### Project_Identifier

**Input Type:** Text Field  
**Definition:** A unique Project Identifier generated by the DPCC by combining the Center-generated Project Code and a random 4-digit number.  
**Format:** Project Code_XXXX  
**Value List:** None  
**Curation:** The entry must be a Project Identifier value registered with the DPCC.  
**Examples:** SJCProj02_4001  
**Notes:** Enter NA if the reagent is not related to a surveillance submission.

### Contributing_Institution

**Input Type:** Text Field  
**Definition:** The institution code for the group that CREATED THE REAGENT. Must be one of the CEIRS institution codes assigned by NIAID.  
**Format:** Text  
**Value List:** None  
**Curation:** Must be an Institution Code value registered with the DPCC  
**Examples:** SJC101  
**Validation:** Must be an Institution Code value registered with the DPCC  
**Message Code:** Error_1_INVALID_VALUE

### Reagent_Name

**Input Type:** Text Field  
**Definition:** Name of the reagent assigned by the investigator  
**Format:** Text  
**Value List:** None  
**Curation:** None  
**Examples:** F225.2  
**Validation:**  
**Message Code:**

### Sample_Identifier

**Input Type:** Text Field  
**Definition:** Identifier assigned to the virus used to create the reagent  
**Format:** Text  
**Value List:** None  
**Curation:** It should match with the Sample_Identifier provided in related data submissions.  
**Examples:** 21145-001a  
**Validation:**  
**Message Code:**

