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## 3.2.S.2.3. CONTROL OF MATERIALS – SOURCE, HISTORY AND GENERATION OF PLASMIDS [AGC]

This section was originally prepared for plasmids used in the manufacture of Original drug substance. Presentations using Original drug substance have been discontinued but the manufacturing process information is continued to be used for plasmids used as starting materials for variant drug substances.

#### 3.2.S.2.3.1. Plasmid Cell Bank and Linear DNA Template Manufacturer(s)

The plasmid master cell bank (MBC) manufacture and associated testing is performed in the Pfizer facility at 875 Chesterfield Parkway West, Chesterfield MO 63017.

The plasmid master cell bank inventory is stored in Pfizer's storage facilities located at 875 Chesterfield Parkway West, Chesterfield MO 63017 and 1 Burtt Road, Andover MA 01810. The master cell bank testing was performed at 4.2 1 ind.

The master cell bank sequence testing was performed at 4.2 1 ind.

The master cell bank sequence testing was performed at 4.2 1 ind.

The plasmid working cell bank (WCB) manufacture, starting material (linear DNA template) manufacture and associated testing are performed at AGC Biologics GmbH, Czernyring 22, 69115 Heidelberg, Germany. The plasmid WCB inventory is stored in AGC's GMP storage facilities located at AGC Biologics GmbH, Germany. The cell bank testing was performed at AGC Biologics GmbH and 4.2 1st ind

The cell bank sequence testing was performed 4.2 1 ind.

#### 3.2.S.2.3.2. Plasmid Cell Banking System, Characterization and Testing

Plasmid cell banks have been prepared in accordance with the following guidelines: ICH Q5D Derivation and characterization of cell substrates used for production of biotechnological/biological products

Cell banking operations were performed in a controlled manufacturing area with appropriate precautions against adventitious contamination and cross-contamination from other cell lines. AGC used the MCB established by Pfizer Chesterfield. Details can be found in Section 3.2.S.2.3 Control of Materials – Source, History, and Generation of Plasmids [Pfizer Chesterfield].

#### 3.2.S.2.3.2.1. Preparation of pST4-1525 Working Cell Bank

Manufacture of the WCB is done according to batch documentation. A pre-culture flask containing 4.21 ind. medium with 4.21 ind. of the master cell bank material is cultivated at  $37^{\circ}$ C and 180 rpm until  $OD_{600nm}$  2-4 is reached. Cells are then harvested by adding cryopreservation media and filling of the cell suspension into labelled vials for the WCB. After cryopreservation of the filled vials using a controlled rate freezer the vials are finally transferred to storage in vapor phase of liquid nitrogen at  $\leq -130$  °C.

#### 3.2.S.2.3.2.2. Release Testing of the Plasmid Working Cell Bank

The analytical methods at AGC for characterization, release testing and retesting of the Working Cell Bank (WCB) include tests for purity and quality (culture purity, contaminating phages, cell viability, retention of expression plasmid, plasmid copy number), identity of host strain, expression plasmid and expression gene (confirmation of *E. coli* species, genetic identity of *E. coli* strain, restriction digest of expression plasmid, sequence confirmation of gene and flanking regions).

Culture purity and identity testing performed on the plasmid WCB C-211901 provide confirmation that the cell bank is free from microbial and bacteriophage contamination and is of an *E. coli* lineage. The studies were designed in accordance with ICH Q5D guidelines.

Table 3.2.S.2.3-1 lists the release tests performed, acceptance criteria, and results for the WCB C-211901.

Table 3.2.S.2.3-1. Release Testing of Plasmid WCB Batch C-211901

Test	Method	Acceptance Criteria	Result
Purity	•		
Culture purity	Ph. Eur. 2.6.12 and 2.6.13	4.2 1 ind.	
Bacteriophage – lytic & lysogenic	Infection with T4 bacteriophage with/without irradiation	Free of bacteriophage and lysogenic prophage	Complies
Identity			
Host cell identity (Genotypic testing)	API 20 E patter by test kit	Identified as derived from Escherichia coli	4.2 1 ind.
Genetic identity of E. coli	RAPD fingerprint analysis of genomic DNA using PAGE/AGE	RAPD fingerprint corresponds to reference RAPD fingerprint.	RAPD fingerprint corresponds to reference RAPD fingerprint
Quality	-		
Cell viability	Plating on TSA	4.2 1 ind.	
Plasmid retention	Replica plating on LB agar with and without antibiotic.	4.21 ind. cells resistant to kanamycin	4.2.1 ind. cells resistant to kanamycin
Identity of expression	on construct and heterologous gene	•	•
Restriction map analysis	Digestion with restriction enzymes and separation of DNA fragments on agarose.	Banding pattern on agarose gel corresponds to banding pattern of reference plasmid	Banding pattern on agarose gel corresponds to banding pattern of reference plasmid
DNA sequencing	DNA sequencing	DNA of the expression cassette corresponds to theoretical sequence	Complies

Abbreviations: WCB = working cell bank; Ph. Eur. = European Pharmacopoeia; CFU = colony forming unit; RAPD = randomly amplified polymorphic DNA; PAGE = polyacrylamide gel electrophoresis; AGE = agarose gel electrophoresis; TSA = tryptic soy agar; LB = lysogeny broth; RP = result pending

# 3.2.S.2.3.2.3. Preparation, Qualification and Storage of Renewal Plasmid Working Cell Banks (WCBs)

At this stage no renewal of plasmid working cell bank is defined.

