

Package ‘RImmPort’

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Type Package

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Description The RImmPort package simplifies access to ImmPort data for analysis in the R environment. It provides a standards-based interface to the ImmPort study data that is in a proprietary format.

License GPL-3

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Adverse Events Domain *Adverse Events Domain*

Description

The Adverse Events data of an ImmPort study is reformatted to the CDISC SDTM Adverse Events (AE) domain model, and is a list of 2 data frames containing 1) Adverse Events data [AE](#) and 2) any supplemental Adverse Events data [SUPP](#)

AE *Adverse Events Domain Variables*

Description

| Variable Name | Variable Label |
|---------------|-------------------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| AESEQ | Sequence Number |
| AESPID | Sponsor-Defined Identifier |
| AETERM | Reported Term for the Adverse Event |
| AEMODIFY | Modified Reported Term |
| AEBODYSYS | Body System or Organ Class |
| AELOC | Location of Event |
| AESEV | Severity/Intensity |

| | |
|----------|-------------------------------------|
| AEACN | Action Taken with Study Treatment |
| AEACNOTH | Other Action Taken |
| AEREL | Causality |
| AERELNST | Relationship to Non-Study Treatment |
| AEOUT | Outcome of Adverse Event |
| AESTDY | Study Day of Start of Adverse Event |
| AEENDY | Study Day of End of Adverse Event |

 APMH

 Associated Persons Medical History Domain Variables

Description

| Variable Name | Variable Label |
|---------------|---------------------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| APID | Associated Persons Identifier |
| MHSEQ | Sequence Number |
| RSUBJID | Related Subject |
| SREL | Subject Relationship |
| MHTERM | Reported Term for the Medical History |
| MHCAT | Category for Medical History |
| MHBODSYS | Body System or Organ Class |
| MHDTC | Date/Time of History Collection |
| MHDY | RStudy Day of History Collection |

 Associated Persons Medical History Domain

 Associated Persons Medical History Domain

Description

The Associated Persons Medical History data of an ImmPort study is reformatted to the CDISC SDTM AAssociated Persons Medical History (APMH) domain model, and is a list of 2 data frames containing 1) Associated Persons Medical History data [APMH](#) and 2) any supplemental Associated Persons Medical History data [SUPP](#)

| | |
|------------------|-------------------------|
| buildNewSqliteDb | <i>buildNewSqliteDb</i> |
|------------------|-------------------------|

Description

The function `buildNewSqliteDb` builds a sqlite db of ImmPort study data. It takes in as input the study files in the TSV (Tab) format.

Usage

```
buildNewSqliteDb(data_dir, db_dir)
```

Arguments

| | |
|-----------------------|---|
| <code>data_dir</code> | File directory where the study TSV files are stored |
| <code>db_dir</code> | File directory where the sqlite database will be stored |

Value

The SQLite database name

Examples

```
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
# set tab_dir to the folder where the zip files are located
tab_dir <- file.path(studies_dir, "Tab")
# set db_dir to the folder where the database file 'ImmPort.sqlite' should be stored
db_dir <- file.path(studies_dir, "Db")
# build a new ImmPort SQLite database with the data in the downloaded zip files
# dbname <- buildNewSqliteDb(tab_dir, db_dir)
```

Cellular Quantification Domain

Cellular Quantification Domain

Description

The ImmPort study data generated from assays of types: Flow and ELISPOT are grouped into the Cellular Quantification Domain. The data is reformatted to a custom Cellular Quantification domain model in CDISC SDTM standards, and is a list of 2 data frames containing 1) Cellular Quantification data [ZB](#) and 2) any supplemental Cellular Quantification data [SUPP](#)

 CM *Concomitant Medications Domain Variables*

Description

| Variable Name | Variable Label |
|----------------------|--|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| CMSEQ | Sequence Number |
| CMTRT | Reported Name of Drug, Med, or Therapy |
| CMCAT | Category for Medication |
| CMDOSE | Dose per Administration |
| CMDOSTXT | Dose Description |
| CMDOSU | Dose Units |
| CMDOSFREQ | Dosing Frequency per Interval |
| CMROUTE | Route of Administration |
| CMSTDTC | Start Date/Time of Medication |
| CMENDTC | End Date/Time of Medication |
| CMSTDY | Study Day of Start of Medication |
| CMENDY | Study Day of End of Medication |

 Concomitant Medications Domain
Concomitant Medications Domain

Description

The Concomitant Medications data of an ImmPort study is reformatted to the CDISC SDTM Concomitant Medications (CM) domain model, and is a list of 2 data frames containing 1) Concomitant Medications data [CM](#) and 2) any supplemental Concomitant Medications data [SUPP](#)

 Demographics Domain *Demographics Domain*

Description

The Demographics data of an ImmPort study is reformatted to the CDISC SDTM Demographics (DM) domain model, and is a list of 2 data frames containing 1) Demographics data [DM](#) and 2) any supplemental Demographics data [SUPP](#)

 DM *Demographics Domain Variables*

Description

| Variable Name | Variable Label |
|----------------------|--|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| AGE | Age |
| AGEU | Age Units |
| SEX | Sex |
| RACE | Race (only for human data) |
| ETHNIC | Ethnicity (only for human data) |
| SPECIES | Species (only for non-human data) |
| STRAIN | Strain/Substrain (only for non-human data) |
| SBSTRAIN | Strain/Substrain Details (only for non-human data) |
| ARMCD | Planned Arm Code |
| ARM | Description of Planned Arm |

