### Study Identifier

- **Definition:** A unique Study Identifier generated by the iDPCC by combining the Center-generated Study Code and a random 5-digit number.

- **Format:** Study_Code_XXXXX
  - Center three-letter code followed by three digits.
  - Maximum length: 50 characters

- **Value List:** None

- **Notes:** Enter NA if the reagent is not related to a surveillance submission.

### Contributing Institution

- **Definition:** The institution code for the group that CREATED THE REAGENT. Must be one of the CEIRR institution codes assigned by NIAID.

- **Format:** Text (variable length)
  - Center-specific
  - Allowed characters include alphanumeric, hyphen, and underscore: a-z, A-Z, 0-9, -
  - Maximum length: 50 characters

- **Value List:** None

- **Notes:** None

### Reagent Name

- **Definition:** Name of the reagent assigned by the investigator.

- **Format:** Text (variable length)
  - Maximum length: 150 characters

- **Value List:** None

- **Notes:** None

### SampleIdentifier

- **Definition:** Identifier assigned to the virus used to create the reagent.

- **Format:** Text (variable length)
  - Center-specific
  - Maximum length: 150 characters

- **Value List:** None

- **Notes:** None

### Input Type

- **Format:** Text Field
  - Maximum length: 50 characters

- **Value List:** None

- **Notes:** None

### Dependent Fields

- **Validation:** Study_identifier should be a valid Study Identifier.
  - Must be an Institution Code value registered with the iDPCC.
  - Validated field length

- **Message Code:** Error_I_STUDY_CODE

- **Validation:** Study_identifier exists but user does not have permission to access or edit the study.
  - Error_I_DENIED_USER_ACCESS

- **Message Code:** Error_I_DENIED_USER_ACCESS

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For any other questions please contact support@ceirr-network.org
**Input Type**: Strain Name

**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]

**Value List**

- Text
- NA

**Validation**

- Field length: Maximum length: 50 characters

**Examples**


**Notes**

- WHO Reference for influenza viruses: http://www.cdc.gov/flu/about/viruses/types.htm
- [HxN2] can be used in cases where a partial subtype has been determined (e.g., H5Nx, HxN2).
- If there are mixed subtypes contained within a single sample use A/chicken/Fujian/4/2002 (mixed) for Strain_name and enter additional subtype information in the Comments field.

**Dependent Fields**

- Strain Name must be valid
- Strain Name must be unique
- Strain Name must be unique

**Message Code**

<table>
<thead>
<tr>
<th>Message Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error_00_INVALID_FIELD_LENGTH</td>
<td>Field length must be valid</td>
</tr>
</tbody>
</table>

**Validation**

- Strain Name must be valid
- Strain Name must be unique
- Strain Name must be unique

**Message Code**

<table>
<thead>
<tr>
<th>Message Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error_01_INVALID_SPECIES_STRAIN_TEXT</td>
<td>Species/strain text is invalid</td>
</tr>
</tbody>
</table>

**Validation**

- Strain Name must be valid
- Strain Name must be unique
- Strain Name must be unique

**Message Code**

<table>
<thead>
<tr>
<th>Message Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error_02_INVALID_LOCATION_STRAIN_TEXT</td>
<td>Location is invalid</td>
</tr>
<tr>
<td>Error_03_INVALID_Number_STRAIN_TEXT</td>
<td>Number is invalid</td>
</tr>
<tr>
<td>Error_04_INVALID_STRAIN_YEAR</td>
<td>Year is invalid</td>
</tr>
</tbody>
</table>

**Validation**

- Strain Name must be valid
- Strain Name must be unique
- Strain Name must be unique

**Message Code**

<table>
<thead>
<tr>
<th>Message Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error_05_INVALID_STRAIN_SUBTYPE</td>
<td>Subtype is invalid</td>
</tr>
</tbody>
</table>

**Validation**

- Strain Name must be valid
- Strain Name must be unique
- Strain Name must be unique

**Message Code**

<table>
<thead>
<tr>
<th>Message Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error_06_INVALID_STRAIN_OPEN_BRACKETS</td>
<td>Open brackets must be present after year in isolation date</td>
</tr>
</tbody>
</table>

**Validation**

- Strain Name must be valid
- Strain Name must be unique
- Strain Name must be unique

**Message Code**

<table>
<thead>
<tr>
<th>Message Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error_07_INVALID_STRAIN_BRAKETS</td>
<td>Brackets cannot be present after year in isolation date</td>
</tr>
</tbody>
</table>

**Validation**

- Strain Name must be valid
- Strain Name must be unique
- Strain Name must be unique

**Message Code**

<table>
<thead>
<tr>
<th>Message Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error_08_INVALID_STRAIN_OPEN_BRAKETS</td>
<td>Open brackets cannot be present after year in isolation date</td>
</tr>
</tbody>
</table>

