

DPCC Data Standard Reference for Ferret Tissue Reagent v1.1

	Project_Identifier	Contributing_Institution	Sample_Identifier	Sample_Material
<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.	Identifier assigned to the reagent	Material from which the reagent was derived
<b>Format</b>	Project_Code_XXXX Maximum length: 21 characters	Center three-letter code followed by three digits. Maximum length: 6 characters	Center-specific Allowed characters include alphanumeric, hyphen, and underscore: a-z, A-Z, 0-9, -, _ Maximum length: 50 characters	Text Maximum length: 30 characters
<b>Value List</b>	None	None	Text NA	AIR BAL BLO CCF CCO CCT CLO FEC LFF LUN NAL NAS NTS ORP OTH- OTT PLS RCS SER SLU SOI SPU TFB TFH TFL TFS TFT TJN TNC TRS WAT U
<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	The entry must be one and only one member of the Value List.  Values are case-sensitive and must be entered in all-caps.
<b>Examples</b>	SJCPrj02_4001	SJC101	SSC-001	LUN, or TFS
<b>Notes</b>				AIR = Air BAL = Bronchoalveolar lavage BLO = Blood CCF = Combined cloacal and fecal CCO = Combined cloacal and orai-pharyngeal CCT = Combined cloacal and tracheal CLO = Cloacal FEC = Feces LFF = Lung lavage fluid LUN = Lungs NAL = Nasal lavage NAS = Nasal swab NTS = Combined nasal throat swab ORP = Orai-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 TJN = Tissue from lymph node TNC = Tissue from nasal cavity TRS = Tracheal swab WAT = Water U = Unknown
<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	Field value should be one of valid values as in list. NOTE: User can enter other value by prefixing 'OTH:'
<b>Message Code</b>	Error_9_PROJECT_NOT_FOUND	Error_1_INVALID_VALUE	Error_70_INVALID_FIELD_LENGTH	Error_1_INVALID_VALUE
<b>Validation</b>	Project_Identifier exists but user does not have permission to access or edit the project.			Validate field length
<b>Message Code</b>	Error_4_DENIED_USER_ACCESS			Error_75_INVALID_FIELD_LENGTH_OTH
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Strain_Name	
<b>Input Type</b>	Text Field
<b>Definition</b>	The WHO or ICTV strain name of the virus that was used to create the reagent
<b>Format</b>	<p><b>Influenza A virus:</b> 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><b>Influenza B, C, or D virus:</b> 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><b>SARS-CoV-2 and other viruses:</b> 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>
<b>Value List</b>	Text U NA
<b>Curation</b>	<p><b>For influenza viruses,</b> 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"> <li>1. The antigenic type (e.g., A, B, C, D)</li> <li>2. The host of origin (e.g., swine, equine, chicken. For human-origin viruses, no host of origin designation is given.)</li> <li>3. Geographical origin (e.g., Denver, Taiwan)</li> <li>4. Strain number (e.g., 15, 7)</li> <li>5. Year of isolation (e.g., 2009, 1934)</li> <li>6. For influenza A viruses, the hemagglutinin and neuraminidase antigen description in parentheses (e.g., (H1N1), (H3N2))</li> </ol> <p><b>For SARS-CoV-2 viruses,</b> 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"> <li>1. Virus name (e.g., SARS-CoV-2)</li> <li>2. The host of origin (e.g., human. Human-origin viruses must include the origin designation.)</li> <li>3. Country of geographical origin as a three-letter code from the DPCC's Country Codes list (e.g., USA, MEX, CAN)</li> <li>4. Strain number (e.g., 15, 7)</li> <li>5. Year of isolation (e.g., 2019, 2020)</li> </ol> <p><b>For all other viruses,</b> please use the following convention: Fields must be ordered as follows and separated with the '/' character:</p> <ol style="list-style-type: none"> <li>1. Virus name (e.g., MERS-CoV, Bat-CoV, etc.)</li> <li>2. The host of origin (e.g., human, bat, camel. Human-origin viruses must include the origin designation.)</li> <li>3. Geographical origin, either regional locality or country (e.g., Denver, Taiwan)</li> <li>4. Strain number (e.g., 15, 7)</li> <li>5. Year of isolation (e.g., 2019, 2020)</li> </ol> <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>
<b>Examples</b>	<p><b>For influenza:</b> A/Hong Kong/1/1968 (H3N2), A/chicken/Fujian/4/2002 (H3N6), A/chicken/Fujian/4/2002 (HbNx), 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/1987/2011, 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><b>For SARS-CoV-2:</b> SARS-CoV-2/human/USA/NY-PV08486/2020</p> <p><b>For other viruses:</b> PHEV-CoV/swine/USA/15TOSU25049/2015</p>
<b>Notes</b>	<p>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></p> <p>(HbNx) 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>
<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