For any other questions please contact support@niaidceirs.org
<table>
<thead>
<tr>
<th>Input Type</th>
<th>Strain_Name</th>
<th>Antibody_Type</th>
<th>Purification</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Definition</strong></td>
<td>The WHO strain name of the virus that was used to create the reagent</td>
<td>Description of the type of antibody or antiserum</td>
<td>Description of the purification of the monoclonal or polyclonal antibody</td>
</tr>
<tr>
<td><strong>Format</strong></td>
<td>Antigenic Type/Host of Origin/Geographical Origin/Strain Number/Year of Isolation (Subtype)</td>
<td>Text</td>
<td>Text</td>
</tr>
<tr>
<td></td>
<td>rg-Antigenic Type/Host of Origin/Geographical Origin/Strain Number/Year of Isolation [rg details] (Subtype)</td>
<td>Maximum length: 3 characters</td>
<td>Maximum length: 3 characters</td>
</tr>
<tr>
<td><strong>Value List</strong></td>
<td>Text</td>
<td>ATS</td>
<td>NA</td>
</tr>
<tr>
<td></td>
<td>U</td>
<td>HAS</td>
<td>MAB</td>
</tr>
<tr>
<td></td>
<td>NA</td>
<td>XA</td>
<td>KG</td>
</tr>
<tr>
<td></td>
<td>IG</td>
<td>GM</td>
<td>IGY</td>
</tr>
<tr>
<td></td>
<td>TIG</td>
<td>NA</td>
<td>U</td>
</tr>
<tr>
<td><strong>Curation</strong></td>
<td>WHO strain naming convention: Fields must be ordered as follows and separated with the '/' character: 1. The antigenic type (e.g., A, B, C, D) 2. The host of origin (e.g., swine, equine, chicken. For human-origin viruses, no host of origin designation is given.) 3. Geographical origin (e.g., Denver, Taiwan) 4. Strain number (e.g., 15, 7) 5. Year of isolation (e.g., 2009, 1934) 6. For influenza A viruses, the hemagglutinin and neuraminidase antigen description in parentheses (e.g., (H1N1), (H3N2)) If the strain is a reverse genetic virus, prefix Strain_Name with rg-. Provide reverse genetic details in brackets between year of isolation and subtype. Enter NA if the reagent is not related to a virus strain.</td>
<td>The entry must be one and only one member of the Value List. Values are case-sensitive and must be entered in all-caps. Enter NA if reagent is ATS or HAS. Enter U if purification is unknown.</td>
<td></td>
</tr>
<tr>
<td><strong>Notes</strong></td>
<td>Reference: <a href="http://www.cdc.gov/flu/about/viruses/types.htm">http://www.cdc.gov/flu/about/viruses/types.htm</a> (H0N0) can be used in cases where a partial subtype has been determined (e.g., H5N1). If there are mixed subtypes contained within a sample use A/chicken/Fujian/4/2002 (mixed), A/chicken/Fujian/4/2002 (mixed), A/swine/owa2/233-56/2011 (H3N2v), A/duck/Alberta/35/1976 (H1N1), B/Hong Kong/432/2014, C/Texas/19876/2011, rg-A/Puerto Rico/8/1934 (H1N1), or rg-A/Egypt/N03072/2010 [PR8 internal R 6+2] (H5N1)</td>
<td>ATS = Antiserum HAS = Hyperimmune antiserum MAB = Monoclonal antibody PAB = Polyclonal antibody XA = IgA KG = IgG GM = IgM IGY = IgY TIG = Total Ig NA = Not Applicable U = Unknown</td>
<td></td>
</tr>
<tr>
<td><strong>Dependent Fields</strong></td>
<td>Purification, Specificity</td>
<td>Antibody_Type</td>
<td></td>
</tr>
<tr>
<td><strong>Validation</strong></td>
<td>Validate field length</td>
<td>Field value should be one of valid values as in list. Field value should be one of valid values as in list.</td>
<td></td>
</tr>
<tr>
<td><strong>Message Code</strong></td>
<td>Error_70_INVALID_FIELD_LENGTH</td>
<td>Error_1_INVALID_VALUE</td>
<td>Error_1_INVALID_VALUE</td>
</tr>
<tr>
<td><strong>Validation</strong></td>
<td>Host of origin element of strain name must be alphanumeric, underscore, dash, period, or single quote: a-z, A-Z, 0-9, _-, ., '</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Message Code</strong></td>
<td>Error_137_INVALID_HOST_SPECIES_STRAIN_TEXT</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Validation</strong></td>
<td>Geographical origin element of strain name must be alphanumeric, underscore, dash, period, or single quote: a-z, A-Z, 0-9, _-, ., '</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Message Code</strong></td>
<td>Error_138_INVALID_LOCATION_STRAIN_TEXT</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Validation</strong></td>
<td>Strain number element of strain name must be alphanumeric, underscore, dash, or period: a-z, A-Z, 0-9, _-, ., '</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Message Code</strong></td>
<td>Error_139_INVALID_STRAIN_NUMBER_STRAIN_TEXT</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Validation</strong></td>
<td>Year of isolation element of strain name must be 4-digit year.</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Message Code</strong></td>
<td>Error_110_INVALID_STRAIN_YEAR</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Validation</strong></td>
<td>If strain is influenza A, subtype must be present as text between parentheses.</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Message Code</strong></td>
<td>Error_112_INVALID_STRAIN_SUBTYPE</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Validation</strong></td>
<td>Brackets cannot be present if strain does not have rg- prefix.</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Message Code</strong></td>
<td>Error_119_INVALID_STRAIN_BRACKETS</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Input Type</td>
<td>Immunogen</td>
<td>Specificity</td>
<td>Produced_in</td>
</tr>
<tr>
<td>------------</td>
<td>-----------</td>
<td>-------------</td>
<td>-------------</td>
</tr>
<tr>
<td>Definition</td>
<td>Text Field</td>
<td>Text Field</td>
<td>Text Field</td>
</tr>
<tr>
<td>Description of the immunogen used to generate the antibody or antiserum</td>
<td>A description of what the antibody or antiserum is specific to</td>
<td>The animal in which the antibody or antiserum originates</td>
<td>Information about the activity or specificity of the antibody or antiserum in laboratory assays</td>
</tr>
<tr>
<td>Format</td>
<td>Text</td>
<td>Text</td>
<td>Text</td>
</tr>
<tr>
<td>Maximum length: 50 characters</td>
<td>Maximum length: 50 characters</td>
<td>Maximum length: 50 characters</td>
<td>Maximum length: 200 characters</td>
</tr>
<tr>
<td>Value List</td>
<td>Text</td>
<td>Text</td>
<td>Text</td>
</tr>
<tr>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>Curation</td>
<td>None</td>
<td>None</td>
<td>None</td>
</tr>
<tr>
<td>The entry must be a valid BEI number.</td>
<td></td>
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<tr>
<td>Examples</td>
<td>BPL-inactivated virus, synthetic peptide, or purified HA protein</td>
<td>H7, H1b, H7 clade, or 2.3.4.4</td>
<td>Human, goat, mouse, mouse (humanized), or ferret</td>
</tr>
<tr>
<td>Notes</td>
<td>For monoclonal and polyclonal antibodies, list a target protein. For antiserum or samples derived from H5N1 viruses, include clade information if available.</td>
<td>Enter NA if activity or specificity are unknown.</td>
<td>Enter NA if the reagent was not deposited with BEI.</td>
</tr>
<tr>
<td>Dependent Fields</td>
<td>Antibody_Type</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Validation</td>
<td>Validate field length</td>
<td>Validate field length</td>
<td>Validate field length</td>
</tr>
<tr>
<td>Message Code</td>
<td>Error_70_INVALID_FIELD_LENGTH</td>
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<td></td>
</tr>
</tbody>
</table>

