Workflow of qcAssayPortal

```
┌─────────────────────────────┐
│   Skyline document file     │
│     (Experiment 1~5)        │
└─────────────────────────────┘
```

Is the value of internal standard preset?

Yes ──────────────────────── **No**

```
┌─────────────────────────┐        ┌─────────────────────────────┐
│  Skyline document file  │        │ Error report of the missing │
│                         │        │     internal standard       │
└─────────────────────────┘        └─────────────────────────────┘
```

Extract the data with necessary attributes.

```
┌─────────────────────────┐
│   Formatted form file   │
└─────────────────────────┘
```

Detect missing values.

```
┌─────────────────────────┐        ┌─────────────────────────────┐
│  Formatted form file    │        │  Error report of miss       │
│    without missing      │        │        values               │
│       values            │        │                             │
└─────────────────────────┘        └─────────────────────────────┘
```

Traverse the peptide sequences and run the R script.
Is the running successful?

Yes ──────────────────────── **No**

```
┌─────────────────────────────┐    ┌─────────────────────────────┐
│ Formatted form file without │    │ Error report of the failed  │
│ errors to stop R script     │    │  peptides and the reason    │
│        running              │    │                             │
└─────────────────────────────┘    └─────────────────────────────┘
```

Randomly sample 5 peptides to infer the internal standard.
Is the internal standard correct?

Yes ──────────────────────── **No**

```
┌─────────────────────────────┐    ┌─────────────────────────────┐
│  Formatted form file        │    │  Error report of the        │
│     without errors          │    │  incorrect internal         │
│                             │    │      standard               │
└─────────────────────────────┘    └─────────────────────────────┘
```

Traverse the peptide sequences and run the R script.

```
┌─────────────────────────────┐
│ Corresponding plots and     │
│        tables               │
└─────────────────────────────┘
```

Evaluate the quality of the plots and tables.
Is the quality of the plots of tables good?

Yes ──────────────────────── **No**

```
┌─────────────────────────────┐    ┌─────────────────────────────┐
│ Approved plots and tables   │    │ Warning report of the       │
│                             │    │ peptide with poor quality   │
│                             │    │      and the reason         │
└─────────────────────────────┘    └─────────────────────────────┘
```

```
                                   ┌─────────────────────────────┐
                                   │        QC report            │
                                   └─────────────────────────────┘
```