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Center for Regulatory Services, Inc.
5200 Wolf Run Shoals Road
Woodbridge, VA 22192-5755
703 590 7337 (Fax 703 580 8637)
smedley@cfr-services.com

May 12, 2022

Dr. Susan Carlson
Director, Division of Biotechnology and GRAS Notice Review (HFS-255)
Office of Food Additive Safety
Center for Food Safety and Applied Nutrition
Food and Drug Administration
5001 Campus Drive
College Park, MD 20740

RECEIVED
MAY 13 2022
OFFICE OF
FOOD ADDITIVE SAFETY

Dear Dr. Carlson:

SUBJECT: Transmittal of the FINK TEC GmbH –
GRAS Notice for Applied Phage Vegetable S2
Antimicrobial to control Salmonella enterica spp. on
Fresh and Processed Fruits and Vegetables

On behalf of FINK TEC GmbH, enclosed you will find the GRAS notice for Applied Phage Meat S2 that contains cocktail contains six out of a set of eleven well characterized bacteriophages, namely: bacteriophages vB_SalM_ELB17 (DSM 26158), vB_SalM_MP82 (DSM 26173), vB_SalM_KAZ99a (DSM 33039), vB_SalM_RMP11k (DSM 33040), vB_SalM_RMS3b (DSM 33043), vB_SalM_TAT2F (DSM 33044), vB_SalM_DIN2 (DSM 33045), vB_SalM_MP75 (DSM 104023), vB_SalS_FV7M4 (DSM 26125), vB_SalS_RMP9 (DSM 26157) and vB_SalS_OBO18 (DSM33041). The substance is formulated under the product name of, "Applied Phage Vegetable S2" for use as antimicrobial to control Salmonella enterica spp. in fresh and processed fruits and vegetables, wherever and whenever a risk of Salmonella contamination occurs.

I have provided a DVD of the GRAS notice and all the cited references.

Should you have any questions on this filing, please contact me, at your convenience.

Sincerely,

Kristi Smedley
Digitally signed by Kristi Smedley
DN: cn=Kristi Smedley, o=Center for Regulatory Services, Inc., ou, email=smedley@cfr-services.com, c=US
Date: 2022.05.12 13:50:07 -04'00'

Kristi O. Smedley, Ph.D.
Consultant to FINK TEC GmbH

Attachments

FDA Form 3667 (Hard Copy and DVD-Copy)
Applied Phage Vegetable S2 GRN NARRATIVE of Notice (Hard Copy and DVD-Copy)
Appendices (as appended to Narrative) (DVD-copy)
Full Complement of References (DVD-copy)

FINK TEC GmbH

GRAS Notification

“*Applied Phage Vegetable S2*”

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Attachment list:

Attachment I: Host spectra

Attachment II: Bioinformatic analyses of phage genomes – confidential

Attachment III: Phage genome sequences – confidential

Attachment IV: Virulence finder data

Attachment V: Genome safety table

Attachment VI: Allergen search

Attachment VII: Efficacy study on lettuce

Attachment VIII: Efficacy study on apple

I. GRAS Exemption Claim

I.1 Claim of Exemption From the Premarket Approval Requirements Pursuant to 21CFR 170 Subpart E

This Notice is submitted in compliance with Subpart E of FDA's GRAS Notification process regulations 21 CFR Subpart E 170.225-170.255.

The bacteriophages vB_SalM_ELB17 (DSM 26158), vB_SalM_MP82 (DSM 26173), vB_SalM_KAZ99a (DSM 33039), vB_SalM_RMP11k (DSM 33040), vB_SalM_RMS3b (DSM 33043), vB_SalM_TAT2F (DSM 33044), vB_SalM_DIN2 (DSM 33045), vB_SalM_MP75 (DSM 104023), vB_SalS_FV7M4 (DSM 26125), vB_SalS_RMP9 (DSM 26157) and vB_SalS_OBO18 (DSM33041), formulated under the product name of, "*Applied Phage Vegetable S2*", have been determined by the scientists of the FINK TEC GmbH to be generally recognized as safe, through scientific procedures, and are exempt from the premarket approval requirements under the intended use conditions described within this notification. The accompanying sections provide the basis for this finding. On behalf of FINK TEC GmbH (notifier), I certify that to the best of my knowledge, this GRAS Notice is complete, representative, and balanced with respect to the information provided, favorable or unfavorable, known to me and pertinent to the evaluation of the safety and GRAS status of our bacteriophage-based antimicrobial product.

