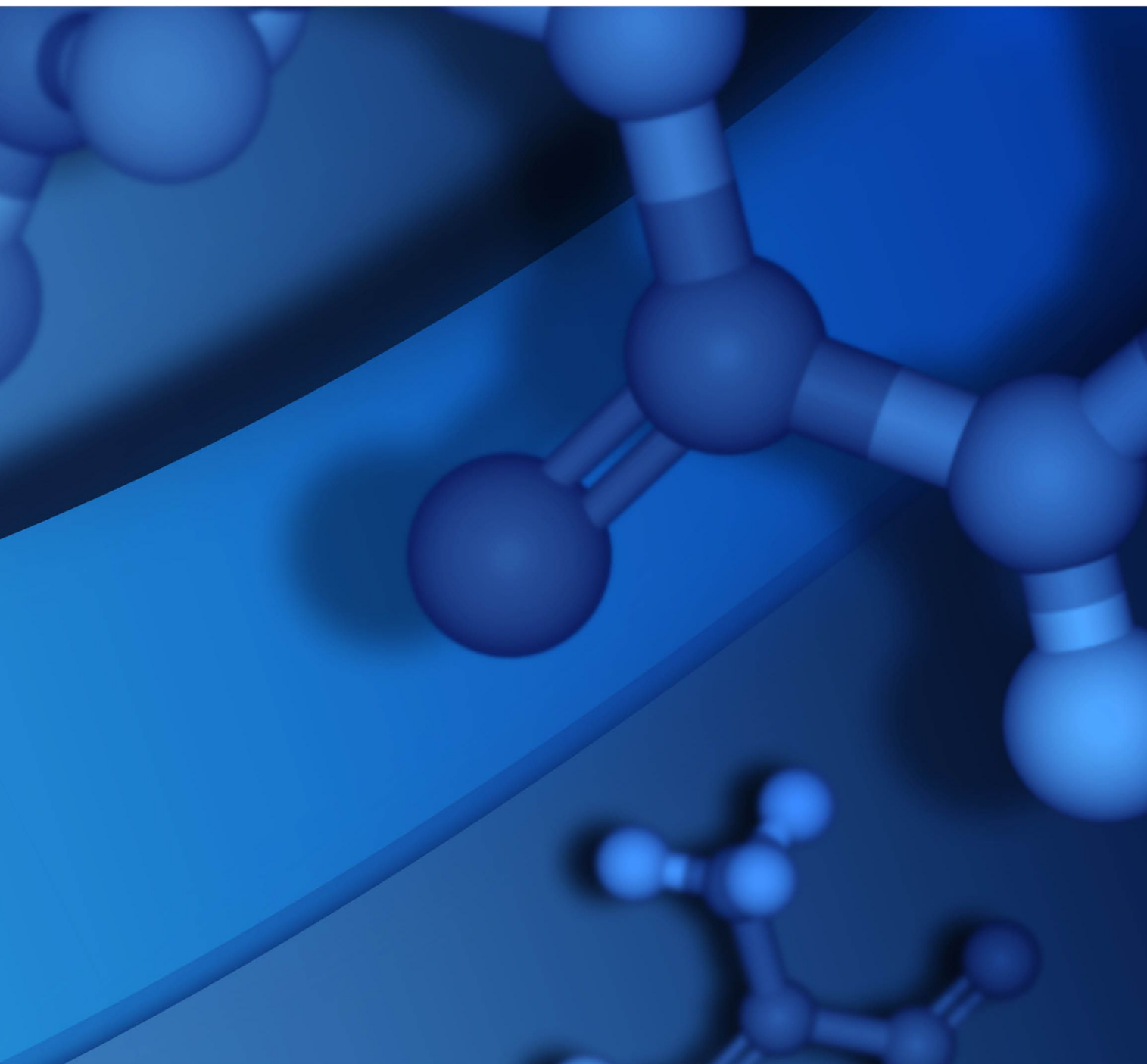


# DEVELOPERS GUIDE

BIOVIA ASSAY 2018



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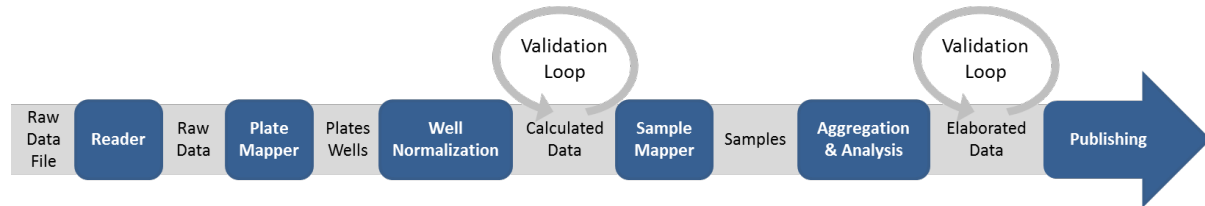
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## Introduction to the Assay Developer Guide

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BIOVIA Assay is a plate-based assay data capture and analysis platform. It helps scientists to automate and standardize the acquisition, validation and publishing of results in a shared workspace. Assay is workflow-based to guide the user through each step of the analysis.

The following is a description of the analysis workflow:



**Reader:** Capture direct output of plate readers and manage data complexity.

**Plate Mapper:** Associate barcode information to plate data.

**Well Normalization:** Transform raw data into normalized results and generate statistics.

**Validation:** Use visual analytics capabilities to exclude outliers on control wells and identify deviation patterns.

**Sample Mapper:** Associate samples IDs and doses to results.

**Aggregation & Analysis:** Manage data aggregation and results consolidation, such as Average, Fitting for IC50 determination.

**Publishing:** Map protocol information and publish results on central repository.

## Customize Assay Resources

---

You can customize BIOVIA Assay by creating custom resources. Create the custom resource using the supported technology: Oracle Package, Pipeline Pilot, Spotfire or R, and then register it into the Administration Tab of Assay.

### Customizable Resources

#### Readers

Readers are used to parse the file output from the plate readers and create the plates and wells in BIOVIA Assay. Assay is installed with a set of Readers that cover the most common formats of plate reader.

#### Normalization Procedures

Normalize raw data using one or several Normalization Processes. BIOVIA Assay is installed with a set of Normalization Procedures that can be enabled/disabled by setting the `Is hidden` status to `Yes` or `No`.

#### Sample and Reference Analysis Procedures

After the Sample or Reference aggregation, perform data analysis on each aggregated group to compute elaborated data. Custom Sample and Reference Analysis Procedures can be added to BIOVIA Assay.

