<table>
<thead>
<tr>
<th>Field Type</th>
<th>Description</th>
<th>Data Type</th>
<th>Max. Length</th>
<th>Value List</th>
</tr>
</thead>
<tbody>
<tr>
<td>Study Identifier</td>
<td>A unique Study Identifier generated by the iDPCC by combining the Center-generated Study Code and a random 5-digit number</td>
<td>Text Field</td>
<td>50 characters</td>
<td>None</td>
</tr>
<tr>
<td>Contributing Institution</td>
<td>The institution code for the group that contributed the reagent. Must be one of the CEIRR institution codes assigned by NIAID.</td>
<td>Text Field</td>
<td>6 characters</td>
<td>None</td>
</tr>
<tr>
<td>Sample Identifier</td>
<td>Identifier assigned to the reagent. Material from which the reagent was derived</td>
<td>Text Field</td>
<td>50 characters</td>
<td>None</td>
</tr>
<tr>
<td>Sample Material</td>
<td>Material from which the reagent was derived.</td>
<td>Text Field</td>
<td>30 characters</td>
<td>AIR, BAL, BLO, CCF, CCO, CCT, CLO, FEC, LLF, LUN, NAL, NAS, NTS, ORP, OTH-, OTT, PLS, RCS, SER, SLU, SOI, SPU, TFB, TFH, TFL, TFS, TFT, TLN, TNC, TRS, WAT, U</td>
</tr>
</tbody>
</table>

**Examples:**
- SJCProj02_00015
- SJC101
- SSC-001
- LUN, or TFS

**Notes:**
- AIR = Air
- BAL = Bronchoalveolar lavage
- BLO = Blood
- CCF = Combined cloacal and fecal
- CCO = Combined cloacal and oral-pharyngeal
- CCT = Combined cloacal and tracheal
- CLO = Cloacal
- FEC = Feces
- LLF = Lung lavage fluid
- LUN = Lungs
- NAL = Nasal lavage
- NAS = Nasal swab
- NTS = Combined nasal throat swab
- ORP = Oral-pharyngeal
- OTH- = Other; append free text to describe
- OTT = Other tissue
- PLS = Plasma
- RCS = Rectal swab
- SER = Serum
- SLU = Slurry
- SOI = Soil
- SPU = Sputum
- TFB = Tissue from brain
- TFH = Tissue from heart
- TFL = Tissue from liver
- TFS = Tissue from spleen
- TFT = Tissue from trachea
- TLN = Tissue from lymph node
- TNC = Tissue from nasal cavity
- TRS = Tracheal swab
- WAT = Water
- U = Unknown

For any other questions please contact support@ceirr-network.org
<table>
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<tr>
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<th>Description</th>
<th>Value List</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sample Material Area</td>
<td>Region of tissue from which the reagent was derived</td>
<td>Left Lung, Upper Left Lung, Lower Left Lung, Right Lung, Upper Right Lung, Middle Right Lung, or Lower Right Lung</td>
</tr>
<tr>
<td>Sample Material Form</td>
<td>Description of the type of material in which the reagent is supplied</td>
<td>Bronchioaveolar Fluid, Cell Suspension, Homogenate, Tissue, PBMC in RNALater, Single Cell Suspension, Trachea cells in RNALater, or Whole Tissue</td>
</tr>
<tr>
<td>Infected</td>
<td>Is the reagent derived from an infected sample?</td>
<td>Y = Yes, N = No</td>
</tr>
<tr>
<td>Notes</td>
<td>For any other questions please contact <a href="mailto:support@ceirr-network.org">support@ceirr-network.org</a></td>
<td></td>
</tr>
</tbody>
</table>
**Strain Name**

**Input Type:** Text Field

**Definition:** The WHO or ICTV strain name of the virus that was used to create the reagent

**Format:** Influenza A virus: Antigenic Type/Host of Origin/Geographical Origin/Strain Number/Year of Isolation (Subtype), or rg-Antigenic Type/Host of Origin/Geographical Origin/Strain Number/Year of Isolation [rg details] (Subtype)