DV

*Protocol Deviations Domain Variables***Description**

| Variable Name | Variable Label |
|----------------------|---------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| DVSEQ | Sequence Number |
| DVTERM | Protocol Deviation Term |

Events-class

*Events class***Description**

Events class

Fields

- ae_1 Adverse Events data [AE](#) and supplemental Adverse Events data [SUPP](#)
- dv_1 Protocol Deviations data [DV](#) and supplemental Protocol Deviations data [SUPPDV](#)
- mh_1 Medical History data [MH](#) and supplemental Medical History data [SUPPMH](#)
- apmh_1 Associated Persons Medical History data [APMH](#) and supplemental Associated Persons Medical History data [SUPP](#)

Examples

```

library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
sdy139 <- getStudy("SDY139")
ae_df <- sdy139$events$ae_l$ae_df

```

EX

*Exposure Domain Variables***Description**

| Variable Name | Variable Label |
|----------------------|---------------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| EXSEQ | Sequence Number |
| EXTRT | Name of Treatment |
| EXCAT | Category of Treatment |
| EXDOSE | Dose |
| EXDOSTXT | Dose Description |
| EXDOSU | Dose Units |
| EXDOSFRQ | Dosing Frequency per Interval |
| EXROUTE | Route of Administration |
| EXSTDTC | Start Date/Time of Treatment |
| EXENDTC | End Date/Time of Treatment |
| EXSTDY | Study Day of Start of Treatment |
| EXENDY | Study Day of End of Treatment |

Exposure Domain

*Exposure Domain***Description**

The Exposure data of an ImmPort study is reformatted to the CDISC SDTM Exposure (EX) domain model, and is a list of 2 data frames containing 1) Exposure data [EX](#) and 2) any supplemental Exposure data [SUPP](#)

FA

*Findings About Domain Variables***Description**

| Variable Name | Variable Label |
|----------------------|---------------------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| FASEQ | Sequence Number |
| FATEST | Findings About Test Name |
| FAOBJ | Object of the Observation |
| FACAT | Category for Findings About |
| FAORRES | Results or Findings in Original Units |
| FAORRESU | Original Units |
| FALOC | Location of the Finding About |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| FADY | Study Day of Collection |

Findings About Domain *Findings About Domain*

Description

The Findings About data of an ImmPort study is reformatted to the CDISC SDTM Findings About (FA) domain model, and is a list of 2 data frames containing 1) Findings About data [FA](#) and 2) any supplemental Findings About data [SUPPFA](#)

Findings-class *Findings class*

Description

Findings class

Fields

lb_1 Laboratory Test Results data [LB](#) and supplemental Laboratory Test Results data [SUPPLB](#)
 pe_1 Physical Examination data [PE](#) and supplemental Physical Examination data [SUPPPE](#)
 vs_1 Vital Signs data [VS](#) and supplemental Vital Signs data [SUPPVS](#)
 qs_1 Questionnaires data [QS](#) and supplemental Questionnaires data [SUPP](#)
 fa_1 Findings About data [FA](#) and supplemental Findings About data [SUPPFA](#)
 sr_1 Skin Response data [SR](#) and supplemental Skin Response data [SUPP](#)
 pf_1 Genetics Findings data [PF](#) and supplemental Genetics Findings data [SUPPPF](#)
 za_1 Protein Quantification data [ZA](#) and supplemental Protein Quantification data [SUPPZA](#)
 zb_1 Cellular Quantification data [ZB](#) and supplemental Cellular Quantification data [SUPP](#)
 zc_1 Nucleic Acid Quantification data [ZC](#) and supplemental Nucleic Acid Quantification data [SUPP](#)
 zd_1 Titer Assay Results data [ZD](#) and supplemental Titer Assay Results data [SUPP](#)

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
sdy139 <- getStudy("SDY139")
zb_df <- sdy139$findings$zb_1$zb_df
```

Genetics Findings Domain

Genetics Findings Domain

Description

The ImmPort study data generated from assays of types: HLA Typing and Array are grouped into the Genetics Findings Domain. The data is reformated to a Pharmacogenomics and Genetics Findings (PF) model in CDISC SDTM standards, and is a list of 2 data frames containing 1) Genetics Findings data [PF](#) and 2) any supplemental Genetics Findings data [SUPP](#)

getAssayDataOfStudies *Get specific assay data of one or more studies from the ImmPort database*

Description

Get specific assay data of one or more studies from the ImmPort database

Usage

```
getAssayDataOfStudies(study_ids, assay_type)
```

Arguments

| | |
|------------|----------------------------|
| study_ids | List of study indentifiers |
| assay_type | Assay Type |

Value

a list of 1) domain data of specific assay technology and 2) any supplemental domain data of the studies

Author(s)

Ravi Shankar

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
elispot_1 <- getAssayDataOfStudies("SDY139", "ELISPOT")
if (length(elispot_1) > 0)
  names(elispot_1)
head(elispot_1$zb_df)
```

| | |
|---------------|--------------------------------------|
| getDomainCode | <i>Get code of a specific domain</i> |
|---------------|--------------------------------------|

