

DPCC Data Standard Reference for Plasmid Reagent v1.2

	Project_Identifier	Contributing_Institution	Reagent_Name	Sample_Identifier
<b>Input Type</b>	Text Field	Text Field	Text Field	Text Field
<b>Definition</b>	A unique Project Identifier generated by the DPCC by combining the Center-generated Project Code and a random 4-digit number	The institution code for the group that CREATED THE REAGENT. Must be one of the CEIRS institution codes assigned by NIAID.	Name of the reagent assigned by the investigator	Identifier assigned to the virus used to create the reagent
<b>Format</b>	Project_Code_XXXX Maximum length: 21 characters	Center three-letter code followed by three digits. Maximum length: 6 characters	Text Maximum length: 150 characters	Center-specific Allowed characters include alphanumeric, hyphen, and underscore: a-z, A-Z, 0-9, -, _ Maximum length: 50 characters
<b>Value List</b>	None	None	None	Text NA
<b>Curation</b>	The entry must be a Project Identifier value registered with the DPCC.	The entry must be an Institution Code value registered with the DPCC.  Center 3-letter codes are case-sensitive and must be entered in all-caps.	None	It should match with the Sample_Identifier provided in related data submissions.
<b>Examples</b>	SJCProj02_4001	SJC101	pHW2000 VN1203 PB2 E627K	21145-001a
<b>Notes</b>				Enter NA if the reagent is not related to a surveillance submission.
<b>Dependent Fields</b>				
<b>Validation</b>	Project_Identifier should be a valid project identifier.	Must be an Institution Code value registered with the DPCC	Validate field length	Validate field length
<b>Message Code</b>	Error_9_PROJECT_NOT_FOUND	Error_1_INVALID_VALUE	Error_70_INVALID_FIELD_LENGTH	Error_70_INVALID_FIELD_LENGTH
<b>Validation</b>	Project_Identifier exists but user does not have permission to access or edit the project.			
<b>Message Code</b>	Error_4_DENIED_USER_ACCESS			
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Input Type	Strain Name
<b>Definition</b> Text Field The WHO or ICTV strain name of the virus that was used to create the reagent	
<b>Format</b>	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
<b>Value List</b>	Text U NA
<b>Curation</b>	For influenza viruses, strain names most follow WHO 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))  For SARS-CoV-2 viruses, strain names most follow ICTV naming convention: Fields must be ordered as follows and separated with the '/' character: 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)  For all other viruses, please use the following convention: Fields must be ordered as follows and separated with the '/' character: 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)  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.
<b>Examples</b>	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  For other viruses: PHEV-CoV/swine/USA/15TOSU25049/2015
<b>Notes</b>	WHO Reference for influenza viruses: <a href="http://www.cdc.gov/flu/about/viruses/types.htm">http://www.cdc.gov/flu/about/viruses/types.htm</a> ICTV Reference for SARS-CoV-2 viruses: <a href="https://pubmed.ncbi.nlm.nih.gov/32123347">https://pubmed.ncbi.nlm.nih.gov/32123347</a>  (HxNx) can be used in cases where a partial subtype has been determined (e.g., H5Nx, HxN2).  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.
<b>Dependent Fields</b>	Infected, Days_Post_Infection
<b>Validation</b>	Validate field length
<b>Message Code</b>	Error_70_INVALID_FIELD_LENGTH
<b>Validation</b>	Host of origin element of strain name must be alphanumeric, underscore, dash, period, or single quote: a-z, A-Z, 0-9, -, ., '
<b>Message Code</b>	Error_137_INVALID_HOST_SPECIES_STRAIN_TEXT
<b>Validation</b>	Geographical origin element of strain name must be alphanumeric, underscore, dash, period, or single quote: a-z, A-Z, 0-9, -, ., '
<b>Message Code</b>	Error_138_INVALID_LOCATION_STRAIN_TEXT
<b>Validation</b>	Strain number element of strain name must be alphanumeric, underscore, dash, or period: a-z, A-Z, 0-9, -, ., '
<b>Message Code</b>	Error_139_INVALID_STRAIN_NUMBER_STRAIN_TEXT
<b>Validation</b>	Year of isolation element of strain name must be 4-digit year.
<b>Message Code</b>	Error_110_INVALID_STRAIN_YEAR
<b>Validation</b>	If strain is influenza A, subtype must be present as text between parentheses.
<b>Message Code</b>	Error_112_INVALID_STRAIN_SUBTYPE
<b>Validation</b>	Brackets cannot be present if strain does not have rg- prefix.
<b>Message Code</b>	Error_119_INVALID_STRAIN_BRACKETS
<b>Validation</b>	If included, the strain must have a matched pair of opening and closing brackets or parentheses.
<b>Message Code</b>	Error_158_INVALID_STRAIN_OPEN_BRACKETS
<b>Validation</b>	The strain must have four or five elements separated by a slash '/' character.
<b>Message Code</b>	Error_159_INVALID_NUMBER_OF_STRAIN_ELEMENTS

