/SeriesFilter	Daq/SeriesFilter	SeriesFilter (categorizes data) (not used)	-	Both	String
ns=2;s=Daq/ChromatographyAlert	Daq/ChromatographyAlerts	Chromatography Alert (in Development)	-	Both	String
ns=2;s=Daq/ChromatographyStats	Daq/ChromatographyStats	ChromatographyStats (In Development)	-	Both	String
ns=2;s=Daq/Username	Daq/Username	Displays the username that initiated data acquisition	-	Both	String
ns=2;s=Daq/UserType	Daq/UserType	Displays the type of user that initiated data acquisition	-	Both	String
ns=2;s=Daq/RunStart	Daq/RunStart	Returns the DateTime data acquisition started - will display minimum DateTime if run has not started	-	Both	String
ns=2;s=Daq/RunEnd	Daq/RunEnd	Returns the DateTime data acquisition started - will display minimum DateTime if run has not ended	-	Both	String
ns=2;s=Daq/KfcTrialRunSettingId	Daq/KfcTrialRunSettingId	Setting trial run id for integrated RPM System (KR2i + FlowVPX)	-	Both	Int32
ns=2;s=Daq/GetDaqStartInfo	Daq/GetDaqStartInfo	If collected data needs to be retrieved at a later time, ViPER's OPC server allows the user to review previously run data. Under the Daq node, select the GetDaqStartInfo node. A start and end date (MM/DD/YYYY format) value can be input, and all runs that have been performed within the specified range will be subsequently retrieved, as shown in the screenshot below.	-	Both	String
ns=2;s=Daq/GetCycleData	Daq/GetCycleData	Will provide cycle data information on all cycles collected within DAQ ID input	-	Both	MethodNodeClass
ns=2;s=Daq/GetCyclesInDaq	Daq/GetCyclesInDaq	Retrieve the cycles Ids in DAQ. Node to enter Daqid. Similar to above, but only shows cycle Ids.	-	Both	String
ns=2;s=Daq	Daq/GetCyclesInDaq/daqID	This will display all the cycles/slopes acquired for that DAQ ID.	-	Both	Int32
ns=2;s=Daq/StopMethod	Daq/StopMethod	Stops method	-	Both	MethodNodeClass
ns=2;s=Daq/RequestNextRep	Daq/RequestNextRep	Request next sample rep measurement when method is set to Replicate	-	Both	MethodNodeClass

ns=2;s=Daq/CreateDaqStart	Daq/CreateDaqStart	Inserts the DAQ to database so that the start of the run can be recorded accurately. MethodId: Enter Id#, Int32 DeviceId: Enter Id#, Int32 UserId: Enter Id#, Int32	-	Both	MethodNodeClass
ns=2;s=Daq/StartCollect	Daq/StartCollect	Starts data collection after entering dId (Int32) from information entered into CreateDaqStart	-	Both	MethodNodeClass
ns=2;s=Daq/StartCollectBool	Daq/StartCollectBool	When True, starts the collection according to nodes that are already set. When False, it will stop the run	-	Both	Boolean
ns=2;s=Daq/GetDaqId	Daq/GetDaqId	Returns current DAQ ID after a call	-	Both	MethodNodeClass
ns=2;s=Daq/GetBaselineDaqId	Daq/GetBaselineDaqId	Returns current baseline DAQ ID after call	-	Both	MethodNodeClass
ns=2;s=Daq/GetDaqRunStart	Daq/GetDaqRunStart	Returns DAQ run start date/time	-	Both	MethodNodeClass