#### Visualization Templates

Visualization Templates are used to display plates or wells data to the user, for a specific visualization step, such as *Validation*, *Reference* or *Sample Analysis*, or to analyze a set of runs (Cross Run functionality). Data can be displayed as a flat or plate-shaped report depending of the Visualization Template and Step. Several visualization templates are available by default on first installation.

#### Publishers

Publishers allow users who have an `ASSAY_PUBLISHER_PROFILE` to publish elaborated data in central repository. Two publishers are available in Assay:

- Warehouse
- Biovia ScienceCloud Project Data.

Publishers can be enabled or disabled by setting `Is hidden` status to `Yes` or `No`.

**Note:** Warehouse publisher is hidden by default. In order to make it available to the users, Warehouse must be installed and `Is hidden` status has to be set to `Yes`. Biovia ScienceCloud Project Data publisher is available on scienceCloud.

### Create Custom Resource

The following technologies are available to create custom resources:

- Oracle Package: packaged PL/SQL function or procedure
- Pipeline Pilot Protocol
- Spotfire Template
- R script

Every technology is not available for each resource. Here are the technologies available to develop each resource:

|                               | Oracle Package | Pipeline Pilot Protocol | Spotfire Template | R Script |
|-------------------------------|----------------|-------------------------|-------------------|----------|
| Readers                       | Yes            | Yes                     | No                | No       |
| Normalization Procedures      | Yes            | Yes                     | No                | No       |
| Sample and Reference Analysis | Yes            | Yes                     | No                | Yes      |
| Visualization Templates       | No             | Yes                     | Yes               | No       |
| Publishers                    | No             | Yes                     | No                | No       |

## Register Custom Resource

To register a custom component into BIOVIA Assay, a connected user must have the ASSAY\_ADMINISTRATOR\_PROFILE (i.e. ASSAY\_SUPER\_USER or ASSAY\_ADMINISTRATOR users).