#### 3.2.S.2.3.2.4. Plasmid Cell Bank Stability Testing

To ensure the quality (shelf-life) of the existing WCB, a re-examination on cell viability, retention of plasmid and DNA sequence confirmation shall be performed every 5 years. If fermentation is carried out routinely, the quality of the WCB may be evaluated by process data generated during production to justify the stability and to ensure the shelf-life of WCB.

#### 3.2.S.2.3.3. Linear DNA Template Manufacturing

Cells from the WCB are thawed and the culture is expanded in shake flasks, which are then used to inoculate the pre-fermenter. An aliquot of the pre-fermenter is used to inoculate the main culture in a 4.2 1 ind. fermenter and the fermentation step is ended by time. The entire fermentation process at AGC is performed without addition of antibiotics. After fermentation the cells are broken by chemical lysis. After filtration, the remaining solution containing plasmid DNA is concentrated, the buffer exchanged and then passed to Chromatography. During DSP, the DNA is purified by two sequential column steps (anion-exchange chromatography and hydrophobic interaction chromatography) and then linearized 4.2 1 ind. Finally, the linearization enzyme is removed by a third column (mixed-mode chromatography) 4.2 1 ind. The linear DNA template is aliquoted, filled and frozen.

Table 3.2.S.2.3-2. Process Flow for Linear DNA Template

Process Step	Process Description
Pre-culture I	One vial from the working cell bank is thawed and used to inoculate a
	shake flask (pre-culture I)
Pre-culture II	One flask of pre-culture I is inoculated in the pre-fermenter (pre-culture II).
Main culture	The pre-culture II is transferred into a 4.2 1 ind. fermenter (total volume) and
	the fermentation is ended by time.
Cell harvest	The production fermenter is harvested by disc separator.
Cell lysis and RNA	Resuspension of cell mass; chemical cell lysis and pDNA preparation using
precipitation	static mixer and subsequent calcium chloride precipitation.
Ultrafiltration/ Diafiltration 1	Ultra- and diafiltration using hollow fiber modules to concentrate and
	buffer exchange in preparation for next chromatography step.
Anion Exchange	4.21 ind. column v4.21 ind. is used for capturing of
Chromatography	pDNA material.
Hydrophobic Interaction	4.2 1 ind. solumn is used for this polishing process step of
Chromatography	pDNA material.
Ultrafiltration/ Diafiltration 2	Ultra- and diafiltration using hollow fiber modules to concentrate and
	buffer exchange followed by a 0.2 µm filtration.
Linearization	Linearization using wave rockers and single use bags.
Mixed-Mode Chromatography	A mixed-mode column with 4.2 1 ind. resin is used for this
	purification process step of the linearized DNA template.
Ultrafiltration/ Diafiltration 3	Ultra- and diafiltration using hollow fiber modules to concentrate and
	buffer exchange with 4.2 1 ind. for final fill.
Filtration and filling	The linear DNA template filtered via 0.2 µm filtration and stored frozen at
	≤ -60 °C.

Purified water manufactured at the facility is used throughout the linear DNA template process and meets compendial requirements. A list of the raw materials used in the manufacture of the linear DNA template is provided in Table 3.2.S.2.3-3. All the materials used in the manufacture of the linear DNA template are animal origin free or the risk of carry-over of any adventitious contaminant from the animal derived material is very low risk to insignificant. Section 3.2.A.2 Adventitious Agents Safety Evaluation [BNT Marburg] is providing the evaluation of adventitious agent risk. All materials are sourced from approved suppliers. Inspection of materials received and examination of vendor certificate of analysis are performed for raw materials.

Table 3.2.S.2.3-3. Raw Materials and External Buffers Used in the Manufacture of Linear DNA Template

Raw Material	Supplier Grade <sup>a,b</sup>		
1,4-Dithiothreitol (DTT)	Non compendial		
Acetic acid	Ph. Eur., JP, USP		
Ammonia solution 25%	Ph. Eur.		
Ammonium sulfate	Ph. Eur., NF		
Boric acid	Ph. Eur., NF		
Calcium chloride dihydrate	Ph. Eur., JP, USP		
Citric acid monohydrate	Ph. Eur., JP, USP		
Cobalt sulfate heptahydrate	Non compendial		
di-Sodium hydrogen phosphate dihydrate	Ph. Eur., USP		
D(+)-Glucose monohydrate	Ph. Eur., USP		
4.2 1 ind.	Non compendial		
EDTA	Ph. Eur., ChP, JP, USP		
Ethanol 96%	Ph. Eur.		
HEPES	Non compendial		
Hydrochloric acid 25%	Ph. Helv.		
Iron(III)-chloride-hexahydrate	Ph. Eur., JPE		
Magnesium acetate tetrahydrate	Ph. Eur.		
Manganese(II) sulfate monohydrate	Ph. Eur., USP		
85-% phosphoric acid	Ph. Eur., JPE, NF		
Polypropylene glycol 2000	Non compendial		
Potassium acetate	Ph. Eur.		
Potassium chloride	Ph. Eur., USP, JP		
Sodium chloride	Ph. Eur., JP, USP		
Sodium dihydrogen phosphate monohydrate	BP, USP		
Sodium dodecyl sulfate	NF		
Sodium hydroxide	Ph. Eur.		
Sodium molybdate dihydrate Ph. Eur.			
Tris(hydroxymethyl)amino methane	Ph. Eur., USP, ChP, JPC		
Tris(hydroxymethyl)amino methane hydrochloride	Non compendial		
Tris(hydroxymethyl)amino methane acetate	Non compendial		
Zinc sulfate heptahydrate Ph. Eur., USP			

a. Equivalent can be used. Supplier Grades of incoming materials listed.