### 3. Flow

Node ID	OPC Tag	Description	Units	Point Source	Data Type
ns=2;s=Flow/CellName	Flow/CellName	Name of the Flow Cell loaded. E.g. 3mm SS GxP Smart	-	FlowVPX	String
ns=2;s=Flow/SerialNumber	Flow/SerialNumber	Serial Number of the Flow Cell	-	FlowVPX	String
ns=2;s=Flow/CycleCount	Flow/CycleCount	Returns Flow Cell Cycle Count	-	FlowVPX	Int32
ns=2;s=Flow/CycleLimit	Flow/CycleLimit	Returns Max Cycle Count of Flow Cell	-	FlowVPX	Int32
ns=2;s=Flow/FlowCellTypeId	Flow/FlowCellTypeId	Returns an identifier for the type (size & material) of the Flow Cell	-	FlowVPX	Enumeration
ns=2;s=Flow/FlowCellId	Flow/FlowCellId	Once a Flow Cell is added to the database, this ID will be assigned. This is unique to the system.	-	FlowVPX	Int32
ns=2;s=Flow/GoToPosition	Flow/GoToPosition	Sends the Pathlength stepper motor to the given step	-	FlowVPX	MethodNodeClass
ns=2;s=Flow/ClearZeroingData	Flow/ClearZeroingData	Clears the zeroing data.	-	FlowVPX	MethodNodeClass
ns=2;s=Flow/FindZero	Flow/FindZero	Finds Zero Position	-	FlowVPX	MethodNodeClass
ns=2;s=Flow/FindMyHome	Flow/FindMyHome	Finds Home Position	-	FlowVPX	MethodNodeClass
ns=2;s=Flow/WaitForMotor	Flow/WaitForMotor	Waits for Motor	-	FlowVPX	MethodNodeClass
ns=2;s=Flow/GotoFlowCellLoadPosition	Flow/GotoFlowCellLoadPosition	Go to Flow Cell Load Position	-	FlowVPX	MethodNodeClass
ns=2;s=Flow/UpdateFlowCellLocalStats	Flow/UpdateFlowCellLocalStats	Updates the stats on the Flow Cell	-	FlowVPX	MethodNodeClass
ns=2;s=Flow/LoadFlowCell	Flow/LoadFlowCell	Loads the Flow Cell by entering the following information: To load a Flow Cell, set the parameters for Flow/LoadFlowCell method call fc = FlowCellTypeId fcd = Flow Cell ID. once a Flow Cell is inserted to the database, an ID will be inserted. This is unique to the system. uld = User ID of who is doing the loading. Use the same User ID in the System/UserId node did = Device ID, should be the same value as System/DeviceId updateDb = to update database (optional)	-	FlowVPX	MethodNodeClass
ns=2;s=Flow/UnloadFlowCell	Flow/UnloadFlowCell	Unloads the Flow Cell and updates the Db.	-	FlowVPX	MethodNodeClass
ns=2;s=Flow/FlowCell/StartUnload	Flow/FlowCell/StartUnload	Before physically unloading the Flow Cell, set this to TRUE to make sure the device is ready to unload	-	FlowVPX	Boolean
ns=2;s=Flow/FlowCell/FinishUnload	Flow/FlowCell/FinishUnload	After physically unloading the Flow Cell, set this to TRUE to let the system know it is unloaded	-	FlowVPX	Boolean

ns=2;s=Flow/FlowCell/StartLoad	Flow/FlowCell/StartLoad	Before physically loading the Flow Cell, set this to TRUE to make sure the device is ready to load	-	FlowVPX	Boolean
ns=2;s=Flow/FlowCell/FinishLoad	Flow/FlowCell/FinishLoad	After physically loading the Flow Cell, set this to TRUE to let the system know it is loaded. It will verify and take a transmission check. Results of transmission check will be displayed in RawData/Absorbance node	-	FlowVPX	Boolean
ns=2;s=Flow/FlowCell/Message	Flow/FlowCell/Message	Any messages/errors when loading or unloading the Flow Cell from OPC UA will be displayed here	-	FlowVPX	String

## 4. Method

Node ID	OPC Tag	Description	Units	Point Source	Data Type
ns=2;s=Method/ID	Method/ID	Method ID number	-	Both	Int32
ns=2;s=Method/Name	Method/Name	Identifies the run. Users make this entry unique for their day-to-day run at their discretion, but in the database, the field is not unique. This property accepts a string input.	-	Both	String
ns=2;s=Method/SearchMode	Method/SearchMode	Defines the type of method that will run: 0 = Quick, or 1 = Fixed. This property accepts an integer as input.	-	Both	Int32
ns=2;s=Method/AveragingTime	Method/AveragingTime	Averaging time per one absorbance measurement. E.g. Cary 60 takes 80 flashes per second.	seconds	Both	Double
ns=2;s=Method/WavelengthList	Method/WavelengthList	Defines the wavelengths at which the spectrophotometer takes its readings. If a single wavelength is defined, wrap the input (which is usually a double type) in quotes. But if multiple wavelengths are being defined, separate each wavelength with a space ( ).	nm	Both	String
ns=2;s=Method/ExtinctionCoefficientList	Method/ExtinctionCoefficientList	Defines the extinction coefficient of the sample per wavelength. This value allows the software to calculate the concentration for every slope. There must be one extinction coefficient value for each wavelength. Similar to the WavelengthList value, the extinction coefficient value must be wrapped in quotes if using one value or separated with a space for multiple values. If the extinction coefficient is unknown, 0 can be entered as a placeholder value.	ml/(mg*cm)	Both	String