Description

The function `getListOfDomains` returns the code of a specific domain

Usage

```
getDomainCode(domain)
```

Arguments

domain Name of a specific domain

Value

A list of of all domain names and codes

Examples

```
domain <- "Demographics"
code <- getDomainCode(domain)
```

| | |
|------------------------|--|
| getDomainDataOfStudies | <i>Get specific domain data of one or more studies from the ImmPort database</i> |
|------------------------|--|

Description

Get specific domain data of one or more studies from the ImmPort database

Usage

```
getDomainDataOfStudies(domain, study_ids)
```

Arguments

| | |
|-----------|----------------------------|
| domain | Name of a specific domain |
| study_ids | List of study indentifiers |

Value

a list of 1) domain data and 2) supplemental domain data of the studies

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
dm_df <- getDomainDataOfStudies("Demographics", "SDY139")
```

getListOfAssayTypes *Get a list of Assay Types*

Description

The function getListOfAssayTypes returns a list of assay types that ImmPort studies have employed in their experimetal assays

Usage

```
getListOfAssayTypes()
```

Value

A list of assay types

Examples

```
at_l <- getListOfAssayTypes()
```

getListOfDomains *Get names of all domains and their codes*

Description

The function getListOfDomains returns a list of all domain names and codes

Usage

```
getListOfDomains()
```

Value

A list of of all domain names and codes

Examples

```
domains_df <- getListOfDomains()
```

| | |
|------------------|----------------------------------|
| getListOfStudies | <i>Get a list of all studies</i> |
|------------------|----------------------------------|

Description

Get a list of all studies

Usage

```
getListOfStudies()
```

Value

List of study indentifiers

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
study_ids <- getListOfStudies()
```

| | |
|---------------------------------|---|
| getStudiesWithSpecificAssayData | <i>Get a list of studies that have specific assay type data</i> |
|---------------------------------|---|

Description

Get a list of studies that have specific assay type data

Usage

```
getStudiesWithSpecificAssayData(assay_type, all_study_ids = c("ALL"))
```

Arguments

| | |
|---------------|---|
| assay_type | Assay Type |
| all_study_ids | List of study indentifiers to search on |

Value

List of study indentifiers

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
study_ids <- getStudiesWithSpecificAssayData("ELISPOT")
```

getStudiesWithSpecificDomainData

Get a list of studies that have specific domain data

Description

Get a list of studies that have specific domain data

Usage

```
getStudiesWithSpecificDomainData(domain, all_study_ids = c("ALL"))
```

Arguments

domain Name of a specific domain
all_study_ids List of study indentifiers to search on

Value

List of study indentifiers

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
study_ids <- getStudiesWithSpecificDomainData("Demographics")
```

| | |
|----------|--|
| getStudy | <i>Get all data of a specific study from the ImmPort data source</i> |
|----------|--|

Description

The function `getStudy` queries the ImmPort data source for data of a specific study in all domains. The data is then structured into `Study` as classes, domains, variables and values.

Usage

```
getStudy(study_id)
```

Arguments

`study_id` Identifier of a specific study

Value

A study data object where in all data are structured as classes, domains, variables and values (in CDISC format)

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
sdy139 <- getStudy("SDY139")
```

| | |
|---------------------|----------------------------|
| Interventions-class | <i>Interventions class</i> |
|---------------------|----------------------------|

Description

Interventions class

Fields

`cm_1` Concomitant Medications data [CM](#) and supplemental Concomitant Medications data [SUPP](#)

`ex_1` Exposure data [EX](#) and supplemental Exposure data [SUPP](#)

`su_1` Substance Use data [SU](#) and supplemental Substance Use data [SUPP](#)

Examples

```

library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
sdy139 <- getStudy("SDY139")
cm_df <- sdy139$interventions$cm_1$cm_df

```

Laboratory Test Results Domain

Laboratory Test Results Domain

Description

The Laboratory Test Results data of an ImmPort study is reformatted to the CDISC SDTM Laboratory Test Results (LB) domain model, and is a list of 2 data frames containing 1) Laboratory Test Results data [LB](#) and 2) any supplemental Laboratory Test Results data [SUPPLB](#)

LB

Laboratory Test Results Domain Variables

Description

| Variable Name | Variable Label |
|----------------------|--|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| LBSEQ | Sequence Number |
| LBTEST | Lab Test or Examination Name |
| LBCAT | Category for Lab Test |
| LBORRES | Result or Finding in Original Units |
| LBORRESU | Original Units |
| LBSPEC | Specimen Type |
| LBREFID | Specimen Identifier |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| LBELTM | Planned Elapsed Time from Time Point Ref |
| LBTPTREF | Time Point Reference |

loadSerializedStudyData

Load the Serialized Data of a Study

Description

Load the serialized data (.rds) file of a specific domain of a study study from the directory where the file is located

Usage

```
loadSerializedStudyData(data_dir, study_id, domain)
```

Arguments

| | |
|----------|---|
| data_dir | Path to a file folder where the .rds study files reside |
| study_id | Study identifier |
| domain | Domain of interest |

Value

A study data object where in all data are structured as classes, domains, variables and values (in CDISC format)

Examples