Influenza B, C, or D virus: Antigenic Type/Host of Origin/Geographical Origin/Strain Number/Year of Isolation, or rg-Antigenic Type/Host of Origin/Geographical Origin/Strain Number/Year of Isolation [rg details]

SARS-CoV-2 and other viruses: Virus Name/Host of Origin/Geographical Origin/Strain Number/Year of Isolation, or rg-Virus Name/Host of Origin/Geographical Origin/Strain Number/Year of Isolation [rg details]

**Maximum length:** 150 characters

**Examples:**

- For influenza:
  - A/Hong Kong/1/1968 (H3N2)
  - A/chicken/Fujian/4/2002 (H3N6)
  - A/chicken/Fujian/4/2002 (HxNx)
  - A/chicken/Fujian/4/2002 (mixed)
  - A/swine/Iowa/233-56/2011 (H3N2)
  - A/duck/Alberta/35/1976 (H1N1)
  - B/Hong Kong/432/2014
  - C/Texas/19876/2011
  - D/swine/Oklahoma/1334/2011
  - rg-A/Puerto Rico/8/1934 (H1N1), or
  - rg-A/Egypt/N03072/2010 [PR8 internal R 6+2] (H5N1)

- For SARS-CoV-2:
  - SARS-CoV-2/human/USA/NY-PV08486/2020
  - SARS-CoV-2/white-tailed deer/USA/OH-001/2021

- For other viruses:
  - PHEV-CoV/swine/USA/15TOSU25049/2015

**WHO Reference for influenza viruses:** [http://www.cdc.gov/flu/about/viruses/types.htm](http://www.cdc.gov/flu/about/viruses/types.htm)


(HxNx) can be used in cases where a partial subtype has been determined (e.g., H5Nx, HxN2).

If there are mixed subtypes combined within a sample use A/chicken/Fujian/4/2002 (mixed) for Strain_Name and enter additional subtype information in the Comments field.

---

**Dependent Fields:**

- Infected
- Days Post Infection

**Message Code:**

- Error_70_INVALID_FIELD_LENGTH

**Notes:**

- The strain is a reverse genetic virus, prefix Strain_Name with rg. Provide reverse genetic details in brackets after the year of isolation and before the subtype.

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<table>
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<th>Field Type</th>
<th>Field Name</th>
<th>Description</th>
<th>Validation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Integer</td>
<td>Days Post Infection</td>
<td>The number of days post-infection at which the reagent was collected.</td>
<td>Number or NA. Valid values are in the Value List.</td>
</tr>
<tr>
<td>Text</td>
<td>Host Identifier</td>
<td>An identifier assigned to the host animal from which the reagent was derived.</td>
<td>Maximum length: 2 characters. Allowed characters include alphanumeric, hyphen, and underscore: a-z, A-Z, 0-9, -, _</td>
</tr>
<tr>
<td>Text</td>
<td>Host Common Name</td>
<td>The English common name given to a particular species as listed in the iDPCC Species Dictionary from which the reagent was derived.</td>
<td>Maximum length: 50 characters.</td>
</tr>
<tr>
<td>Text</td>
<td>Host Sex</td>
<td>Gender of host animal from which the sample was taken.</td>
<td>Maximum length: 1 character. Valid values are M, F, U.</td>
</tr>
<tr>
<td>Text</td>
<td>Supplied as</td>
<td>A description of the reagent's storage and shipping condition.</td>
<td>Maximum length: 30 characters.</td>
</tr>
</tbody>
</table>

**Value List:***
- **Days Post Infection:** Integer
  - Valid values: 1, 2, 3, ..., 30
- **Host Identifier:** Text
  - Maximum length: 2 characters
- **Host Common Name:** Text
  - Maximum length: 50 characters
- **Host Sex:** Text
  - Maximum length: 1 character
  - Valid values: M, F, U
- **Supplied as:** Text
  - Maximum length: 30 characters

**Examples:**
- Days Post Infection: 3, 5, 10, 15, 20, 25, 30
- Host Identifier: F001, H002, H003
- Host Common Name: ferret, dog, cat
- Host Sex: M, F, U
- Supplied as: Aliquot, Stock, Frozen, Liquid

**Notes:**
- If multiple samples are collected from a host, then all reagents must reference the same Host_IDentifier.
- Do not enter an unknown or unknown field. If no value is entered for a field, then all reagents must reference the same Host_IDentifier.
- All values are case-sensitive and must be entered in all-caps.