For more information on how to register a component, see the section dedicated to the resource:

- [Register New Normalization Procedure in Assay](#)
- [Register New Publisher in Assay](#)
- [Register New Reader in Assay](#)
- [Register New Sample and Reference Analysis Procedure in Assay](#)
- [Register New Visualization Template in Assay](#)

## Assay Configuration

---

### Pipeline Pilot Server

The Pipeline Pilot Server must be configured in BIOVIA Assay.

Contact your Assay administrator or refer to the *BIOVIA Assay Installation Guide*.

### TIBCO Spotfire Server

The TIBCO Spotfire server must to be configured in BIOVIA Assay.

Contact your Assay administrator or refer to *BIOVIA Assay Installation Guide*.

### Daughter Application Concept

Some Assay resources are open to Oracle customization. A **Daughter Application** is made of a dedicated ORACLE schema that consumes the Assay API represented by ASA\_WS\_\* packages and views. BIOVIA recommends an Oracle developer perform the following:

The following Oracle schema must be registered after new Assay install, that is after the DNG\_ASSAY Oracle schema has been created.

- Grant ORACLE schema named `<tenant>_DNG_ASSAY` to execute the package that implements a custom PROCEDURE in the daughter application schema:

```
GRANT EXECUTE ON <daughter_application>.<package_name> TO <tenant>_DNG_ASSAY
```

- Create SYNONYM on ORACLE schema named `<tenant>_DNG_ASSAY` from package that implement custom PROCEDURE in daughter application schema:

```
CREATE OR REPLACE SYNONYM <package_name>  
FOR <daughter_application>.<package_name>
```



## Readers

---

### Create Custom Reader Using Pipeline Pilot Protocol

Default reader protocols are provided within the BIOVIA Assay collection in Pipeline Pilot at the following path: `Protocols/Discngine/Assay/Readers/`

A Reader protocol needs two main components:

- The component *Discngine Assay Get Raw Data File* gets raw data from Assay database.
- The component *Discngine Assay Insert Raw Data* inserts data from files in the Assay database and creates datapoints.

The file parser must be wrapped into a subprotocol and implemented with the *run to completion* mode.

Once the protocol is created in Pipeline Pilot, register it in Assay as a Reader. For More information, see [Register new Reader in Assay](#).

### Create Custom Reader Using Daughter Application

Create package.procedure in your custom schema. The procedure inserts rows in the `asa_datapoint` table:

| COLUMN_NAME           | DATA_TYPE           | NULLABLE | DATA_DEFAULT | COLUMN_ID | COMMENTS |
|-----------------------|---------------------|----------|--------------|-----------|----------|
| 1 DATAPOINT_ID        | NUMBER (38,0)       | No       | (null)       | 1 (null)  |          |
| 2 LOGICAL_PLATE_INDEX | NUMBER (38,0)       | No       | (null)       | 2 (null)  |          |
| 3 PLATE_NAME          | VARCHAR2 (30 BYTE)  | No       | (null)       | 3 (null)  |          |
| 4 ROW_INDEX           | NUMBER (38,0)       | No       | (null)       | 4 (null)  |          |
| 5 COLUMN_INDEX        | NUMBER (38,0)       | No       | (null)       | 5 (null)  |          |
| 6 READ_VALUE          | NUMBER              | Yes      | (null)       | 6 (null)  |          |
| 7 RUN_ID              | NUMBER (38,0)       | No       | (null)       | 7 (null)  |          |
| 8 VALUE_NAME          | VARCHAR2 (400 BYTE) | No       | 'READOUT'    | 8 (null)  |          |
| 9 IS_PLATE_MAPPED     | VARCHAR2 (1 BYTE)   | Yes      | 'N'          | 9 (null)  |          |
| 10 IS_WELL_MAPPED     | VARCHAR2 (1 BYTE)   | Yes      | 'N'          | 10 (null) |          |

For kinetic data, your procedure inserts rows in the `asa_datapoint_k` table and can also insert into the `asa_datapoint` table.