```
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
# the folder where the .rds files will be stored
rds_dir <- file.path(studies_dir, "Rds")
# load the serialized data of study `SDY208`
loadSerializedStudyData(rds_dir, 'SDY208', "Demographics")
```

Medical History Domain

Medical History Domain

Description

The Medical History data of an ImmPort study is reformatted to the CDISC SDTM Medical History (MH) domain model, and is a list of 2 data frames containing 1) Medical History data [MH](#) and 2) any supplemental Medical History data [SUPPMH](#)

mergeDomainAndSupplemental

Merge the Domain dataframe and Supplemental dataframe (long form)

Description

The Domain data list comprises of the the Domain dataframe that is in wide form, and any Supplemental dataframe that is in long form. The function mergeDomainAndSupplemental transposes the Supplemental dataframe into a wide form, and merges it with the Domain dataframe.

Usage

```
mergeDomainAndSupplemental(data_list)
```

Arguments

`data_list` A list of 1) Domain dataframe and 2) any Supplemental dataframe

Value

The merged dataframe

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
l <- getDomainDataOfStudies("Cellular Quantification", "SDY208")
df <- mergeDomainAndSupplemental(l)
```

MH

Medical History Domain Variables

Description

| Variable Name | Variable Label |
|----------------------|---------------------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| MHSEQ | Sequence Number |
| MHTERM | Reported Term for the Medical History |
| MHCAT | Category for Medical History |
| MHBODSYS | Body System or Organ Class |
| MHDY | Study Day of History Collection |

Nucleic Acid Quantification Domain

Nucleic Acid Quantification Domain

Description

The ImmPort study data generated from assays of types: PCR are grouped into the Nucleic Acid Quantification Domain. The data is reformatted to a custom Nucleic Acid Quantification domain model in CDISC SDTM standards, and is a list of 2 data frames containing 1) Nucleic Acid Quantification data [ZC](#) and 2) any supplemental Nucleic Acid Quantification data [SUPP](#)

PE

*Physical Examination Domain Variables***Description**

| Variable Name | Variable Label |
|----------------------|-----------------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| PESEQ | Sequence Number |
| PETEST | Body System Examined |
| PECAT | Category for Examination |
| PEBODSYS | Body System or Organ Class |
| PEORRES | Verbatim Examination Finding |
| PEORRESU | Original Units |
| PELOC | Location of Physical Exam Finding |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| PEDY | Study Day of Examination |

PF

*Genetics Findings Domain Variables***Description**

| Variable Name | Variable Label |
|----------------------|--|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| PFSEQ | Sequence Number |
| PFGRPID | Group Identifier |
| PFTEST | Test Name |
| PFCAT | Category for Test |
| PFMETHOD | Method of the Test |
| PFGENRI | Genetic Region of Interest |
| PFORRES | Result or Finding in Original Units |
| PFALLELC | Allele (Chromosome) Identifier |
| PFSPEC | Specimen Type |
| PFREFID | Reference ID (Specimen Identifier) |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| PFELTM | Planned Elapsed Time from Time Point Ref |
| PFTPTREF | Time Point Reference |
| PFXFN | Raw Data File or Life Science Identifier |

Physical Examination Domain

Physical Examination Domain

Description

The Physical Examination data of an ImmPort study is reformatted to the CDISC SDTM Physical Examination (PE) domain model, and is a list of 2 data frames containing 1) Physical Examination data [PE](#) and 2) any supplemental Physical Examination data [SUPPPE](#)

Protein Quantification Domain

Protein Quantification Domain

Description

The ImmPort study data generated from assays of types: ELISA and MBAA are grouped into the Cellular Quantification Domain. The data is reformatted to a custom Protein Quantification domain model in CDISC SDTM standards, and is a list of 2 data frames containing 1) Protein Quantification data [ZA](#) and 2) any supplemental Protein Quantification data [SUPP](#)

Protocol Deviations Domain

Protocol Deviations Domain

Description

The Protocol Deviations data of an ImmPort study is reformatted to the CDISC SDTM Protocol Deviations (DV) domain model, and is a list of 2 data frames containing 1) Protocol Deviations data [DV](#) and 2) any supplemental Protocol Deviations data [SUPPDV](#)

QS

Questionnaires Domain Variables

Description

| Variable Name | Variable Label |
|---------------|---------------------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| QSSEQ | Sequence Number |
| QSTEST | Questionnaires Test Name |
| QSCAT | Category for Questionnaires |
| QSORRES | Results or Findings in Original Units |
| QSORRESU | Original Units |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| QSDY | Study Day of Finding |

Questionnaires Domain *Questionnaires Domain*

Description

The Questionnaires data of an ImmPort study is reformatted to the CDISC SDTM Questionnaires (QS) domain model, and is a list of 2 data frames containing 1) Questionnaires data [QS](#) and 2) any supplemental Questionnaires data [SUPP](#)

RImmPort

RImmPort: Enabling ready-for-analysis immunology research data

Description

The ‘RImmPort’ package simplifies access to ImmPort data for analysis, as the name implies, in the R statistical environment. It provides a standards-based interface to the ImmPort study data that is in a proprietary format.

serializeStudyData

Serialize the Study Data

Description

Load specific studies from the database and save it in .rds format in a local file directory