**Validation**

- Strain Name must be valid
- Strain Name must be unique
- Strain Name must be unique

**Message Code**

<table>
<thead>
<tr>
<th>Message Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error_09_INVALID_STRAIN_CLOSED_BRAKETS</td>
<td>Closing brackets cannot be present after year in isolation date</td>
</tr>
</tbody>
</table>

**Validation**

- Strain Name must be valid
- Strain Name must be unique
- Strain Name must be unique

**Message Code**

<table>
<thead>
<tr>
<th>Message Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error_10_INVALID_STRAIN_NUMBER_STRAIN_ELEMENTS</td>
<td>Number is invalid</td>
</tr>
</tbody>
</table>

For any other questions please contact support@ceirr-network.org
<table>
<thead>
<tr>
<th>Input Type</th>
<th>Definition</th>
<th>Format</th>
<th>Value List</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Segment</td>
<td>Text Field</td>
<td>Text</td>
<td>NA, HA, NP, NA, NS, P42, PA, PB1, PB2, OTH-</td>
<td>The entry must be one and only one member of the Value List. Enter NA if the reagent was not deposited with BEI. The entry must use the HGVS reference for annotation guidelines to describe mutations, insertions, or deletions in any gene segment order. <a href="http://www.hgvs.org/mutnomen/quickref.html">http://www.hgvs.org/mutnomen/quickref.html</a></td>
</tr>
<tr>
<td>Mutations</td>
<td>Text Field</td>
<td>Text</td>
<td>NA, PB2, or OTH-Luciferase</td>
<td>Enter NA if the gene segment has no mutation. Format for amino acid mutation: protein_name:p.[mutation_information] For a single mutation, list the original amino acid, its position, and the new amino acid in brackets: PB2:p.[E627K] For a deletion within a single protein, list the amino acid, its position, and 'del': NS:p.[H155del] For a stop codon, use an asterisk: NA:p.[K471_*472insHHHHHH] Format for non-coding mutation: gene_segment_name:c.[mutation_information] For a single mutation, enter the position, the original nucleotide, &gt;, and the new nucleotide: PB2:c.[273C&gt;T] For a deletion: enter the position, del, and the nucleotide deleted: NA:c.[73delT] To list both amino acid and non-coding changes, comma-separate the individual mutation information in any order: HA:p.[N220K;Q222L],PB1:c.[273C&gt;T;274A&gt;G;275G&gt;T] Enter NA if the field length is not deposited with BEI. Enter NA if the reagent was not deposited with BEI.</td>
</tr>
<tr>
<td>Dependent Fields</td>
<td>Validation</td>
<td>Value should be one of valid values as in list.</td>
<td>Value should be one of valid values as in list.</td>
<td></td>
</tr>
</tbody>
</table>

For any other questions please contact support@ceirr-network.org
<table>
<thead>
<tr>
<th>Input Type</th>
<th>Definition</th>
<th>Format</th>
<th>Value List</th>
<th>Curation</th>
<th>Notes</th>
<th>Dependent Fields</th>
<th>Validation</th>
<th>Message Code</th>
<th>Validation</th>
<th>Message Code</th>
</tr>
</thead>
<tbody>
<tr>
<td>Contact Name</td>
<td>The name of the point-of-contact for reagent requests or the name of the BEI depositor</td>
<td>Text Field</td>
<td>None</td>
<td>None</td>
<td>The entry must be a valid email address.</td>
<td>Validate field length</td>
<td>Error_70_INVALID_FIELD_LENGTH</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Contact Email</td>
<td>Email address for the point-of-contact</td>
<td>Text Field</td>
<td>None</td>
<td>N</td>
<td>Must be a valid email address.</td>
<td>Validate field length</td>
<td>Error_70_INVALID_FIELD_LENGTH</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Availability</td>
<td>Whether the reagent is available to share with other laboratories on the reagents page of the CEIRR Public Website.</td>
<td>Text</td>
<td>Y</td>
<td>Y</td>
<td>If the reagent was referenced in multiple publications, comma-separate the individual PMIDs. Enter NA if the reagent was not referenced in a publication.</td>
<td>Validate field length</td>
<td>Error_1_INVALID_VALUE</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Publication PMID</td>
<td>The PubMed Unique Identifier (PMID) for the publication in which the reagent was published.</td>
<td>Text</td>
<td>NA</td>
<td>NA</td>
<td>If there are no comments, enter NA.</td>
<td>Validate field length</td>
<td>Error_70_INVALID_FIELD_LENGTH</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Examples:
Jane Smith, or Davey M. Jones
jsmith@email.edu
Y
19465683, or NA
NA

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