ns=2;s=Method/RepMode	Method/RepMode	<p>Defines how the system performs repetitions of a method. The possible integer inputs for the different modes of method repetition are</p> <ul style="list-style-type: none"> <li>• 0 = Off, will run the method only once;</li> <li>• 1 = Repeat, will run the method to a specified amount (specified by the Repeats property);</li> <li>• 2 = Replicates, similar to Repeat but pauses between runs for the user to change the Fibrette and/or sample before continuing (<b>Note:</b> Not applicable to the FlowVPX System); and</li> <li>• 4 = Continuous, runs the method continuously until the method is manually stopped.</li> </ul>	-	Both	Int32
ns=2;s=Method/RepMode	Method/Repeats	Defines the number of times the method will run. If RepMode is set to 0 or 4 (Off or Continuous), this field should be set to 0. This property accepts an integer input.	-	Both	Int32
ns=2;s=Method/SearchPathlengthList	Method/SearchPathlengthList	Defines the pathlengths at which it attempts to find the specified TargetThresholdAbsorbance. Normally, three pathlength values (double type) are input to have the best outcome.	-	Both	String
ns=2;s=Method/TargetThresholdAbsorbance	Method/TargetThresholdAbsorbance	When SearchMode is set to 0, a value for <b>TargetThresholdAbsorbance</b> must then be defined. This property defines the absorbance value that the Quick Slope algorithm aims for when searching for the most optimal absorbance to start the slope collection.	Abs	Both	Double
ns=2;s=Method/StartingPathlengthsList	Method/StartingPathlengthList	When SearchMode is set to 1, <b>StartingPathlengthsList</b> must then be defined. This informs the VPT instrument at which pathlength to start the slope collection. This property accepts a double type as input.	mm	Both	Double
ns=2;s=Method/StepPathlengthList	Method/StepPathlengthList	Defines the steps from one data point to another. For example, if the value for StartingPathlengthsList is specified to 1.000 mm and the value for StepPathlengthList is specified to 0.001 mm with five data points, the VPT instrument first takes a measurement at 1.000 mm, steps down to 0.999 mm and performs a reading, then to 0.998 mm and performs a reading, and so on until five data points have been collected.	mm	Both	Double