Usage

```
serializeStudyData(study_ids, data_dir)
```

Arguments

`study_ids` List of study identifiers
`data_dir` Path to a file folder where the .rds study files will be saved into

Value

List of study identifiers that were serialized successfully

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
# the folder where the .rds files will be stored
rds_dir <- file.path(studies_dir, "Rds")
study_ids <- c('SDY139', 'SDY208')
serializeStudyData(study_ids, rds_dir)
```

setImmPortDataSource *Set ImmPort data ource*

Description

The function `setImmPortDataSource` sets the data source variable in RImmPort environment, to the connection handle to the MySQL or SQLite database, or to the file directory where the pre-created RImmPort-formatted files are stored.

Usage

```
setImmPortDataSource(data_src)
```

Arguments

`data_src` A connection handle to ImmPort (MySQL or SQLite) database instance or a directory handle to folder where study RImmPort-formatted (.rds) files located

Value

1 if successful

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
```

Skin Response Domain *Skin Response Domain*

Description

The Skin Response data of an ImmPort study is reformatted to the CDISC SDTM Skin Response (SR) domain model, and is a list of 2 data frames containing 1) Skin Response data [SR](#) and 2) any supplemental Skin Response data [SUPP](#)

SpecialPurpose-class *Special Purpose class*

Description

Special Purpose class

Fields

dm_1 Demographics data [DM](#) and supplemental Demographics data [SUPP](#)

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
sdy139 <- getStudy("SDY139")
dm_df <- sdy139$special_purpose$dm_1$dm_df
```

SR

Skin Response Domain Variables

Description

| Variable Name | Variable Label |
|----------------------|--|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| SRSEQ | Sequence Number |
| SRTEST | Skin Response Test or Examination Name |
| SROBJ | Object of the Observation |
| SRCAT | Category for Test |
| SRORRES | Results or Findings in Original Units |
| SRORRESU | Original Units |
| SRLOC | Location used for Measurement |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| SRDY | Study Day of Visit/Collection/Exam |

Study-class

Study class

Description

Study class

Fields

special_purpose [SpecialPurpose](#)
 interventions [Interventions](#)
 events [Events](#)
 findings [Findings](#)
 trial_design [TrialDesign](#)

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
sdy139 <- getStudy("SDY139")
```

 SU

Substance Use Domain Variables

Description

| Variable Name | Variable Label |
|----------------------|-------------------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| SUSEQ | Sequence Number |
| SUTRT | Reported Name of Substance |
| SUCAT | Category of Substance Use |
| SUDOSE | Substance Use Consumption |
| SUDOSTXT | Substance Use Consumption Text |
| SUDOSU | Consumption Units |
| SUDOSFRQ | Use Frequency per Interval |
| SURROUTE | Route of Administration |
| SUSTDTC | Start Date/Time of Substance Use |
| SUENDTC | End Date/Time of Substance Use |
| SUSTDY | Study Day of Start of Substance Use |
| SUENDY | Study Day of End of Substance Use |

 Subject Visits Domain *Subject Visits Domain*

Description

Actual subject visits data of an ImmPort study is reformatted to the CDISC SDTM Subject Visits (SV) domain model, and is a list of 2 data frames containing 1) Subject Visits data [SV](#) and 2) any supplemental Subject Visits data [SUPP](#)

Substance Use Domain *Substance Use Domain*

Description

The Substance Use data of an ImmPort study is reformatted to the CDISC SDTM Substance Use (SU) domain model, and is a list of 2 data frames containing 1) Substance Use data [SU](#) and 2) any supplemental Substance Use data [SUPP](#)

SUPP *Supplemental Variables*

Description

| Variable Name | Variable Label |
|----------------------|-----------------------------|
| STUDYID | Study Identifier |
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

SUPPDV *Protocol Deviations Domain Supplemental Variables*

Description

| Variable Name | Variable Label |
|----------------------|-----------------------------|
| STUDYID | Study Identifier |
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

Note

The following table enumerates the values in QNAM and QLABEL variables

| QNAM | QLABEL |
|-------------|---|
| DVRELAE | Is Deviation Related to an Adverse Event? |
| DVREASON | Reason for Deviation |
| DVRESOL | Resolution of Deviation |
| DVCONT | Did Subject continued in Study? |
| DVSTDY | Study Day of Start of Deviation |
| DVENDY | Study Day of End of Deviation |

 SUPPFA

Findings About Domain Supplemental Variables

Description

| Variable Name | Variable Label |
|----------------------|-----------------------------|
| STUDYID | Study Identifier |
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| FASEQ | Sequence Number |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

Note

The following table enumerates the values in QNAM and QLABEL variables

| QNAM | QLABEL |
|-------------|---------------------------|
| FATOD | Time of Day of Collection |

 SUPPLB

Laboratory Test Results Domain Supplemental Variables

Description

| Variable Name | Variable Label |
|----------------------|-----------------------|
| STUDYID | Study Identifier |

| | |
|----------|-----------------------------|
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

Note

The following table enumerates the values in QNAM and QLABEL variables

| QNAM | QLABEL |
|----------|---------------------------------|
| LBSPECSB | Specimen Subtype |
| VISITMIN | Planned Visit Minimum Start Day |
| VISITMAX | Planned Visit Maximum Start Day |