HEPES = 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid; DTT = DL-dithiothreitol; EDTA = edetate disodium dihydrate or ethylenediaminetetraacetic acid; NF = National Formulary; USP = United States Pharmacopeia; JP= Japan Pharmacopeia; Ph. Eur. = European Pharmacopeia; ChP = Chinese Pharmacopoeia; Ph. Helv. = Swiss Pharmacopoeia; JPE = Japanese Pharmacopoeia Excipients; JPC = Japanese Pharmaceutical Codex; BP = British Pharmacopoeia

b. Gross visual, CoA check and ID test.

The chromatography resins and filters used in linear DNA template manufacture are described in Table 3.2.S.2.3-4.

Table 3.2.S.2.3-4. Chromatography Resins and Filters Used in Linear DNA Template Manufacture

4.2 1 ind.	esin	
4.2 1 ind.	resin	
4.2 1 ind.	resin	
30 kDa MWCC	Dultrafiltration membrane	
Depth filters (de	leep bed filtration)	
0.2 μm filters		

#### 3.2.S.2.3.4. Linear DNA Template Specifications

The release specifications for the linear DNA template are given in Table 3.2.S.2.3-5. The analytical control strategy includes sampling and testing of a selected number of attributes prior to linearization and the remainder of the attributes on the final linear DNA template. Those attributes analyzed prior to linearization are listed first (circular plasmid DNA) and those analyzed after linearization are listed second (linear DNA template).

Table 3.2.S.2.3-5. Linear DNA Template Specifications

<b>Analytical Procedure</b>	Quality Attribute	Acceptance Criteria	
CIRCULAR PLASMID DNA			
Characteristics	•		
UV260	DNA Concentration	4.2 1 ind.	
Restriction map	Poly A tail integrity	Bands at approximately 4.2 1 ind.	
Identity			
Sanger sequencing	Identity of transcribed region	Homology to reference <sup>a</sup>	
	Identity of poly A tail	Report results	
Purity		•	
AEX-HPLC	Plasmid topology	Supercoiled form: 4.2 1 ind. Linear form: 4.2 1 ind.	
<b>Process-Related Impurities</b>			
Assay RNA analysis	Residual host cell RNA	4.2 1 ind.	
qPCR DNA analysis	Assay RNA analysis		
LINEAR DNA TEMPLATE			
Characteristics			
Appearance (clarity)	Clarity	Clear to slightly opalescent (not more turbid than reference suspension II)	
Appearance (coloration)	Coloration	Colorless to slightly colored (not more colored than reference solution	
pН	pH	4.2 1 ind.	
UV260	DNA Concentration		
Purity	<u> </u>	<u>-</u>	
AEX-HPLC	Linearization Efficiency (Plasmid topology)	Linear form: 4.2 1 ind.	
<b>Process-Related Impurities</b>			
Total residual protein by μBCA	Residual protein	4.2 1 ind.	
Safety			
Bioburden	Bioburden	4.2 1 ind.	
Endotoxin	Endotoxin		

a. Defined as 100% identity with DNA reference sequence in transcribed region excluding poly(dA:dT)-tract Abbreviations: AEX-HPLC = anion exchange high pressure liquid chromatography; CFU = colony forming units; EU = endotoxin unit

#### 3.2.S.2.3.5. Linear DNA Template Method Descriptions

Specific analytical procedures, including compendial and non-compendial methods, were used to assess characteristics, identity, purity and safety of the circular plasmid DNA and linear DNA template. Descriptions of the analytical procedures are provided below

#### 3.2.S.2.3.5.1. Appearance (Clarity and Coloration)

The linear DNA template is assessed for clarity and coloration in accordance with the current European Pharmacopoeia procedure, Ph. Eur. 2.2.1 and Ph. Eur. 2.2.2, respectively.

#### 3.2.S.2.3.5.2. pH

The linear DNA template is analyzed for pH in accordance with the current European Pharmacopoeia procedure, Ph. Eur. 2.2.3.

#### 3.2.S.2.3.5.3. DNA Concentration by Spectroscopy

Using a spectrophotometer, the absorbance at 260 nm is used to determine the concentration of the circular plasmid DNA and linear DNA template. The specific absorption coefficient or absorptivity ( $a_{260}$ ) for dsDNA (given below) is used for the concentration calculation.

 $a_{260} = 4.2 1 \text{ ind.}$ 

#### 3.2.S.2.3.5.4. Identity by Restriction Mapping\*

## \*Identification by Restriction Mapping was removed for future circular plasmid DNA batch analysis. The method summary is retained for historical purposes.