	Vector	Segment	Mutations	BEI Number
<b>Input Type</b>	Text Field	Text Field	Text Field	Text Field
<b>Definition</b>	Name of the vector used to create the plasmid	The influenza virus segment or other element that the plasmid contains	A description of the mutation(s) or non-coding change(s) made in the plasmid reagent	The identification number assigned to the reagent by BEI
<b>Format</b>	Text Maximum length: 50 characters	Text Maximum length: 30 characters	An HGVS-formatted list describing sequence changes Maximum length: 400 characters	BEI Number Maximum length: 20 characters
<b>Value List</b>	None	HA HE MP NA NP NS P3 P42 PA PB1 PB2 OTH-	Text NA	Text NA
<b>Curation</b>	None	The entry must be one and only one member of the Value List.	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>	The entry must be a valid BEI number.
<b>Examples</b>	pHW2000	PB2, or OTH-Luciferase	PB2:p.[E627K;T255K;H155del]	NR-12277
<b>Notes</b>			<p><b>Format for amino acid mutation:</b> 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 multiple mutations within a single protein, separate individual mutations by a semicolon: HA:p.[N220K;Q222L] 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]</p> <p><b>Format for non-coding mutation:</b> 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 multiple mutations within a single gene, separate individual mutations by a semicolon: PB1:c.[273C&gt;T;274A&gt;G;275G&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],HA:c.[273C&gt;T;274A&gt;G;275G&gt;T] Enter NA if the gene segment has no mutation.</p>	Enter NA if the reagent was not deposited with BEI.
<b>Dependent Fields</b>				
<b>Validation</b>	Validate field length	Field value should be one of valid values as in list.	Validate field length	Validate field length
<b>Message Code</b>	Error_70_INVALID_FIELD_LENGTH	Error_1_INVALID_VALUE	Error_70_INVALID_FIELD_LENGTH	Error_70_INVALID_FIELD_LENGTH
<b>Validation</b>		Validate field length		
<b>Message Code</b>		Error_75_INVALID_FIELD_LENGTH_OTH		
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	Contact Name	Contact Email	Availability	Publication PMID	Comments
<b>Input Type</b>	Text Field	Text Field	Text Field	Text Field	Text Field
<b>Definition</b>	The name of the point-of-contact for reagent requests or the name of the BEI depositor	Email address for the point-of-contact	Whether the reagent is available to share with other investigators on the reagent's 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
<b>Format</b>	FirstName LastName FirstName MI. LastName Maximum length: 50 characters	Text@domain.com Maximum length: 50 characters	Text Maximum length: 1 character	PMID Maximum length: 50 characters	Text Maximum length: 2000 characters
<b>Value List</b>	None	None	Y N	Text NA	Text NA
<b>Curation</b>	None	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. <a href="http://www.nlm.nih.gov/bsd/mms/medlineelements.htm#pmid">http://www.nlm.nih.gov/bsd/mms/medlineelements.htm#pmid</a>	None
<b>Examples</b>	Jane Smith, or Davey M. Jones	jsmith@email.edu	Y	19465683, or NA	NA
<b>Notes</b>			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.
<b>Dependent Fields</b>					
<b>Validation</b>	Validate field length	Validate field length	Field value should be one of valid values as in list.	Validate field length	Validate field length
<b>Message Code</b>	Error_70_INVALID_FIELD_LENGTH	Error_70_INVALID_FIELD_LENGTH	Error_1_INVALID_VALUE	Error_70_INVALID_FIELD_LENGTH	Error_70_INVALID_FIELD_LENGTH
<b>Validation</b>		Must be a valid email address.		Must be a valid PMID.	
<b>Message Code</b>		Error_114_INVALID_EMAIL		Error_96_INVALID_PMID	
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