 SUPPMH

Medical History Domain Supplemental Variables

Description

| Variable Name | Variable Label |
|---------------|-----------------------------|
| STUDYID | Study Identifier |
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| MHSEQ | Sequence Number |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

Note

The following table enumerates the values in QNAM and QLABEL variables

| QNAM | QLABEL |
|--------|--------------------|
| MHAGE | Age at Onset |
| MHAGEU | Age at Onset Units |
| MHTOD | Time of Day |

SUPPPE

*Physical Examination Domain Supplemental Variables***Description**

| Variable Name | Variable Label |
|----------------------|-----------------------------|
| STUDYID | Study Identifier |
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| PESEQ | Sequence Number |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

Note

The following table enumerates the values in QNAM and QLABEL variables

| QNAM | QLABEL |
|-------------|---------------|
| PETOD | Time of Day |

SUPPPF

*Genetics Findings Domain Supplemental Variables***Description**

| Variable Name | Variable Label |
|----------------------|-----------------------------|
| STUDYID | Study Identifier |
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

Note

The following table enumerates the values in QNAM and QLABEL variables

| QNAM | QLABEL |
|-------------|--------------------------------------|
| PFPOPAR | Geographic Area of the Population |
| PFSPECSB | Specimen Subtype |
| PFREFIDP | Source Specimen Identifier |
| VISITMIN | Planned Visit Minimum Start Day |
| VISITMAX | Planned Visit Maximum Start Day |
| PFSPTRT | Specimen Treatment |
| PFTRTAMV | Specimen Treatment Amount Value |
| PFTRTAMU | Specimen Treatment Amount Unit |
| PFTRTDUV | Specimen Treatment Duration Value |
| PFTRTDUU | Specimen Treatment Duration Unit |
| PFTRTTMV | Specimen Treatment Temperature Value |
| PFTRTTMU | Specimen Treatment Temperature Unit |

 SUPPVS

Vital Signs Domain Supplemental Variables

Description

| Variable Name | Variable Label |
|----------------------|-----------------------------|
| STUDYID | Study Identifier |
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| VSSEQ | Sequence Number |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

Note

The following table enumerates the values in QNAM and QLABEL variables

| QNAM | QLABEL |
|-------------|---------------|
| VSTOD | Time of Day |

 SUPPZA

Protein Quantification Domain Supplemental Variables

Description

| Variable Name | Variable Label |
|----------------------|-----------------------|
|----------------------|-----------------------|

| | |
|----------|-----------------------------|
| STUDYID | Study Identifier |
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

Note

The following table enumerates the values in QNAM and QLABEL variables

| QNAM | QLABEL |
|-------------|--------------------------------------|
| ZAMFI | MFI |
| ZAMFICRD | MFI Coordinate |
| ZASPECSB | Specimen Subtype |
| ZAREFIDP | Source Specimen Identifier |
| VISITMIN | Planned Visit Minimum Start Day |
| VISITMAX | Planned Visit Maximum Start Day |
| ZASPTRT | Specimen Treatment |
| ZARTAMV | Specimen Treatment Amount Value |
| ZARTAMU | Specimen Treatment Amount Unit |
| ZARTDUV | Specimen Treatment Duration Value |
| ZARTDUU | Specimen Treatment Duration Unit |
| ZARTTMV | Specimen Treatment Temperature Value |
| ZARTTMU | Specimen Treatment Temperature Unit |

 SUPPZB

Cellular Quantification Domain Supplemental Variables

Description

| Variable Name | Variable Label |
|----------------------|-----------------------------|
| STUDYID | Study Identifier |
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

Note

The following table enumerates the values in QNAM and QLABEL variables

| QNAM | QLABEL |
|-------------|--------------------------------------|
| ZBSPECSB | Specimen Subtype |
| ZBREFIDP | Source Specimen Identifier |
| ZBFCF | Control Files Names |
| VISITMIN | Planned Visit Minimum Start Day |
| VISITMAX | Planned Visit Maximum Start Day |
| ZBSPTRT | Specimen Treatment |
| ZBTRTAMV | Specimen Treatment Amount Value |
| ZBTRTAMU | Specimen Treatment Amount Unit |
| ZBTRTDUV | Specimen Treatment Duration Value |
| ZBTRTDUU | Specimen Treatment Duration Unit |
| ZBTRTTMV | Specimen Treatment Temperature Value |
| ZBTRTTMU | Specimen Treatment Temperature Unit |

SUPPZC

*Nucleic Acid Quantification Domain Supplemental Variables***Description**

| Variable Name | Variable Label |
|----------------------|-----------------------------|
| STUDYID | Study Identifier |
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

Note

The following table enumerates the values in QNAM and QLABEL variables

| QNAM | QLABEL |
|-------------|--------------------------------------|
| ZCSPECSB | Specimen Subtype |
| ZCREFIDP | Source Specimen Identifier |
| VISITMIN | Planned Visit Minimum Start Day |
| VISITMAX | Planned Visit Maximum Start Day |
| ZCSPTRT | Specimen Treatment |
| ZCTRTRAMV | Specimen Treatment Amount Value |
| ZCTRTRAMU | Specimen Treatment Amount Unit |
| ZCTRTRDUV | Specimen Treatment Duration Value |
| ZCTRTRDUU | Specimen Treatment Duration Unit |
| ZCTRRTTMV | Specimen Treatment Temperature Value |