A restriction endonuclease mapping method is used to determine identity of the circular plasmid DNA. The reference material and test samples are subjected to digestion using the following enzymes or groups of enzymes: 4.2 1 ind. all of which cleave at specific sites. The enzymatic digest produces a set of nucleic acid fragments which are separated through sieving via agarose gel electrophoresis and visualized by addition of a detection reagent. The bands of test samples are compared to the expected band pattern to confirm identity of the circular plasmid DNA by ensuring that all appropriate bands are present.

#### 3.2.S.2.3.5.5. Identity of the Transgene Region by DNA Sanger Sequencing

Using Sanger sequencing the identity of the transgene region of circular plasmid DNA is determined. By involving electrophoresis and incorporation of chain-termination dideoxynucleotides by DNA polymerase the output sequence is compared to the nucleotide reference sequence.

#### 3.2.S.2.3.5.6. Poly A Tail Integrity by Restriction Digestion

A restriction endonuclease mapping method is used to determine poly A tail integrity of the circular plasmid DNA. The test samples are subjected to digestion using the following enzymes or groups of enzymes: 4.2 1 ind. all of which cleave at specific sites. The enzymatic digest produces a set of nucleic acid fragments which are separated through sieving via agarose gel electrophoresis and visualized by addition of a detection reagent. The bands of test samples are compared to the theoretical band size values at approximately and approximately using the DNA ladder as a size reference to confirm integrity of the poly A tail by ensuring that all appropriate bands are present.

#### 3.2.S.2.3.5.7. Plasmid Topology and Linearization Efficiency by AEX-HPLC

Anion-exchange chromatography is used to separate negatively charged nucleic acids and determine plasmid topology for circular plasmid DNA and linearization efficiency for linear DNA template. Chromatograms are compared to the respective reference material and amount of supercoiled and linear form evaluated by integration of peak area.

#### 3.2.S.2.3.5.8. Total Residual Protein by µBCA

Quantification of protein impurities in linear DNA template using a protein assay kit. Residual protein in samples reduce Cu<sup>2+</sup> to Cu<sup>+</sup> ions, which form a purple-colored reaction product by chelation with bicinchoninic acid (BCA). Absorption of measured samples at 562 nm.

#### 3.2.S.2.3.5.9. Host Cell DNA by qPCR

This assay for determination of host cell DNA of the circular plasmid DNA is based on the principle of the quantitative PCR. DNA is first isolated and purified. During the purification step, samples are digested by proteinase K, lysed and washed. The qPCR assay contains altogether 4.2 1 ind.

A reporter dye is used as a fluorescent probe (4.2 1 ind.)

The emitted fluorescence is proportional to the initial amount of target DNA amplified by 40 cycles of denaturation and elongation. The absolute quantification of the residual DNA in the sample is performed using the standard curve generated by the DNA Standard.

#### 3.2.S.2.3.5.10. Host Cell RNA by Assay Kit

Before host cell RNA analysis of the circular plasmid DNA, the samples is treated with 4.2 1 ind to prevent possible interference of DNA with the assay reagent. Following DNA digestion, residual RNA is analyzed with a selective fluorophore. RNA concentration is calculated based on a linear regression of a RNA standard curve (4.2 1 ind. 4.2 1 ind.

#### 3.2.S.2.3.5.11. Residual Kanamycin by HPLC-FLD and ELISA

High performance liquid chromatography (HPLC) with fluorescence detection (FLD) is used as analytical procedure for detection residual kanamycin in circular plasmid DNA. The test method is a limit test based on a standard addition.

Wherever the samples matrix is not allowing for a determination of residual kanamycin by HPLC, an Enzyme-linked Immunosorbent Assay (ELISA) is used.

#### 3.2.S.2.3.5.12. Bacterial Endotoxin Assay (Limulus Amebocyte Lysate [LAL])

The linear DNA template is assessed for bacterial endotoxin in accordance with the current European Pharmacopoeia procedure, Ph. Eur. 2.6.14, Method D.

#### 3.2.S.2.3.5.13. Bioburden

The linear DNA template is tested for microbiological contamination in accordance with the current European Pharmacopoeia procedure, Ph. Eur. 2.6.12.

#### 3.2.S.2.3.6. Linear DNA Template Method Verification/Qualification Data

The plasmid-specific methods are listed in Table 3.2.S.2.3-6. The compendial methods were verified following applicable Pharmacopoeias. The non-compendial methods for linear DNA template were qualified/verified to ensure analytical methods are sound and suitable for their intended use. A gap analysis will be performed and documented to identify any supplemental qualification to align with ICH requirements. The gaps identified will be addressed either prior to transferring the methods to relevant sites or during the transfer activities. The qualification/verification results are summarized in Table 3.2.S.2.3-6.

 Table 3.2.S.2.3-6.
 Product Specific Qualification or Verification Summaries

Attribute	Method	Qualification-Verification Summaries				
CIRCULAR PLASMID DNA						
DNA	UV 260	Parameter	Acceptance criteria	Result		
Concentration <sup>a</sup>		System suitability	RSD of standard curve and controls 4.2 1 ind.	RSD = 4.21  ind.		
		H	4.2 1 ind.			
		Specificity	4.2 1 ind.			
		Linearity	Visual inspection of the plot demonstrates linearity	Visual inspection of the plot demonstrates linearity		
		Accuracy	4.2 1			
		Precision/	<b>14</b> / 1			
		Repeatability				
		Precision/ Intermediate				
		Precision				
		Range	The range is defined as the concentration interval for which all target criteria for linearity, accuracy and precision are fulfilled	4.2 1 ind.		
		buffers used buffers will	ation identified that the concent was too high. The method was be used. easurement with diluted buffers.	amended and diluted		
		J. Robuit of Inc	man diller man diller bullets.			
Plasmid	AEX-HPLC	Parameter	Acceptance criteria	Result		
Topology <sup>a</sup>		Specificity	The chromatogram of the formulation buffer injection does not contain any	The chromatogram of the formulation buffer injection does not contain		
			interfering peaks.	any interfering peaks.		