| COLUMN_NAME           | DATA_TYPE           | NULLABLE | DATA_DEFAULT | COLUMN_ID | COMMENTS |
|-----------------------|---------------------|----------|--------------|-----------|----------|
| 1 DATAPOINT_K_ID      | NUMBER (38,0)       | No       | (null)       | 1 (null)  |          |
| 2 LOGICAL_PLATE_INDEX | NUMBER (38,0)       | No       | (null)       | 2 (null)  |          |
| 3 PLATE_NAME          | VARCHAR2 (30 BYTE)  | No       | (null)       | 3 (null)  |          |
| 4 ROW_INDEX           | NUMBER (38,0)       | No       | (null)       | 4 (null)  |          |
| 5 COLUMN_INDEX        | NUMBER (38,0)       | No       | (null)       | 5 (null)  |          |
| 6 TIME_INDEX          | NUMBER (38,0)       | No       | (null)       | 6 (null)  |          |
| 7 TIME_VALUE          | NUMBER              | No       | (null)       | 7 (null)  |          |
| 8 TIME_UNIT_ID        | NUMBER (38,0)       | Yes      | (null)       | 8 (null)  |          |
| 9 READ_VALUE          | NUMBER              | Yes      | (null)       | 9 (null)  |          |
| 10 RUN_ID             | NUMBER (38,0)       | No       | (null)       | 10 (null) |          |
| 11 VALUE_NAME         | VARCHAR2 (400 BYTE) | No       | 'READOUT'    | 11 (null) |          |
| 12 IS_PLATE_MAPPED    | VARCHAR2 (1 BYTE)   | Yes      | 'N'          | 12 (null) |          |
| 13 IS_WELL_MAPPED     | VARCHAR2 (1 BYTE)   | Yes      | 'N'          | 13 (null) |          |

To generate `datapoint_id` or `datapoint_k_id` (primary key), use `ASA_DATAPOINT_SQ` sequence or `ASA_DATAPOINT_K_SQ` sequence respectively.

## Register New Reader in Assay

To register a new Reader in BIOVIA Assay, login to the application as a user who is a member of the `ASSAY_ADMINISTRATOR_PROFILE` user group.

1. Click on the **Administration** tab.
2. Select **Readers** from the *Administration Utilities* menu.
3. Click **Create** to add a new Reader.
4. On the *Create or Edit* page, fill in the form as described below.
  - Reader Name: The name of the reader
  - **Resource Path**: The path of the reader
  - **Plate Format**: The plate format supported by the reader
  - **Is Hidden**: If the reader is hidden to end users or not
  - **Process type**: The technology used to develop the reader
  - **Kinetic**: If the reader handles kinetic data or not
  - **Delimiter**: the file delimiter (not shown for Pipeline Pilot/Pipeline Pilot interactive process type)
  - **Description**: The description of the readerClick **Create** to save the information.

## Delete Reader from Assay

To delete a Reader from BIOVIA Assay, go to *Administration > Administration utilities > Readers* and click on the name of the Reader you want to delete.

Click **Delete**.

**Note:** A reader can't be deleted if it is used in at least one run. The reader's implementation is still available in Pipeline Pilot server or in the oracle schema of the daughter application.

## Normalization Procedures

---

### Create Custom Normalization Procedure Using Pipeline Pilot Protocol

Default Normalization protocols are provided within the BIOVIA Assay collection in Pipeline Pilot at: [Protocols/Discngine/Assay/Calculation/](#).

To create a Normalization protocol, use the following components:

- *Discngine Assay Get Well*: normalizes the raw well data
- *Discngine Assay Insert Plate Data*: inserts the calculated data for plates into the appropriate table
- *Discngine Assay Insert Well Calculated Data*: inserts the calculated data for wells into the appropriate table

Once the protocol is created in Pipeline Pilot, it must be registered in Assay. For more information, see [Register New Normalization Procedure in Assay](#).

### Create Custom Normalization Procedure Using Daughter Application

Create the package .procedure in your custom schema. The procedure must have the following signature:

```
PROCEDURE <my_procedure>(
    val_run_id    IN asa_ws_run_vw.run_id%TYPE,
    val_plate_id  IN asa_ws_plate_vw.plate_id%TYPE,
    val_run_calc_id IN asa_ws_run_calc_vw.run_calc_id%TYPE);
```

The value <val\_run\_calc\_id> allows you to get the calculation parameters. For example to get the parameter type *readout*:

```
SELECT b.parameter_value, a.calc_procedure_alias calc_alias
FROM asa_ws_run_calc_vw a
JOIN ASA_WS_RUN_CALC_PARAMETER_VW b ON a.run_calc_id = b.run_calc_
id
WHERE a.run_id = val_run_id
AND parameter_type_name = 'readout'
AND a.run_calc_id = val_run_calc_id;
```