ZCTRRTMU Specimen Treatment Temperature Unit

SUPPZD

*Titer Assay Results Domain Supplemental Variables***Description**

| Variable Name | Variable Label |
|----------------------|-----------------------------|
| STUDYID | Study Identifier |
| RDOMAIN | Related Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| IDVAR | Identifying Variable |
| IDVARVAL | Identifying Variable Value |
| QNAM | Qualifier Variable Name |
| QLABEL | Qualifier Variable Label |
| QVAL | Data Value |

Note

The following table enumerates the values in QNAM and QLABEL variables

| QNAM | QLABEL |
|-------------|--------------------------------------|
| ZDSPECSB | Specimen Subtype |
| ZDREFIDP | Source Specimen Identifier |
| VISITMIN | Planned Visit Minimum Start Day |
| VISITMAX | Planned Visit Maximum Start Day |
| ZDSPTRT | Specimen Treatment |
| ZDTRTAMV | Specimen Treatment Amount Value |
| ZDTRTAMU | Specimen Treatment Amount Unit |
| ZDTRTDUV | Specimen Treatment Duration Value |
| ZDTRTDUU | Specimen Treatment Duration Unit |
| ZDTRTTMV | Specimen Treatment Temperature Value |
| ZDTRTTMU | Specimen Treatment Temperature Unit |

SV

*Subject Visits Domain Variables***Description**

| Variable Name | Variable Label |
|----------------------|-----------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| SVSTDY | Study Day of Start of Visit |

TA *Trial Arms Domain Variables*

Description

| Variable Name | Variable Label |
|----------------------|----------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| ARMCD | Planned Arm Code |
| ARM | Name of Planned Arm |
| ARMDESC | Description of Planned Arm |
| ARMRULE | Population Selection Rule |

TI *Trial Inclusion Exclusion Criteria Domain Variables*

Description

| Variable Name | Variable Label |
|----------------------|-------------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| IETEST | Inclusion/Exclusion Criterion |
| IECAT | Inclusion/Exclusion Category |

Titer Assay Results Domain
Titer Assay Results Domain

Description

The ImmPort study data generated from assays of types: HAI and Neut Ab Titer are grouped into the Titer Assay Results Domain. The data is reformatted to a custom Titer Assay Results domain model in CDISC SDTM standards, and is a list of 2 data frames containing 1) Titer Assay Results data [ZD](#) and 2) any supplemental Titer Assay Results data [SUPP](#)

Trial Arms Domain *Trial Arms Domain*

Description

The Trial Arms data of an ImmPort study is reformatted to the CDISC SDTM Trial Arms (TA) domain model, and is a list of 2 data frames containing 1) Trial Arms data [TA](#) and 2) any supplemental Trial Arms data [SUPP](#)

Trial Inclusion Exclusion Criteria Domain
Trial Inclusion Exclusion Criteria Domain

Description

The Trial Inclusion Exclusion Criteria data of an ImmPort study is reformatted to the CDISC SDTM Trial Inclusion Exclusion Criteria (TI) domain model, and is a list of 2 data frames containing 1) Trial Inclusion Exclusion Criteria data [TI](#) and 2) any supplemental Trial Inclusion Exclusion Criteria data [SUPP](#)

Trial Summary Domain *Trial Summary Domain*

Description

The Trial Summary data of an ImmPort study is reformatted to the CDISC SDTM Trial Summary (TS) domain model, and is a list of 2 data frames containing 1) Trial Summary data [TS](#) and 2) any supplemental Trial Summary data [SUPP](#)

Trial Visits Domain *Trial Visits Domain*

Description

Information on the planned visits of an ImmPort study is reformatted to the CDISC SDTM Trial Visits (TV) domain model, and is a list of 2 data frames containing 1) Trial Visits data [TV](#) and 2) any supplemental Trial Visits data [SUPP](#)

TrialDesign-class *Trial Design class*

Description

Trial Design class

Fields

ta_1 Trial Arms data [TA](#) and supplemental Trial Arms data [SUPP](#)

tv_1 Trial Visits data [TA](#) and supplemental Trial Visits data [SUPP](#)

ti_1 Trial Inclusion Exclusion Criteria data [TI](#) and supplemental Trial Inclusion Exclusion Criteria data [SUPP](#)

ts_1 Trial Summary data [TS](#) and supplemental Trial Summary data [SUPP](#)

Examples

```
library(DBI)
library(sqldf)
studies_dir <- system.file("extdata", "ImmPortStudies", package = "RImmPort")
db_dir <- file.path(studies_dir, "Db")
sqlite_conn <- dbConnect(SQLite(), dbname=file.path(db_dir, "ImmPort.sqlite"))
setImmPortDataSource(sqlite_conn)
sdy139 <- getStudy("SDY139")
ts_df <- sdy139$trial_design$ts_1$ts_df
```

TS

Trial Summary Domain Variables

Description

| Variable Name | Variable Label |
|----------------------|------------------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| TSSEQ | Sequence Number |
| TSPARMCD | Trial Summary Parameter Short Name |
| TSPARM | Trial Summary Parameter |
| TSVAL | Parameter Value |