Table 3.2.S.2.3-6. Product Specific Qualification or Verification Summaries

Attribute	Method	Qualification-Verification Summaries		
			The main peak is visually separated from product related species or degradation products, if visible.	The main peak is visually separated from product related species and degradation products for stressed material.
		Linearity	Visual inspection of the plot demonstrates linearity	Visual inspection of the plot demonstrates linearity
		Accuracy Precision/ Repeatability Precision/ Intermediate Precision	4.2 1	ind.
		Range	The range is defined as concentration for which all target criteria for linearity, accuracy and precision are fulfilled	4.2 1 ind.
		Limit of quantification	Lowest concentration which passes the following criteria:  4.2 1 ind.	4.2 1 ind.
Residual host cell RNA	Assay RNA analysis	Repeatability: 4.2 Specificity: Positive result Limit of quantifications	ve controls show positive result,	negative controls show
Residual host cell DNA	qPCR DNA analysis	Repeatability: 4.2 Accuracy: 4.2 1 Specificity: 1. Positive control result	2 1 ind. ind. s show positive result, negative tals above LOQ in product matri	<u> </u>
LINEAR DNA T	EMPLATE	-	<del>-</del>	
DNA Concentration <sup>a</sup>	UV 260	Parameter System suitability	Acceptance criteria  RSD of standard curve and controls 4.2 1 ind.	Result 4.2 1 ind.

Table 3.2.S.2.3-6. Product Specific Qualification or Verification Summaries

Method	Qualification-Verification Summaries		
	Specificity	Mean A <sub>260</sub> of formulation buffer measurements 4.2 1 ind.	4.2 1 ind.
	Linearity	Visual inspection of the plot demonstrates linearity	Visual inspection of the plot demonstrates linearity
	Accuracy Precision/	4 2 1	ind
	Repeatability		III IG.
	Intermediate Precision		
	Range	The range is defined as the concentration interval for which all target criteria for linearity, accuracy and precision are fulfilled.	4.2 1 ind.
AEX-HPLC	Specificity	The chromatogram of the formulation buffer injection does not contain any interfering peaks.  The main peak is visually	Result The chromatogram of the formulation buffer injection does not contain any interfering peaks. The main peak is visually separated from product
		related species or degradation products, if visible.	related species and degradation products for stressed material.
	Linearity	Visual inspection of the plot demonstrates linearity	Visual inspection of the plot demonstrates
			linearity
	Accuracy	4.2 1	
	Accuracy  Precision/ Repeatability Precision/ Intermediate	4.2 1	
	AEX-HPLC	Accuracy Precision/ Repeatability Precision/ Intermediate Precision Range  AEX-HPLC Parameter Specificity	Specificity  Mean A <sub>260</sub> of formulation buffer measurements 4.2 1 ind.  Linearity  Visual inspection of the plot demonstrates linearity  Accuracy Precision/ Repeatability Precision  Range  The range is defined as the concentration interval for which all target criteria for linearity, accuracy and precision are fulfilled.  AEX-HPLC  Parameter Specificity  The chromatogram of the formulation buffer injection does not contain any interfering peaks.  The main peak is visually separated from product related species or degradation products, if visible.  Linearity  Visual inspection of the plot

Table 3.2.S.2.3-6. Product Specific Qualification or Verification Summaries

Attribute	Method	Qualification-Verification Summaries		
		Limit of quantification	accuracy and precision are fulfilled  Lowest concentration which passes the following criteria:  4.2 1 inc.	4.2 1 ind.
Total Residual Protein <sup>a</sup>	μBCA Assay	Parameter	Acceptance criteria 4.2 1 ind.	Result
riotem	Assay	System suitability	RSD of standard curve and controls 4.2 1 ind.	4.2 1 ind.
			Mean of calculated negative control 4.2 1 ind.  Recovery of positive control 4.2 1 ind.	4.2 1 ind.
		Specificity	Mean A <sub>562</sub> of diluted formulation buffer is below mean A <sub>562</sub> of 4.2 1 ind.  BSA standard	$A_{562}$ formulation buffer: 4.21 ind $A_{562}$ Standard: 4.21 ind.
		Linearity	Visual inspection of the plot demonstrates linearity	Visual inspection of the plot demonstrates linearity
		Accuracy Precision/ Repeatability	4.2 1 in	id.
		Limit of quantitation	The range is defined as that interval of BSA concentration for which all target criteria for linearity, accuracy and precision are fulfilled	All acceptance criteria are fulfilled for spiked BSA concentrations between 4.2 1 ind.