ns=2;s=Method/MultiDatapointsList	Method/MultiDatapointsList	Defines how many readings the Cary 60 spectrophotometer measures to complete one slope. The best practice is to set a lower limit of five data points, but technically only two data points are needed to create a slope between them.	-	Both	Int32
ns=2;s=Method/ScatterMode	Method/ScatterMode	Defines the type of scatter correction (single wavelength or dual wavelength) that will be applied for each slope collection. The acceptable values are 0 = Off, 1 = Single, 2 = Dual.	nm	Both	Int32
ns=2;s=Method/Scatter1WavelengthList	Method/Scatter1WavelengthList	If ScatterMode is set to 1 (Single), a value for <b>Scatter1WavelengthList</b> is required.	nm	Both	Double
ns=2;s=Method/Scatter2WavelengthList	Method/Scatter2WavelengthList	If ScatterMode is set to 2 (Dual), values for <b>Scatter1WavelengthList</b> and <b>Scatter2WavelengthList</b> are both required.	nm	Both	Double
ns=2;s=Method/CollectTopDown	Method/CollectTopDown	Collects Data moving from longer pathlengths to smaller pathlengths	-	Both	Boolean
ns=2;s=Method/CollectionMode	Method/CollectionMode	Determines if the method is for discrete reads (if set to 0) or scan (if set to 1). For example, Quick Slope would be 0 but Quick Survey is 1	-	Both	Int32
ns=2;s=Method/CollectTimeInterval	Method/CollectTimeInterval	Amount of time in between cycles. If set to 0, it is Continuous (ie. it will collect the next cycle right after it finishes the current cycle)	seconds	Both	Int32
ns=2;s=Method/CollectTimeIntervalType	Method/CollectTimeIntervalType	(Unused) Determines if method is continuous or will pause between cycles	-	Both	String
ns=2;s=Method/AlternateCollectDirection	Method/AlternateCollectDirection	Alternates direction of collection (Down-up to up-down)	-	Both	Boolean
ns=2;s=Method/AppID	Method/AppID	(Used only by ViPER Web Interface) Determines which app in ViPER the method belongs to	-	Both	Int32
ns=2;s=Method/BaselineRequired	Method/BaselineRequired	Sets if Baseline is Required into Method	-	Both	Boolean
ns=2;s=Method/IsBaselineCollect	Method/IsBaselineCollect	Collects Baseline	-	Both	Boolean
ns=2;s=Method/BaselineConcentration	Method/BaselineConcentration	Sets Extinction Coefficient to Baseline collected to method	-	Both	Double
ns=2;s=Method/CreatedByID	Method/CreatedByID	Shows the User ID of the user who created the method	-	Both	Int32
ns=2;s=Method/CTechCreatedID	Method/CTechCreatedID	(Unused) Shows if the method was pre-built method by the manufacturer	-	Both	Int32
ns=2;s=Method/DataInterval	Method/DataInterval	Determines the interval between StartWavelength and StopWavelength when scanning	-	Both	Double
ns=2;s=Method/Datapoints	Method/Datapoints	<i>Obsoleted by MultiDatapointsList</i>	-	Both	Int32
ns=2;s=Method/KnownConcentrationList	Method/KnownConcentrationList	Define Concentrations, if known, in order to calculate Extinction Coefficient	-	Both	String
ns=2;s=Method/PathlengthList	Method/PathlengthList	Defines which pathlengths will be used while scanning	-	Both	String

ns=2;s=Method/SampleName	Method/SampleName	Sample Name	-	Both	String
ns=2;s=Method/SampleVesselId	Method/SampleVesselId	ID of Sample Vessel used for measurement (micro, small, PV, etc.)	-	SoloVPE PLUS	Int32
ns=2;s=Method/SavedMethod	Method/SaveMethod	Saves a method in JSON format to DB	-	Both	MethodNodeClass
ns=2;s=Method/Scans	Method/Scans	Applies scans to method.	-	Both	Int32
ns=2;s=Method/StartWavelength	Method/StartWavelength	Start Wavelength of Scan	nm	Both	Double
ns=2;s=Method/StopWavelength	Method/StopWavelength	Stop Wavelength of Scan	nm	Both	Double
ns=2;s=Method/UserResultFormulaList	Method/UserResultsFormulaList	List of premade formulas for User Results	-	Both	String
ns=2;s=Method/UserResultFormula	Method/UserResultFormula	<i>Obsoleted by UserResultsFormulaList.</i> Allows for backwards compatibility with older methods. Creates a node for a user-defined calculation.	-	Both	String
ns=2;s=Method/VPTDeviceTypeID	Method/VPTDeviceTypeID	Defines which device type the method belongs to	-	Both	Int32
ns=2;s=Method/FlowCellTypeID	Method/FlowCellTypeID	Defines which Flow Cell the method was intended for	-	FlowVPX	Int32
ns=2;s=Method/FlowRate	Method/FlowRate	(Unused) Defines the expected flow rate to calculate Chromatography-related values	-	Both	Double
ns=2;s=Method/ElutionThreshold	Method/ElutionThreshold	(Unused) Defines the sensitivity to detect elution during Chromatography	-	Both	Double
ns=2;s=Method/FlowSimDataFile	Method/FlowSimDataFile	(Unused) For development purposes, defines the file path of the simulated dataset	-	Both	String
ns=2;s=Method/OverPathlength	Method/OverPathlength	Defines the backlash correction to ensure unintentional device movement does not affect measurements	-	Both	Double
ns=2;s=Method/ErrorMessage	Method/ErrorMessage	Outputs any error messages encountered during method functions	-	Both	String
ns=2;s=Method/SaveMethod	Method/SaveMethod	Saves a method in JSON format to DB	-	Both	MethodNodeClass
ns=2;s=Method/SaveMethodBool	Method/SaveMethodBool	Creates/Saves a method according to the node values of the Method folder	-	Both	Boolean
ns=2;s=Method/GetMethodsByDateRange	Method/GetMethodsByDateRange	Get a list of methods saved during the specified range	-	Both	MethodNodeClass
ns=2;s=Method/OpenMethod	Method/OpenMethod	Populates the tags from the method of the specified method id	-	Both	MethodNodeClass
ns=2;s=Method/ClearMethod	Method/ClearMethod	Clears all method nodes	-	Both	MethodNodeClass
ns=2;s=Method/ClearMethodBool	Method/ClearMethodBool	Clears all method nodes	-	Both	Boolean
ns=2;s=Method/OpenMethodByIdBool	Method/ OpenMethodByIdBool	Populates the tags from the method of the specified Method/ID node value	-	Both	MethodNodeClass
ns=2;s=Method/IOChannel/IOChannel0Enabled	Method/IOChannel/IOChannel0Enabled	Determines if Analog output for Channel 0 is enabled	-	Both	Boolean
ns=2;s=Method/IOChannel/IOChannel0AnalogType	Method/IOChannel/IOChannel0AnalogType	Determines if the channel will send Voltage (0) or Current (1)	-	Both	Int32
ns=2;s=Method/IOChannel/IOChannel0Channel	Method/IOChannel/IOChannel0Channel	Flag used in software to determine the channel	-	Both	Int32
ns=2;s=Method/IOChannel/IOChannel0StartSignal	Method/IOChannel/IOChannel0StartSignal	Determines the lowest signal (either current or voltage)	-	Both	Double