Signed,

[redacted]

Date: 05.05.2022

Michael Fink
Chief Executive Officer
FINK TEC GmbH
Oberster Kamp
23 D-59069
Hamm
Germany

I.2 Name and Address of Notifier

FINK TEC GmbH
Dr. Michael Fink
Chief Executive Officer
Oberster Kamp 23
D-59069 Hamm
Germany
Ph: +49 (0)2385 73 300
Fax: +49 (0)2385 73 389
Michael.Fink@finktec.com

Notifier's US Representative
Kristi O. Smedley, Ph.D.
Center for Regulatory Services, Inc.
5200 Wolf Run Shoals Rd.
Woodbridge, VA 22192
Office: 703-590-7337
Fax: 703-580-8637
smedley@cfr-services.com

I.3 Common or Usual Name of the Notified Substance

The FINK TEC GmbH produces a bacteriophage cocktail with potent lytic activity against *Salmonella enterica* spp. under the trade name "***Applied Phage Vegetable S2***". The cocktail contains six out of a set of eleven well characterized bacteriophages, namely: vB_SalM_ELB17, vB_SalM_MP82, vB_SalM_KAZ99a, vB_SalM_RMP11k, vB_SalM_RMS3b, vB_SalM_TAT2F, vB_SalM_DIN2, vB_SalM_MP75, vB_SalS_FV7M4, vB_SalS_RMP9 and vB_SalS_OBO18.

I.4 Conditions of Use

The bacteriophage cocktail, formulated as "*Applied Phage Vegetable S2*", is intended for use as antimicrobial to control *Salmonella enterica* spp. in fresh and processed fruits and fresh and processed vegetables, wherever and whenever a risk of *Salmonella* contamination occurs.

I.5 Basis for the GRAS Determination

In accordance with 21 CFR § 170.30(b), the intended use of bacteriophages vB_SalM_ELB17, vB_SalM_MP82, vB_SalM_KAZ99a, vB_SalM_RMP11k, vB_SalM_RMS3b, vB_SalM_TAT2F, vB_SalM_DIN2, vB_SalM_MP75, vB_SalS_FV7M4, vB_SalS_RMP9 and vB_SalS_OBO18 has been determined to be generally recognized as safe (GRAS), based on scientific procedures and a comprehensive search of the scientific literature.

I.6 Availability of Information

The data and information that serve as the basis for this GRAS notification are available for review and copying at the offices of FINK TEC GmbH. Copies are available upon request to:

FINK TEC GmbH
Dr. Michael Fink
Chief Executive Officer
Oberster Kamp 23
D-59069 Hamm
Germany
Ph: +49 (0)2385 73 300
Fax: +49 (0)2385 73 389
Michael.Fink@finktec.com

I.7 Public Disclosure

FOIA (Freedom of Information Act): Parts 2 through 8 of this notification as well as the data provided in the Attachments I and IV-VIII to this notification do not contain data or information that is exempt from disclosure under the FOIA (Freedom of Information Act, 5 U.S.C. 552).

The data provided in the Attachments II and III to this notification are considered confidential business information and should be exempt from disclosure under the FOIA (Freedom of Information Act, 5 U.S.C. 552).

II. Identity of Substance

II.1 Identity

Common and Usual Name of the Food Grade Substance: *Salmonella*-specific phage preparation

Quantitative Composition: The *Salmonella*-specific phage preparation is comprised of eleven (11) bacteriophages (phages) to be used six (6) at a time in the final commercial product "*Applied Phage Vegetable S2*". All phages used in the phage preparation are strictly lytic as determined by an analysis of phage genomes.