Table 3.2.S.2.3-6. Product Specific Qualification or Verification Summaries

Attribute	Method	Qualification-Verification Summaries						
Endotoxin <sup>c</sup>	USP <85>; Ph Eur. 2.6.14 & JP 4.01	Compendial qualification performed per local compendia. The criteria of the standard curve was found to be valid (i.e. correlation coefficient (r) must be $\geq  0.980 $ . The sample solution must not interfere with the test (e.g. inhibition/enhancement). The sample must have a maximum valid dilution (MVD) established. Summary of Inhibition/Enhancement Data						
		Endotoxin	λ	Calculated MVD	Qualified			
		Limit	(EU/mL)		Dilution			
		4.2 1 ind.   0.005 EU/mL 1:4000 1:50						
		Inhibition/Enhancement Results from the first two manufactured by Sample Dilution Spike Recovery (%) Results Batch 71703-212002: 1:50 127 % < 0.250 Batch 71703-211901: 1:50 143 % < 0.250						
	I		701. 1.50	13 70	▼ 0.230 LC/IIIL			
Bioburden <sup>c</sup>	Ph. Eur. 2.6.12	Challenge Recove	ry Testing (base	ed on Compendial guida ecovery of inoculated of	ance to ensure test			
Bioburden <sup>c</sup>		Challenge Recove	ry Testing (base	ed on Compendial guid	ance to ensure test			
Bioburden <sup>c</sup>		Challenge Recove articles are non-ini Organism Pseudomonas ae	ry Testing (base	ed on Compendial guide ecovery of inoculated of	ance to ensure test			
Bioburden <sup>c</sup>		Challenge Recove articles are non-ini Organism Pseudomonas ae Bacillus subtilis	ry Testing (base hibitory to the re ruginosa	od on Compendial guida ecovery of inoculated of %Recovery 94 % 115 %	ance to ensure test			
Bioburden <sup>c</sup>		Challenge Recove articles are non-ini Organism Pseudomonas ae Bacillus subtilis Staphylococcus a	ry Testing (base hibitory to the re ruginosa	od on Compendial guida ecovery of inoculated of %Recovery 94 % 115 % 116 %	ance to ensure test			
Bioburden <sup>c</sup>		Challenge Recove articles are non-ini Organism Pseudomonas ae Bacillus subtilis	ry Testing (base hibitory to the re ruginosa nureus	od on Compendial guida ecovery of inoculated of %Recovery 94 % 115 %	ance to ensure test			

- a. Platform Method Verification
- b. Compendial Verified
- c. Compendial Qualified

Abbreviations: AEX-HPLC = anion exchange high pressure liquid chromatography; BCA = bicinchoninic acid; USP = United States Pharmacopoeia; Ph. Eur. = European Pharmacopoeia; RSD = relative standard deviation; R<sup>2</sup> = regression coefficient; OP = operator; MVD = maximum valid dilution; EU = endotoxin unit; LOQ = limit of quantification

#### 3.2.S.2.3.7. Linear DNA Template Batch Analysis

The batch analysis data for representative commercial scale batches of the linear DNA template are given in Table 3.2.S.2.3-7 below. At the time of manufacture of these batches, for some parameters different acceptance criteria compared to the commercial specifications (Table 3.2.S.2.3-5) applied. These differences are footnoted in the table below.

Table 3.2.S.2.3-7. Circular and Linear DNA Template Batch Analysis for Commercial Scale Batches

Analytical	Acceptance Criteria		Results 1	for Batch	
Procedure		71703- 211901	71703- 212002	71703- 214504	71703- 214605
CIRCULAR PLA	SMID DNA				
Characteristics					
DNA	4.2 1 ind.				
Concentration					
(UV260)					
Identity					
Restriction map by agarose gel <sup>d</sup>	Comparable to reference <sup>d</sup>	Complies	Complies	Complies	Complies
Sanger	100% homology to	Complies	Complies	Complies	Complies
sequencing -	reference				
identity of the transcribed					
region					
Sanger	Report results	Complies <sup>c</sup>	Complies <sup>c</sup>	Complies <sup>c</sup>	Compliesc
sequencing -	Report results	Compiles	Compiles	Compiles	Compiles
identity of the					
poly A tail					
Poly A tail	Comparable to reference	Complies	Complies	Complies	Complies
integrity by	Comparable to reference	compiles	Compiles	Compiles	Compiles
agarose gel					
Purity					
Plasmid topology by AEX-HPLC	Supercoiled form: 4.2 1 ind. Linear form 4.2 1 ind.		2 1		
Process Related I		-//			
Residual Host					
Cell RNA	4.2 1 ind.				
Residual Host	+				
Cell DNA					
LINEAR DNA TE	EMPLATE				ı
Characteristics					
Appearance	Clear to slightly opalescent	Complies	Complies	Complies	Complies
(clarity)	(not more turbid than	Compiles	Compiles	Compiles	Compiles
()	reference suspension II)				
Appearance	Colorless to slightly	Complies	Complies	Complies	Complies
(coloration)	colored (not more colored	1			1
` ′	than reference solution				
pН	$\mathbf{I}$ $\mathbf{I}$ $\mathbf{I}$ $\mathbf{I}$ $\mathbf{I}$				
DNA	ij4.∠ I IIIQ.				
Concentration					
(UV260)					
Purity					
AEX-HPLC	Linear form: 4.2 1 ind.				
<b>Process Related I</b>					
Total residual					
protein					
Safety	4.2 1				
Bioburden					
Endotoxin					

Table 3.2.S.2.3-7. Circular and Linear DNA Template Batch Analysis for Commercial Scale Batches

Analytical	Acceptance Criteria					
Procedure		71703- 71703- 71703- 71703-				
		211901	212002	214504	214605	

- a. Defined as 100% identity with DNA reference sequence in transcribed region excluding poly(dA:dT)-tract
- b. Denotes specification at time of release of the batch. Specification was subsequently updated as shown in Table 3.2.S.2.3-5.
- c. Accurate number of A (poly A stretch) upstream from sequence pattern GCATATGACT could not be verified.
- d. Identification by Restriction Mapping was removed for future circular plasmid DNA batch analysis. Results are retained for historical purposes.