- If the parameter type is *readout*, your procedure gets information from the ASA\_WS\_WELL\_RAW\_DATA\_VW and ASA\_WS\_WELL\_CALC\_DATA\_VW views and filters on the VALUE\_NAME column.
- If the parameter type is *kinetic\_readout*, your procedure gets information from the ASA\_WS\_WELL\_RAW\_DATA\_K\_VW table.
- If the parameter type is *well\_type*, your procedure gets information the ASA\_WS\_WELL\_TYPE\_VW view.

Other parameter types (*number*, *text*) can be used as they are.

Output is rows inserted into the `asa_well_calc_data` table:

| COLUMN_NAME         | DATA_TYPE          | NULLABLE | DATA_DEFAULT | COLUMN_ID | COMMENTS |
|---------------------|--------------------|----------|--------------|-----------|----------|
| 1 WELL_ID           | NUMBER(38,0)       | No       | (null)       | 1         | (null)   |
| 2 VALUE             | BINARY_FLOAT       | Yes      | (null)       | 2         | (null)   |
| 3 READ_INDEX        | NUMBER(38,0)       | No       | 1            | 3         | (null)   |
| 4 VALUE_NAME        | VARCHAR2(400 BYTE) | No       | (null)       | 4         | (null)   |
| 5 RUN_ID            | NUMBER(38,0)       | No       | (null)       | 5         | (null)   |
| 6 VALUE_DESC        | VARCHAR2(400 BYTE) | Yes      | (null)       | 6         | (null)   |
| 7 WELL_CALC_DATA_ID | NUMBER(38,0)       | No       | (null)       | 7         | (null)   |

To generate well\_calc\_data\_id (primary key), use the sequence ASA\_WELL\_CALC\_DATA\_SEQ.

## Register New Normalization Procedure in Assay

To register a new Normalization Procedure in BIOVIA Assay, log in to the application with a user account that is a member of the ASSAY\_ADMINISTRATOR\_PROFILE user group.

1. Click on the **Administration** tab.
2. Select **Normalization Procedures** from the *Administration Utilities* menu.
3. Click **Create** to register a new Normalization Procedure.
4. On the *Create or Edit* page, fill in the form as described below for each step of the wizard.
  - a. Define the new normalization procedure.
    - **Name:** The name of the normalization procedure
    - **Alias:** The alias of the normalization procedure
    - **ProcessType:** The technology used to develop the normalization procedure
    - **Kinetic:** If the normalization procedure handles kinetic data or not
    - **Resource Path:** The path of the normalization procedure
    - **Description:** The description of the normalization procedure
    - **Is Hidden:** If the normalization procedure is hidden to end users or not
  - b. Select the well types on which the normalization procedure will be applied.
  - c. Define the parameters of the Normalization procedure.
  - d. Check and save the Normalization procedure.

## Delete Normalization Procedure from Assay

To delete a Normalization Procedure from BIOVIA Assay:

1. Go to *Administration > Administration utilities > Normalization Procedures*.
2. Click the summary icon of the Normalization Procedure you want to delete.
3. Navigate to the summary page, then click **Delete**.

**Note:** A Normalization Procedure cannot be deleted if it is used in at least one run. To remove it, change the Normalization Procedure used in each run before deleting it. The procedure is still available in Pipeline Pilot Server or in the Oracle schema of the daughter application.

## Sample and Reference Analysis Procedures

---

### Create Custom Sample and Reference Analysis Procedure Using Pipeline Pilot Protocol

A protocol is dedicated to sample analysis step or reference analysis step.