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<table>
<thead>
<tr>
<th>Input Type</th>
<th>Contact_Name</th>
<th>Contact_Email</th>
<th>Availability</th>
<th>Publication_PMID</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Definition</td>
<td>The name of the point-of-contact for reagent requests or the name of the BEI depositor</td>
<td>Email address for the point-of-contact</td>
<td>Whether the reagent is available to share with other investigators on the reagents page of the CEIRS Public Website</td>
<td>The PubMed Unique Identifier (PMID) for the publication in which the reagent was published.</td>
<td>Text describing anything else of interest related to the submission</td>
</tr>
<tr>
<td>Format</td>
<td>FirstName LastName</td>
<td><a href="mailto:Email@domain.com">Email@domain.com</a></td>
<td>Text</td>
<td>PMID</td>
<td>Text</td>
</tr>
<tr>
<td></td>
<td>FirstName MI. LastName</td>
<td>Maximum length: 50 characters</td>
<td>Maximum length: 1 character</td>
<td>Maximum length: 50 characters</td>
<td>Maximum length: 2000 characters</td>
</tr>
<tr>
<td>Value List</td>
<td>None</td>
<td>None</td>
<td>Y</td>
<td>Text</td>
<td>Text</td>
</tr>
<tr>
<td>Curation</td>
<td>None</td>
<td>The entry must be a valid email address.</td>
<td>The entry must be one and only one member of the Value List.</td>
<td>The entry must be a valid PMID number: 7 or 8-digit number with no leading zeros. <a href="http://www.nlm.nih.gov/bsd/mms/medlineelements.html#pmid">http://www.nlm.nih.gov/bsd/mms/medlineelements.html#pmid</a></td>
<td>None</td>
</tr>
<tr>
<td>Examples</td>
<td>Jane Smith, or Davey M. Jones</td>
<td><a href="mailto:jsmith@email.edu">jsmith@email.edu</a></td>
<td>Y</td>
<td>19465683, or NA</td>
<td>NA</td>
</tr>
<tr>
<td>Notes</td>
<td>Y = Yes N = No</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>If there are no comments, enter NA.</td>
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<td>Dependent Fields</td>
<td>Validate field length</td>
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<tr>
<td>Validation</td>
<td>Must be a valid email address.</td>
<td>Must be a valid PMID.</td>
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<td>Message Code</td>
<td>Error_114_INVALID_EMAIL</td>
<td>Error_96_INVALID_PMID</td>
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</table>

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