Abbreviations: AEX-HPLC = Anion exchange high pressure liquid chromatography; CFU = colony forming units; EU = endotoxin units; ND = not determined; RP = result pending

#### 3.2.S.2.3.8. Circular and Linear DNA Template Standards

AGC used the circular plasmid DNA and linear DNA template standard materials provided by Pfizer (see Section 3.2.S.2.3 Control of Materials – Source, History, and Generation of Plasmids [Pfizer Chesterfield]) for the analysis of the circular and linear DNA template batches described above as well as for the characterization of their own standard materials. AGC prepared a circular plasmid DNA Control Standard (Contr.Std.-ES-71703-211901) and linear plasmid DNA Reference Standard (Ref.-Std.-71703-211901) from the first commercial batch 71703-211901 for future use. The test results for the standards are provided in Table 3.2.S.2.3-8 and Table 3.2.S.2.3-9. Two hundred 2.0 mL cryogenic vials were filled with 1000  $\mu$ L for each standard. Storage at  $\leq$  -60°C and retesting of the standard is done every year. The parent batch is also part of the stability program.

Table 3.2.S.2.3-8. Circular Plasmid DNA Reference Material Batch Contr.Std.-ES-71703-211901

Test	Method	Result
DNA Concentration	UV spectroscopy at 260	4.2 1 ind.
	nm	
Supercoiled form	AEX-HPLC	
Residual host cell DNA	Assay RNA analysis	

Abbreviations: AEX-HPLC = Anion exchange high pressure liquid chromatography

Table 3.2.S.2.3-9. Linear DNA Template Reference Material Batch Ref.-Std.-71703-211901

Test	Method	Result
DNA Concentration	UV spectroscopy at 260 nm	4.2 1 ind.
Linearization efficiency	AEX-HPLC	

Abbreviations: AEX-HPLC = Anion exchange high pressure liquid chromatography

# 3.2.S.2.3.9. Linear and Circular DNA Template Stability and Period of Use 3.2.S.2.3.9.1. Stability Plan

The shelf life of 18 months is established for both the circular plasmid DNA and the linear DNA template as described in Section 3.2.S.2.3 Control of Materials - Source, History and Generation of Plasmids [Pfizer Chesterfield].

The stability of circular plasmid DNA and linear DNA template is monitored using two representative batches at each stage (71703-211901 and 71703-212002). The stability samples are stored in representative 5 mL and 30 mL downscale versions of the 1000 mL PETG bottles used for long-term storage of linear DNA template, with a filling volume of 5 mL or 20 mL per stability container, respectively.

The stability programs have been established according to the protocols detailed in Table 3.2.S.2.3-10 through Table 3.2.S.2.3-13. In addition to DNA Concentration and Topology, Appearance (Clarity and Coloration) and pH of linear DNA template will be monitored during the stability study.

Table 3.2.S.2.3-10. Stability Protocol for Circular Plasmid DNA Stored at ≤ -60 °C (Long Term Storage Condition)

Analytical Procedure	Test Intervals (Months) a
UV (DNA concentration)	0, 4, 6, 12, 18, 24, 36
AEX HPLC (Topology)	0, 4, 6, 12, 18, 24, 36
Bioburden	0
Endotoxin	0

Initial data (t0) are from release testing.

Table 3.2.S.2.3-11. Stability Protocol for Circular Plasmid DNA Stored at 5 ± 3°C (Accelerated Storage Condition)

Analytical Procedure	Test Intervals (Months) <sup>a</sup>
UV (DNA concentration)	0, 4, 6
AEX HPLC (Topology)	0, 4, 6

a. Initial data (t0) are from release testing.

Table 3.2.S.2.3-12. Stability Protocol for Linear DNA Template Stored at ≤ -60 °C (Long Term Storage Condition)

Analytical Procedure	Test Intervals (Months) a
Appearance (Clarity)	0, 4, 6, 12, 18, 24, 36
Appearance (Coloration)	0, 4, 6, 12, 18, 24, 36
pH	0, 4, 6, 12, 18, 24, 36
UV (DNA concentration)	0, 4, 6, 12, 18, 24, 36
AEX HPLC (Topology) (Topology)	0, 4, 6, 12, 18, 24, 36

Initial data (t0) are from release testing.

Table 3.2.S.2.3-13. Stability Protocol for Linear DNA Template Stored at  $5 \pm 3$  °C (Accelerated Storage Condition)

Analytical Procedure	Test Intervals (Months) a
Appearance (Clarity)	0, 4, 6
Appearance (Coloration)	0, 4, 6
pH	0, 4, 6
UV (DNA concentration)	0, 4, 6
AEX HPLC (Topology)	0, 4, 6

Initial data (t0) are from release testing.

