

	Strain_Name
Input Type	Text Field
Definition	The WHO or ICTV strain name of the virus that was used to create the reagent
Format	<p>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)</p> <p>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]</p> <p>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]</p> <p>Maximum length: 150 characters</p>
Value List	Text U NA
Curation	<p>For influenza viruses, strain names most follow WHO naming convention: Fields must be ordered as follows and separated with the '/' character:</p> <ol style="list-style-type: none"> 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)) <p>For SARS-CoV-2 viruses, strain names most follow ICTV naming convention: Fields must be ordered as follows and separated with the '/' character:</p> <ol style="list-style-type: none"> 1. Virus name (e.g., SARS-CoV-2) 2. The host of origin (e.g., human. Human-origin viruses must include the origin designation.) 3. Country of geographical origin as a three-letter code from the DPCC's Country Codes list (e.g., USA, MEX, CAN) 4. Strain number (e.g., 15, 7) 5. Year of isolation (e.g., 2019, 2020) <p>For all other viruses, please use the following convention: Fields must be ordered as follows and separated with the '/' character:</p> <ol style="list-style-type: none"> 1. Virus name (e.g., MERS-CoV, Bat-CoV, etc.) 2. The host of origin (e.g., human, bat, camel. Human-origin viruses must include the origin designation.) 3. Geographical origin, either regional locality or country (e.g., Denver, Taiwan) 4. Strain number (e.g., 15, 7) 5. Year of isolation (e.g., 2019, 2020) <p>If 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.</p>
Examples	<p>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)</p> <p>For SARS-CoV-2: SARS-CoV-2/human/USA/NY-PV08486/2020</p> <p>For other viruses: PHEV-CoV/swine/USA/15TOSU25049/2015</p>
Notes	<p>WHO Reference for influenza viruses: http://www.cdc.gov/flu/about/viruses/types.htm ICTV Reference for SARS-CoV-2 viruses: https://pubmed.ncbi.nlm.nih.gov/32123347</p> <p>(HxNx) can be used in cases where a partial subtype has been determined (e.g., H5Nx, HxN2).</p> <p>If there are mixed subtypes contained within a sample use A/chicken/Fujian/4/2002 (mixed) for Strain_Name and enter additional subtype information in the Comments field.</p>
Dependent Fields	Infected, Days_Post_Infection
Validation	Validate field length
Message Code	Error_70_INVALID_FIELD_LENGTH
Validation	Host of origin element of strain name must be alphanumeric, underscore, dash, period, or single quote: a-z, A-Z, 0-9, _, -, ., ' ,
Message Code	Error_137_INVALID_HOST_SPECIES_STRAIN_TEXT
Validation	Geographical origin element of strain name must be alphanumeric, underscore, dash, period, or single quote: a-z, A-Z, 0-9, _, -, ., ' ,
Message Code	Error_138_INVALID_LOCATION_STRAIN_TEXT
Validation	Strain number element of strain name must be alphanumeric, underscore, dash, or period: a-z, A-Z, 0-9, _, -, . ,
Message Code	Error_139_INVALID_STRAIN_NUMBER_STRAIN_TEXT
Validation	Year of isolation element of strain name must be 4-digit year.
Message Code	Error_110_INVALID_STRAIN_YEAR
Validation	If strain is influenza A, subtype must be present as text between parentheses.
Message Code	Error_112_INVALID_STRAIN_SUBTYPE
Validation	Brackets cannot be present if strain does not have rg- prefix.
Message Code	Error_119_INVALID_STRAIN_BRACKETS
Validation	If included, the strain must have a matched pair of opening and closing brackets or parentheses.
Message Code	Error_158_INVALID_STRAIN_OPEN_BRACKETS
Validation	The strain must have four or five elements separated by a slash '/' character.
Message Code	Error_159_INVALID_NUMBER_OF_STRAIN_ELEMENTS

	Antibody_Type	Purification	Immunogen	Specificity
Input Type	Text Field	Text Field	Text Field	Text Field
Definition	Description of the type of antibody or antiserum	Description of the purification of the monoclonal or polyclonal antibody	Description of the immunogen used to generate the antibody or antiserum	A description of what the antibody or antiserum is specific to
Format	Text Maximum length: 3 characters	Text Maximum length: 3 characters	Text Maximum length: 50 characters	Text Maximum length: 50 characters
Value List	ATS HAS MAB PAB	IGA IGG IGM IGY TIG NA U	Text NA	Text NA
Curation	The entry must be one and only one member of the Value List. Values are case-sensitive and must be entered in all-caps.	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.	None	None
Examples	MAB	IGA	BPL-inactivated virus, synthetic peptide, or purified HA protein	H7, H1b, H7 clade, or 2.3.4.4
Notes	ATS = Antiserum HAS = Hyperimmune antiserum MAB = Monoclonal antibody PAB = Polyclonal antibody	IGA = IgA IGG = IgG IGM = IgM IGY = IgY TIG = Total Ig NA = Not Applicable U = Unknown		For monoclonal and polyclonal antibodies, list a target protein. For antiserum or samples derived from H5N1 viruses, include clade information if available.
Dependent Fields	Purification, Specificity	Antibody_Type		Antibody_Type
Validation	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
Message Code	Error_1_INVALID_VALUE	Error_1_INVALID_VALUE	Error_70_INVALID_FIELD_LENGTH	Error_70_INVALID_FIELD_LENGTH
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	Contact_Email	Availability	Publication_PMD	Comments
Input Type	Text Field	Text Field	Text Field	Text Field
Definition	Email address for the point-of-contact	Whether the reagent is available to share with other investigators on the reagents page of the CEIRS Public Website	The PubMed Unique Identifier (PMID) for the publication in which the reagent was published.	Text describing anything else of interest related to the submission
Format	Text@domain.com Maximum length: 50 characters	Text Maximum length: 1 character	PMID Maximum length: 50 characters	Text Maximum length: 2000 characters
Value List	None	Y N	Text NA	Text NA
Curation	The entry must be a valid email address.	The entry must be one and only one member of the Value List.	The entry must be a valid PMID number: 7 or 8-digit number with no leading zeros. http://www.nlm.nih.gov/bsd/mms/medlineelements.html#pmid	None
Examples	jsmith@email.edu	Y	19465683, or NA	NA
Notes		Y = Yes N = No	If the reagent was referenced in multiple publications, comma-separate the individual PMIDs. Enter NA if the reagent was not referenced in a publication.	If there are no comments, enter NA.
Dependent Fields				
Validation	Validate field length	Field value should be one of valid values as in list.	Validate field length	Validate field length
Message Code	Error_70_INVALID_FIELD_LENGTH	Error_1_INVALID_VALUE	Error_70_INVALID_FIELD_LENGTH	Error_70_INVALID_FIELD_LENGTH
Validation	Must be a valid email address.		Must be a valid PMID.	
Message Code	Error_114_INVALID_EMAIL		Error_96_INVALID_PMD	
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