The Pipeline Pilot protocol must have the following parameters:

- Data Source
- Discngine Assay Run ID
- Parameter Set ID

### Create Custom Sample and Reference Analysis Procedure Using Daughter Application

Create package . procedure in your custom schema. Your procedure must get information from asa\_ws\_agg\_source\_result\_vw view:

| ◇ COLUMN_NAME       | ◇ DATA_TYPE       | ◇ NULLABLE | DATA_DEFAULT | ◇ COLUMN_ID | ◇ COMMENTS |
|---------------------|-------------------|------------|--------------|-------------|------------|
| 1 AGG_SERIE_ID      | NUMBER(38)        | No         | (null)       | 1 (null)    |            |
| 2 AGG_GROUP_ID      | NUMBER(38)        | No         | (null)       | 2 (null)    |            |
| 3 AGG_GROUP_NAME    | VARCHAR2(400)     | No         | (null)       | 3 (null)    |            |
| 4 AGG_GROUP_DESC    | VARCHAR2(400)     | Yes        | (null)       | 4 (null)    |            |
| 5 AGG_SERIE_NAME    | VARCHAR2(240)     | No         | (null)       | 5 (null)    |            |
| 6 AGG_SERIE_DESC    | VARCHAR2(240)     | Yes        | (null)       | 6 (null)    |            |
| 7 AGG_SERIE_COMMENT | VARCHAR2(4000)    | Yes        | (null)       | 7 (null)    |            |
| 8 AGG_SERIE_INDEX   | NUMBER(38)        | No         | (null)       | 8 (null)    |            |
| 9 IS_REF            | VARCHAR2(2)       | No         | (null)       | 9 (null)    |            |
| 10 SOURCE_RESULT_ID | NUMBER(38)        | No         | (null)       | 10 (null)   |            |
| 11 RESPONSE         | BINARY_FLOAT()    | No         | (null)       | 11 (null)   |            |
| 12 DOSE             | NUMBER            | Yes        | (null)       | 12 (null)   |            |
| 13 DOSE_UNIT_ID     | NUMBER(38)        | Yes        | (null)       | 13 (null)   |            |
| 14 DOSE_UNIT        | VARCHAR2(20 CHAR) | Yes        | (null)       | 14 (null)   |            |
| 15 IS_VALID         | VARCHAR2(1)       | No         | (null)       | 15 (null)   |            |
| 16 IS_SELECTED      | VARCHAR2(1)       | No         | (null)       | 16 (null)   |            |
| 17 CREATED_BY       | VARCHAR2(240)     | No         | (null)       | 17 (null)   |            |
| 18 CREATED_DATE     | DATE              | No         | (null)       | 18 (null)   |            |
| 19 UPDATED_BY       | VARCHAR2(240)     | No         | (null)       | 19 (null)   |            |
| 20 UPDATED_DATE     | DATE              | No         | (null)       | 20 (null)   |            |
| 21 RUN_ID           | NUMBER(38)        | No         | (null)       | 21 (null)   |            |
| 22 SAMPLE_NAME      | VARCHAR2(400)     | Yes        | (null)       | 22 (null)   |            |
| 23 SOLVENT_NAME     | VARCHAR2(80)      | Yes        | (null)       | 23 (null)   |            |
| 24 WEIGHT           | NUMBER            | No         | (null)       | 24 (null)   |            |
| 25 WELL_ID          | NUMBER(38)        | Yes        | (null)       | 25 (null)   |            |

And insert rows in `asa_agg_final_result` table:

|    | COLUMN_NAME         | DATA_TYPE           | NULLABLE | DATA_DEFAULT |
|----|---------------------|---------------------|----------|--------------|
| 1  | FINAL_RESULT_NAME   | VARCHAR2 (70 BYTE)  | No       | (null)       |
| 2  | FINAL_RESULT_DESC   | VARCHAR2 (240 BYTE) | No       | (null)       |
| 3  | VALUE_NUMERIC       | BINARY_FLOAT        | Yes      | (null)       |
| 4  | CREATED_BY          | VARCHAR2 (240 BYTE) | No       | USER         |
| 5  | CREATED_DATE        | DATE                | No       | SYSDATE      |
| 6  | UPDATED_BY          | VARCHAR2 (240 BYTE) | No       | USER         |
| 7  | UPDATED_DATE        | DATE                | No       | SYSDATE      |
| 8  | AGG_SERIE_ID        | NUMBER (38,0)       | No       | (null)       |
| 9  | RUN_ID              | NUMBER (38,0)       | No       | (null)       |
| 10 | FINAL_RESULT_ID     | NUMBER (38,0)       | No       | (null)       |
| 11 | VALUE_TEXT          | VARCHAR2 (4000 B... | Yes      | (null)       |
| 12 | RUN_POST_TRANSFO_ID | NUMBER (38,0)       | No       | (null)       |

To generate `final_result_id` (primary key), use the sequence `ASA_AGG_FINAL_RESULT_SQ`.