ns=2;s=Method/IOChannel/IoChannel0EndSignal	Method/IOChannel/IoChannel0EndSignal	Determines the highest signal (either current or voltage)	-	Both	Double
ns=2;s=Method/IOChannel/IoChannel0StartDatum	Method/IOChannel/IoChannel0StartDatum	Determines the lowest expected value for the data type	-	Both	Double
ns=2;s=Method/IOChannel/IoChannel0EndDatum	Method/IOChannel/IoChannel0EndDatum	Determines the highest expected value for the data type	-	Both	Double
ns=2;s=Method/IOChannel/IoChannel0TestSignal	Method/IOChannel/IoChannel0TestSignal	Transmits signal for testing purposes	-	Both	Double
ns=2;s=Method/IOChannel/IoChannel0DatumType	Method/IOChannel/IoChannel0DatumType	Determines the type of data (slope, concentration, or R <sup>2</sup> ) that the I/O will convert to analog signal	-	Both	Int32
ns=2;s=Method/IOChannel/IoChannel1Enabled	Method/IOChannel/IoChannel1Enabled	Determines if Analog output for Channel 1 is enabled	-	Both	Boolean
ns=2;s=Method/IOChannel/IoChannel1AnalogType	Method/IOChannel/IoChannel1AnalogType	Determines if the channel will send Voltage (0) or Current (1)	-	Both	Int32
ns=2;s=Method/IOChannel/IoChannel1Channel	Method/IOChannel/IoChannel1Channel	Flag used in software to determine the channel	-	Both	Int32
ns=2;s=Method/IOChannel/IoChannel1StartSignal	Method/IOChannel/IoChannel1StartSignal	Determines the lowest signal (either current or voltage)	-	Both	Double
ns=2;s=Method/IOChannel/IoChannel1EndSignal	Method/IOChannel/IoChannel1EndSignal	Determines the highest signal (either current or voltage)	-	Both	Double
ns=2;s=Method/IOChannel/IoChannel1StartDatum	Method/IOChannel/IoChannel1StartDatum	Determines the lowest expected value for the data type	-	Both	Double
ns=2;s=Method/IOChannel/IoChannel1EndDatum	Method/IOChannel/IoChannel1EndDatum	Determines the highest expected value for the data type	-	Both	Double
ns=2;s=Method/IOChannel/IoChannel1TestSignal	Method/IOChannel/IoChannel1TestSignal	Transmits signal for testing purposes	-	Both	Double
ns=2;s=Method/IOChannel/IoChannel1DatumType	Method/IOChannel/IoChannel1DatumType	Determines the type of data (slope, concentration, or R <sup>2</sup> ) that the I/O will convert to analog signal	-	Both	Int32
ns=2;s=Method/GenomeTiter/IsConcentrationOptimization	Method/GenomeTiter/IsConcentrationOptimization	(Unused) For Gene Therapy application	-	Both	Boolean
ns=2;s=Method/GenomeTiter/ExtinctionCoefficientListMatrix	Method/GenomeTiter/ExtinctionCoefficientListMatrix	(Unused) For Gene Therapy application	-	Both	String
ns=2;s=Method/GenomeTiter/Ecc260	Method/GenomeTiter/Ecc260	Extinction Coefficient of Capsid at 260nm	-	Both	Float
ns=2;s=Method/GenomeTiter/Ecc280	Method/GenomeTiter/Ecc280	Extinction Coefficient of Capsid at 280nm	-	Both	Float
ns=2;s=Method/GenomeTiter/Ecd260	Method/GenomeTiter/Ecd260	Extinction Coefficient of Genome at 260nm	-	Both	Float
ns=2;s=Method/GenomeTiter/Ecd280	Method/GenomeTiter/Ecd280	Extinction Coefficient of Genome at 280nm	-	Both	Float
ns=2;s=Method/GenomeTiter/AggregateMode	Method/GenomeTiter/AggregateMode	Sets additional wavelength (320nm) for aggregate measurement in method	-	Both	Boolean
ns=2;s=Method/GenomeTiter/SearchWavelength	Method/GenomeTiter/SearchWavelength	Creates node for Method wavelength	nm	Both	Int32
ns=2;s=Method/Adc/AntibodyEc1	Method/Adc/AntibodyEc1	Creates node for Method extinction coefficient for antibody 1	ml/(mg*cm)	Both	Float
ns=2;s=Method/Adc/AntibodyEc2	Method/Adc/AntibodyEc2	Creates node for Method extinction coefficient for antibody 2	ml/(mg*cm)	Both	Float
ns=2;s=Method/Adc/DrugEc1	Method/Adc/DrugEc1	Creates node for Method extinction coefficient for drug 1	ml/(mg*cm)	Both	Float
ns=2;s=Method/Adc/DrugEc2	Method/Adc/DrugEc2	Creates node for Method extinction coefficient for drug 2	ml/(mg*cm)	Both	Float