Note

The following table enumerates the values in TSPARMCD and TSPARM variables

| TSPARMCD | TSPARM |
|-----------------|-------------------|
| TITLE | Trial Title |
| DESCR | Trial Description |

| | |
|----------|--------------------------------------|
| INDIC | Trial Indication |
| TRT | Investigational Therapy or Treatment |
| HYPOTHS | Trial Hypotheses |
| SSTDTC | Study Start Date |
| SENDTC | Study End Date |
| PLANSUB | Planned Number of Subjects |
| ACTSUB | Actual Number of Subjects |
| AGEMAX | Planned Maximum Age of Subjects |
| AGEMIN | Planned Minimum Age of Subjects |
| AGEU | Age Units |
| SEXPOP | Sex of Participants |
| SPONSOR | Clinical Study Sponsor |
| PUBRLDAT | Public Release Date |
| ISTRIAL | Study Type |
| RESFOCUS | Trial Research Focus |

TV

*Trial Visits Domain Variables***Description**

| Variable Name | Variable Label |
|----------------------|-----------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| ARMCD | Planned Arm Code |
| ARM | Name of Planned Arm |
| TVSTRL | Visit Start Rule |
| TVENRL | Visit End Rule |

Vital Signs Domain

*Vital Signs Domain***Description**

The Vital Signs data of an ImmPort study is reformatted to the CDISC SDTM Vital Signs (VS) domain model, and is a list of 2 data frames containing 1) Vital Signs data [VS](#) and 2) any supplemental Vital Signs data [SUPPVS](#)

VS

*Vital Signs Domain Variables***Description**

| Variable Name | Variable Label |
|----------------------|-------------------------------------|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| VSSEQ | Sequence Number |
| VSTEST | Vital Signs Test Name |
| VSCAT | Category for Vital Signs |
| VSORRES | Result or Finding in Original Units |
| VSORRESU | Original Units |
| VSLOC | Location of Vital Signs Measurement |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| VSDY | Study Day of Vital Signs |

ZA

Protein Quantification Domain Variables

Description

| Variable Name | Variable Label |
|----------------------|--|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| ZASEQ | Sequence Number |
| ZATEST | Protein Quantification Test Name |
| ZACAT | Category for Protein Quantification |
| ZAMETHOD | Measurement Technique |
| ZANALYT | Analyte |
| ZAORRES | Result or Finding in Original Units |
| ZAORRESU | Original Units |
| ZASPEC | Specimen Type |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| ZAELTM | Planned Elapsed Time from Time Point Ref |
| ZATPTREF | Time Point Reference |
| ZAREFID | Specimen Identifier |
| ZAXFN | Raw Data File or Life Science Identifier |

ZB

Cellular Quantification Domain Variables

Description

| Variable Name | Variable Label |
|----------------------|--|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| ZBSEQ | Sequence Number |
| ZBTEST | Cellular Quantification Test Name |
| ZBCAT | Category for Cellular Quantification |
| ZBMETHOD | Measurement Technique |
| ZBPOPDEF | Cell Population Definition |
| ZBPOPNAM | Cell Population Name |
| ZBORRES | Result or Finding in Original Units |
| ZBORRESU | Original Units |
| ZBBASPOP | Base Parent Population |
| ZBSPEC | Specimen Type |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| ZBELTM | Planned Elapsed Time from Time Point Ref |
| ZBTPTREF | Time Point Reference |
| ZBREFID | Specimen Identifier |
| ZBXFN | Raw Data File or Life Science Identifier |

ZC

Nucleic Acid Quantification Domain Variables

Description

| Variable Name | Variable Label |
|----------------------|--|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| ZCSEQ | Sequence Number |
| ZCTEST | Nucleic Acid Quantification Test Name |
| ZCCAT | Category for Nucleic Acid Quantification |
| ZCMETHOD | Measurement Technique |
| ZCENTRZD | Entrez Gene ID |
| ZCGENNAM | Gene Name |
| ZCGENSYM | Gene Symbol |
| ZCORRES | Result or Finding in Original Units |
| ZCORRESU | Original Units |
| ZCSPEC | Specimen Type |
| ZCREFID | Specimen Identifier |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| ZCELTM | Planned Elapsed Time from Time Point Ref |
| ZCTPTREF | Time Point Reference |

ZD

*Titer Assay Results Domain Variables***Description**

| Variable Name | Variable Label |
|----------------------|--|
| STUDYID | Study Identifier |
| DOMAIN | Domain Abbreviation |
| USUBJID | Unique Subject Identifier |
| ZDSEQ | Sequence Number |
| ZDTEST | Titer Assay Results Test Name |
| ZDCAT | Category for Titer Assay Results |
| ZDMETHOD | Measurement Technique |
| ZDSTRAIN | Virus Strain |
| ZDORRES | Result or Finding in Original Units |
| ZDORRESU | Original Units |
| ZDSPEC | Specimen Type |
| ZDREFID | Specimen Identifier |
| VISITNUM | Visit Number |
| VISIT | Visit Name |
| ZDELTM | Planned Elapsed Time from Time Point Ref |
| ZDTPTREF | Time Point Reference |
| ZDXFN | Raw Data File or Life Science Identifier |

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