## Register New Sample and Reference Analysis Procedure in Assay

To register a new Sample and Reference Analysis Procedure in Assay, log in to the application with a user account that is a member of the `ASSAY_ADMINISTRATOR_PROFILE` user group.

1. Click the **Administration** tab.
2. Select **Sample and Reference Analysis Procedures** from the *Administration Utilities* menu.
3. Click **Create** to register a new Sample and Reference Analysis Procedure.
4. Fill in the form as described below for each step of the wizard.
  - a. Define the new Analysis procedure.
    - **Name:** The name of the Sample and Reference Analysis Procedure
    - **Resource Path:** The path of the Sample and Reference Analysis Procedure
    - **Step:** The analysis step where the Sample and Reference Analysis Procedure can be processed
    - **Process type:** The technology used to develop the Sample and Reference Analysis Procedure
    - **Description:** The description of the Sample and Reference Analysis Procedure
  - b. Click on **Create** button to save the information.
  - c. (Optional) Define the input parameters of the Analysis procedure. Click **Next** to continue.
  - d. (Optional) Define the output parameters of the Analysis procedure. Click **Next** to continue.
  - e. Check and save the Normalization procedure. Click **Create**.

## Delete Sample and Reference Analysis Procedure from Assay

To delete a Sample and Reference Analysis Procedure from Assay:

1. Go to *Administration > Administration utilities > Sample and Reference Analysis Procedures*.
2. Click the name of the Analysis Procedure you want to delete.
3. In the Edit window that opens, click **Delete**.

**Note:** The Sample and Reference Analysis Procedure cannot be deleted if it is used in at least one run. To remove it, change the Sample and Reference Analysis Procedure used in each run before deleting it. The Sample and Reference Analysis Procedure is still available in the Pipeline Pilot Server or in the Oracle schema of the daughter application.

## Visualization Templates

---

To create the appropriate template for data visualization, the step is required:

- Validation
- Reference Analysis
- Sample Analysis

The elements used to create a new template are different for each step.

For Cross Run visualization templates, you can use any element.

### Create Custom Visualization Template Using Pipeline Pilot Protocol

Default visualization protocols are provided within the BIOVIA Assay collection in Pipeline Pilot at the following path: `Protocols/Discngine/Assay/Viewers/`.

#### Well Validation Visualization

Several components are available in the Pipeline Pilot Assay Collection to get data from a run.

For well validation visualization, the parameter collected and set by the well validation protocol is *Dng\_AssayRunID*, or *Sci\_UniqueWellID* for PDA collection.

A visualization protocol for this step needs three main components:

- *Discngine Assay Get Well* gets data from Assay database.
- The *Data Connector* listens to the selection.
- The *Discngine Assay Web Connector* is used to transmit the selection. (Optional): If this component is missing, users can see the visualization but cannot interact with Assay through it.

The visualization protocol is composed of these three components, together with other components that you may wish to have in your visualization. These components expose the `well_id` from Assay application.

Once the protocol is created in Pipeline Pilot, register it in Assay as a visualization template. For more information, see [Register New Visualization Template in Assay](#).

#### Sample Analysis Visualization

For the well reference/sample analysis step, the parameter collected and set, is *Dng\_AssayRunID*

Components used to get the appropriate data are:

- *Discngine Assay Get Final Data*
- *Discngine Assay Get Validated Data*

These components expose the `source_result_id` which is listened to and set in Assay application.

To adapt the visualization according to the Reference Analysis step or to the Sample Analysis step, add a filter component after the above components to filter out incorrect data. Test if the property `Dng_AssayIsReference` is true or false

The *Data Connector* component and the *Discngine Assay Web Connector* component shown above must be added, the first one in order to listen to the user selection and the last one to transmit the selection.

Once the protocol is created in Pipeline Pilot, register it in Assay as a visualization template. For more information, see [Register New Visualization Template in Assay](#).



## Create Custom Visualization Template Using TIBCO Spotfire Analyst

To create new TIBCO Spotfire template:

1. Open Spotfire analyst
2. Add data tables and custom visualization. The data tables available to build visualization are:

| Data Table        | Usual Step                |
|-------------------|---------------------------|
| well_data         | Well Validation           |
| well_kinetic_data | Well Validation           |
| plate_data        | Well Validation           |
| validated_data    | Reference/Sample Analysis |
| aggregated_data   | Reference/Sample Analysis |

you can also to import a dxp file.