ns=2;s=Method/Adc/AntibodyMolarMass	Method/Adc/AntibodyMolarMass	The Antibody Molar Mass used to convert the Antibody Concentration from (mol/L) to (mg/ml) or from (mg/ml) to (mol/L)	g/mol	Both	Float
ns=2;s=Method/Adc/DrugMolarMass	Method/Adc/DrugMolarMass	The Drug Molar Mass used to convert the Drug Concentration from (mol/L) to (mg/ml) or from (mg/ml) to (mol/L)	g/mol	Both	Float
ns=2;s=Method/Adc/ExtCoefUnits	Method/Adc/ExtCoefUnits	Determines if the ADC Extinction Coefficients will be in (ml/(mg*cm)) (0) or (M <sup>-1</sup> cm <sup>-1</sup> ) (1)	-	Both	Int32
ns=2;s=Method/AcceptanceCriteria/AddAcceptanceCriteria	Method/AcceptanceCriteria/AddAcceptanceCriteria	Creates a new empty Acceptance Criteria Node node.	-	Both	MethodNodeClass
ns=2;s=Method/AcceptanceCriteria/AddAcceptanceCriteriaNodeBool	Method/AcceptanceCriteria/AddAcceptanceCriteriaNodeBool	Creates a new empty Acceptance Criteria node.	-	Both	Boolean
ns=2;s=Method/Search/MethodID	Method/Search/MethodID	Input argument for the GetMethodByldBool operation	-	Both	Int32
ns=2;s=Method/Search/MethodName	Method/Search/MethodName	Input argument for the GetMethodsByNameBool operation	-	Both	String
ns=2;s=Method/Search/StartDate	Method/Search/StartDate	First input argument for the GetMethodsByDateRangeBool. (e.g. MM/dd/YYYY)	-	Both	String
ns=2;s=Method/Search/EndDate	Method/Search/EndDate	Second input argument for the GetMethodsByDateRangeBool. (e.g. MM/dd/YYYY)	-	Both	String
ns=2;s=Method/Search/Results	Method/Search/Results	Json String result for methods queried by GetMethodsByDateRangeBool, GetMethodsByNameBool, GetMethodsLast25CreatedBool	-	Both	String
ns=2;s=Method/Search/ErrorMessage	Method/Search/ErrorMessage	Returns any error messages encountered during a search query	-	Both	String
ns=2;s=Method/Search/GetMethodsByDateRangeBool	Method/Search/GetMethodsByDateRangeBool	When set to true, will look up the values in Method/Search/StartDate and Method/Search/EndDate and find the methods in that range into the Method/Search/Results node	-	Both	Boolean
ns=2;s=Method/Search/GetMethodByldBool	Method/Search/GetMethodByldBool	When set to true, will look up the value in Method/Search/MethodID and return the method corresponding to that ID into the Method/Search/Results node	-	Both	Boolean
ns=2;s=Method/Search/GetMethodsByNameBool	Method/Search/GetMethodsByNameBool	When set to true, will look up the value in Method/Search/MethodName and return the methods containing that string into the Method/Search/Results node	-	Both	Boolean
ns=2;s=Method/Search/GetMethodsLast25CreatedBool	Method/Search/GetMethodsLast25CreatedBool	When set to true, will return the last 25 methods created into the Method/Search/Results node	-	Both	Boolean
ns=2;s=Method/Search/ClearSearchBool	Method/Search/ClearSearchBool	Clears all Method/Search nodes	-	Both	Boolean