**Message Codes:**
- **Invalid Field Length:** Error_70_INVALID_FIELD_LENGTH
  - **Value:** 1, 2, 3, ..., 30
  - **Message Code:** `Error_70_INVALID_FIELD_LENGTH` (For any other questions please contact support@ceirr-network.org)
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<tr>
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<th>Definition</th>
<th>Format</th>
<th>Value List</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Concentration</td>
<td>The concentration of the reagent</td>
<td>Text</td>
<td>Maximum length: 30 characters</td>
<td>None</td>
</tr>
<tr>
<td>Publication PMID</td>
<td>The PubMed Unique Identifier (PMID) for the publication in which the reagent was published</td>
<td>Number</td>
<td>Maximum length: 50 characters</td>
<td>None</td>
</tr>
<tr>
<td>Quantity Available</td>
<td>The quantity of reagent available on the reagent request interface</td>
<td>Integer</td>
<td>Maximum length: 4 characters</td>
<td>None</td>
</tr>
<tr>
<td>Quantity Minimum</td>
<td>The minimum quantity of reagent to remain available on the reagent request interface</td>
<td>Integer</td>
<td>Maximum length: 4 characters</td>
<td>None</td>
</tr>
<tr>
<td>Make Public</td>
<td>Whether the reagent should be displayed on the CEIRR Public Website in addition to the iDPCC Portal</td>
<td>Text</td>
<td>Maximum length: 1 character</td>
<td>None</td>
</tr>
<tr>
<td>Availability</td>
<td>Whether the reagent is available to share with other investigators on the reagents page of the CEIRR Public Website</td>
<td>Text</td>
<td>Maximum length: 1 character</td>
<td>None</td>
</tr>
<tr>
<td>Contact Name</td>
<td>The name of the point-of-contact for reagent requests</td>
<td>Text</td>
<td>Maximum length: 50 characters</td>
<td>None</td>
</tr>
<tr>
<td>Contact Email</td>
<td>Email address for the point-of-contact</td>
<td>Text</td>
<td>Maximum length: 50 characters</td>
<td>None</td>
</tr>
<tr>
<td>Comments</td>
<td>Text describing anything else of interest related to the submission</td>
<td>Text</td>
<td>Maximum length: 2000 characters</td>
<td>None</td>
</tr>
</tbody>
</table>

### Examples

**Concentration**

- 1x10E6/ml
- 19465683, or NA
- 5
- 5
- Y
- Y
- Jane Smith, or Davey M. Jones
- jsmit@email.edu
- NA

### Notes

- The concentration and publication PMID are mandatory fields.
- The entry must be a valid PMID number: 7 or 8-digit number with no leading zeros.
- The entry must be a valid integer between 0-9999
- The entry must be a valid integer between 0-9999
- The entry must be one and only one member of the Value List.
- The entry must be one and only one member of the Value List.
- The entry must be a valid email address.
- If there are no comments, enter NA.

### Validate

- Field value should be one of valid values as in list.
- Field value should be one of valid values as in list.
- Validate field length
- Validate field length
- Validate field length
- Validate field length
- Validate field length
- Validate field length
- Validate field length
- Validate field length
- Validate field length

### Message Codes

- Error_70_INVALID_FIELD_LENGTH
- Error_96_INVALID_PMID
- Error_18_ATTRIBUTE_VALUE_TYPE
- Error_114_INVALID_EMAIL

For any other questions please contact support@ceirr-network.org