The template must be registered in TIBCO Spotfire Analyst library to be used in Assay.

Once the template is created in TIBCO Spotfire Analyst, register it in Assayas a visualization template. For more information, see [Register New Visualization Template in Assay](#).

## Register New Visualization Template in Assay

To register a Pipeline Pilot protocol or a Spotfire template in Assay application, you need to declare the protocol or library path in Assay application.

Path example:

- Pipeline Pilot: `Protocols/Discngine/Assay/Viewers/<Protocol Name>`
- TIBCO Spotfire: `DNG_ASSAY/<LocalPrefix>/TEMPLATES/<Library Template Name>`

To add a new visualization template, log in to the application with a user account that is a member of the ASSAY\_ADMINISTRATOR\_PROFILE user group. :

1. Click the **Administration** tab.
2. Select **Visualization Templates** from the *Administration Utilities* menu.
3. Click **Create** to register a new visualization.
4. On the *Create or Edit* page, fill in the form as described below.
  - **Resource Path:** The path of the visualization
  - **Process type:** Select Pipeline Pilot interactive if the visualization is a Pipeline Pilot protocol or TIBCO Spotfire if the visualization is Spotfire template
  - **Visualization Step:** Select the step at which the visualization will be used (Validation, Sample Analysis or Reference Analysis step, or Cross Run Analysis option)
  - **Is default:** Select “Yes” if you want this visualization to be the default visualization for the step and process type define above
  - **Show Validation Region:** Select No if you want to allow users to do validation/invalidation with the interactive visualization template in the run. This will hide validation and comment regions
  - **Is Hidden:** If the visualization template is hidden to end users or not
  - **Description:** Add a description for your visualization
5. Click **Create** to save the information.

## Delete Visualization Template from Assay

To delete a Visualization Template from BIOVIA Assay:

1. Go to *Administration > Administration utilities > Visualization Templates*
2. Click the name of the visualization you want to delete.
3. Click **Delete**.

**Note:** A Visualization cannot be deleted if it is used in at least one run. To remove it, change the Visualization used in each run before deleting it. If the visualization to remove is default visualization, please select a different Visualization to be the default for a step and a process type. The Visualization is still available in Pipeline Pilot Server or in the TIBCO Spotfire library.

## Publishers

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### Create Custom Publisher Using Pipeline Pilot Protocol

To create a custom publisher, you need to create the protocol using Pipeline Pilot components and then register the protocol in BIOVIA Assay.

Default publisher protocols are provided within the Assay collection in Pipeline Pilot at: `Protocols/Discngine/Assay/Publisher/`.

To create a new publisher protocol, use the *Discngine Assay Get Final Data* component to get the final results published. Set the following parameters for this component:

- *Data source*
- *Discngine Assay Run ID*

Then, add the component you need to create the new protocol.

Once your protocol is created, you will need to register this publisher in Assay.

### Register New Publisher in Assay

You need a `ASSAY_ADMINISTRATOR` or `ASSAY_SUPER_USER` profile to register a new publisher.

1. On the *Administration* tab, select *Publishers* in the *Administration Utilities* section.
2. On the *Publishers* list page, click **Create**.
3. Fill in the form with the required details:
  - **Name:** Name of the publisher
  - **Code:** A code for publisher, for example “WH” for Warehouse
  - **Resource Path:** The path to the Publisher protocol on Pipeline Pilot Server starting with `Protocols/Discngine/Assay/Publisher/`
  - **Description:** Description of the publisher
  - **Is hidden:** Indicate if you want this publisher to be made available for publishing or if you want to hide it if it is not yet installed/available
4. Once you have entered the required publisher information, click **Create** to save the information.

### Delete Publisher from Assay

To delete a Publisher from BIOVIA Assay:

1. Go to *Administration > Administration utilities > Publishers*
2. Click the name of the publisher you want to delete.
3. Click **Delete**. The corresponding publisher is removed from the Assay database.

**Note:** A Publisher cannot be deleted if it is used in at least one run. To remove it, change the publisher used in each run before deleting it. The publisher will be still available in Pipeline Pilot Server.