#### 3.2.S.2.3.9.2. Stability Data

The results of the stability studies for the circular plasmid DNA batches 71703-211901 and 71703-212002 stored at  $\leq$  -60 °C and 5  $\pm$  3 °C are provided in Table 3.2.S.2.3-14 through Table 3.2.S.2.3-17.

Table 3.2.S.2.3-14. Circular Plasmid DNA Batch 71703-211901 - Stability Data at ≤ -60°C Storage Condition

Assay	Acceptance Criteria	Time points					
		0	4M	6M	12M	18M	24M
DNA	4.2 1 ind.						S
Concentration			9	1	In (		
	Supercoiled form: 4.2 1 ind.  Linear form: 4.2 1 ind.						S

Abbreviations: M = months; S = scheduled for testing

Table 3.2.S.2.3-15. Circular Plasmid DNA Batch 71703-211901 - Stability Data at  $5 \pm 3$  °C Storage Condition

Assay	Acceptance Criteria	Time points				
		0	4M	6M		
DNA	4.2 1 ind.					
Concentration			1 Inc			
Plasmid	Supercoiled form: 4.2 1 ind.	<b>1</b> 4.2		/		
topology	Linear form: 4.2 1 ind.					

Table 3.2.S.2.3-16. Circular Plasmid DNA Batch 71703-212002 - Stability Data at ≤ -60°C Storage Condition

Assay	Acceptance Criteria	Time points					
		0	4M	6M	12M	18M	24M
DNA Concentration	4.2 1 ind.	1	7 1	ir	nd		
Plasmid	Supercoiled form: ≥ 80.0 %				<b>1 .</b> .		
topology	Linear form: ≤ 5.0 %						

Abbreviations: M = months; S = scheduled for testing

Table 3.2.S.2.3-17. Circular Plasmid DNA Batch 71703-212002 - Stability Data at  $5 \pm 3$  °C Storage Condition

Assay	Acceptance Criteria	Time points					Time points		
		0	4M	6M					
DNA	4.2 1 ind.								
Concentration			1 100						
Plasmid	Supercoiled form: 4.2 1 ind.	<b></b>	THIM.						
topology	Linear form 4.2 1 ind.								

Abbreviations: M = months; S = scheduled for testing

The results of the stability testing for the linear DNA template batches 71703-211901 and 71703-212002 stored at  $\leq$  -60 °C and 5  $\pm$  3 °C are provided in Table 3.2.S.2.3-18 through Table 3.2.S.2.3-21.

Table 3.2.S.2.3-18. Linear DNA Template Batch 71703-211901 - Stability Data at ≤ -60°C Storage Condition

Assay	Acceptance Criteria	Time points					
	-	0	4M	6M	12M	18M	24M
Clarity	Clear to slightly opalescent (not more turbid than reference suspension II)	Complies	Complies	Complies	Complies	Complies	S
Coloration	Colorless to slightly colored (not more colored than reference solution	Complies	Complies	Complies	Complies	Complies	S
pН	reference solution 4.2 1 ind.	1	•	1			S
DNA Concentration		<b>14</b> .			nc		S
Linearization	Linear form: 4.2 1 ind.						S
Efficiency (Plasmid topology)							

Table 3.2.S.2.3-19. Linear DNA Template Batch 71703-211901 - Stability Data at  $5 \pm 3$  °C Storage Condition

Assay	Acceptance Criteria	Time points					
		0	4M	6M			
Clarity	Clear to slightly opalescent (not more turbid than reference suspension II)	Complies	Complies	Complies			
Coloration	Colorless to slightly colored (not more colored than reference solution	Complies	Complies	Complies			
pН	4.2 1 ind.	4	4 - 1				
DNA	1.2 1		1 100				
Concentration		7.4	1 ind.				
Linearization	Linear form: 4.2 1 ind.						
Efficiency							
(Plasmid							
topology)							

Abbreviations: M = months; S = scheduled for testing

Table 3.2.S.2.3-20. Linear DNA Template Batch 71703-212002 - Stability Data at ≤-60 °C Storage Condition

Assay	Acceptance Criteria	Time points					
		0	4M	6M	12M	18M	24M
Clarity	Clear to slightly opalescent (not more turbid than reference suspension II)	Complies	Complies	Complies	Complies	Complies	S
Coloration	Colorless to slightly colored (not more colored than reference solution	Complies	Complies	Complies	Complies	Complies	S
pН	4.2 1 ind.	1	9	1:	100		S
DNA Concentration		<b>64</b> .		1 i			S
Linearization	Linear form: 4.2 1 ind.						S
Efficiency							
(Plasmid							
topology)	1 0 1 1	1.6:					

Table 3.2.S.2.3-21. Linear DNA Template Batch 71703-212002 - Stability Data at  $5\pm3$  °C Storage Condition

Assay	Acceptance Criteria	Time points				
		0	4M	6M		
Clarity	Clear to slightly opalescent (not more turbid than reference suspension II)	Complies	Complies	Complies		
Coloration	Colorless to slightly colored (not more colored than reference solution	Complies	Complies	Complies		
pН	4.2 1 ind.	1 0	1:4			
DNA Concentration		<b>14. /</b>	1 in			
Linearization Efficiency (Plasmid topology)	Linear form: 4.2 1 ind.					