## 5. RawData

Node ID	OPC Tag	Description	Units	Point Source	Data Type
ns=2;s=RawData/ID	RawData/ID	Uniquely identifies the raw data (pathlength, absorbance, etc.) with an ID	-	Both	Int32
ns=2;s=RawData/CycleCountId	RawData/CycleCountId	Groups raw value ids into a specific cycle count.	-	Both	Int32
ns=2;s=RawData/Wavelength	RawData/Wavelength	Displays wavelength of raw datapoint.	nm	Both	Float
ns=2;s=RawData/Pathlength	RawData/Pathlength	Displays Pathlength of raw datapoint.	mm	Both	Float
ns=2;s=RawData/Absorbance	RawData/Absorbance	Displays Absorbance value of raw datapoint.	Abs	Both	Float
ns=2;s=RawData/DateAcquired	RawData/DateAcquired	Record of date acquired for each raw datapoint (pathlength, absorbance, wavelength).	-	Both	String
ns=2;s=RawData/ReplicateID	RawData/ReplicateID	Dictates the current repetition ID this data is associated with.	-	Both	Int32
ns=2;s=RawData/SeriesTag	RawData/SeriesTag	Series Tag of the raw data (it is unique per cycle)	-	Both	String
ns=2;s=RawData/GetRawInfo	RawData/GetRawInfo	Takes RawDataId input into node and provides specific information such as wavelength, pathlength, absorbance, date acquired, etc.	-	Both	MethodNodeClass

## 6. System


Node ID	OPC Tag	Description	Units	Point Source	Data Type
ns=2;s=System/UserId	System/UserId	UserId is a mandatory node to filled in to know which user started a method	-	Both	Int32
ns=2;s=System/DeviceId	System/DeviceId	Device ID for FlowVPX	-	Both	Int32
ns=2;s=System/SoftwareVersion	System/SoftwareVersion	ViPER Software Version	-	Both	String
ns=2;s=System/FirmwareVersion	System/FirmwareVersion	Firmware version of FlowVPX	-	Both	String
ns=2;s=System/GetUsers	System/GetUsers	Get a list of users (Item1 = Id, Item2 = Username)	-	Both	MethodNodeClass
ns=2;s=System/GetDevices	System/GetDevices	Get a list of devices (Item1 = Id, Item2 = Serial Number)	-	Both	MethodNodeClass
ns=2;s=System/GetFlowCellTypes	System/GetFlowCellTypes	Get a list of Flow Cell Types (Item1 = FlowCellTypeID, Item2 = CellName)	-	Both	MethodNodeClass
ns=2;s=System/GetFlowCells	System/GetFlowCells	Get a list of Flow Cell by Type (Item1 = ID, Item2 = Serial Number)	-	Both	MethodNodeClass


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