An application of the food ingredient will use a mixture of equal proportions of six (6) phages selected from the designated eleven (11) phage preparation components, with specificity against the target bacterium *Salmonella enterica* spp. The applied preparation will contain a total phage concentration ranging between 5 x 10^9 and 1 x 10^{10} active "Plaque Forming Units" per milliliter of solution" (PFU/mL).

The ability to utilize a blend of selected phages in a particular processing plant is necessary to guarantee the broad scope of lytic activity of the blend against the target *Salmonella* strains. In addition, a rotation in the composition of the cocktail, using a subset of the eleven (11) phages that are the subject of this notice, reduces the risk that the targeted bacterial pathogen might develop resistance against the applied preparation product. The possibility to create diversity within the preparation composition will also provide the producers and processors of fruit and vegetables with the means to rapidly react to outbreaks of novel *Salmonella* strains.

The final phage preparation is a colorless and odorless liquid suspension of phages that is produced as a concentrate to be diluted with water at the site of application to generate a working solution ranging in concentration from 1 x 10^5 to 1 x 10^7 PFU/mL, depending on the actual application.

Phages that comprise the preparation are deposited with the Leibniz Institute DSMZ – German Collection of Microorganisms and Cultures as designated below (https://www.dsmz.de/home.html):

Order: Caudovirales

Family: Myoviridae
Species: DSM 26158 (ELB17)
DSM 26173 (MP82)
DSM 33039 (KAZ99a)
DSM 33040 (RMP11k)
DSM 33043 (RMS3b)
DSM 33044 (TAT2F)
DSM 33045 (DIN2)
DSM 104023 (MP75)

Host bacteria: *Salmonella enterica* spp.

Order: Caudovirales
Family: Siphoviridae
Species: DSM 26125 (FV7M4)
DSM 26157 (RMP9)
DSM33041 (OBO18)

Host bacteria: *Salmonella enterica* spp.

Eight (8) of the preparation phages belong to the structural family of Myoviridae, three (3) preparation phages to the family of Siphoviridae. All bacteriophages are strictly lytic as determined by the analysis of their genomes as described below.

Host range: FINK TEC GmbH conducted host range studies on phage preparation component phages. The results of these studies are shown in Attachment I. Since the individual host ranges varied and none of the phages were lytic against all *Salmonella* strains tested, the different phages complement each other, increasing the total coverage, which is important for the composition of an efficient targeted anti-microbial phage product.

Phage Type: All phage preparation phage components are exclusively lytic. The biology of phages has been exhaustively studied in the 100 years since their discovery. Two major phage classes have been described, lytic and temperate. Temperate phages do not necessarily kill their host bacterium. They have the ability to passively invade a host and thereby are transferring their own genes from one host bacterium to the next, in a process called lysogenic conversion (Brüssow et al. 2004)(Fortier and Sekulovic 2013). As some temperate phages may carry toxin genes (Davis et al. 2000)(Beutin et al. 2004)(Smith et al. 2012), they are not suited to be components of a phage cocktail produced and applied on an industrial scale.

Lytic phages, on the other hand, lack the genes responsible for lysogenic conversion and an infection by a lytic phage always leads to the death of the bacterial host. Thus, lytic phages are safe for use in food, as they do not disseminate toxin or other genes that pose risks for humans.

II.2 Method of Manufacture

II.2.1 Maintenance of host bacteria and bacteriophage stocks to insure purity

Frozen aliquots of the non-pathogenic *E. coli* host strain MG1655 (ATCC 47076) (Guyer et al. 1981) or the non-human pathogenic *Salmonella* host strains *Salmonella bongori* (ATCC 43975) (Reeves et al. 1989) and *Salmonella paratyphi* B var. Java (ATCC BAA-1584) (Boyd et al. 1993) are stored at -80°C as glycerol stocks. For each production cycle the respective strain is streaked out on an agar plate and a single colony is used to start a pre-culture to be used in the fermentation process.

Stocks of bacteriophage lysates are sterilized by 0.22 µm filtration and stored at 4°C. Immediately before use in the fermentation process, the bacteriophage stocks are sterilized anew by 0.22 µm filtration to minimize the risk of contamination.

II.2.2 Description of the manufacturing process

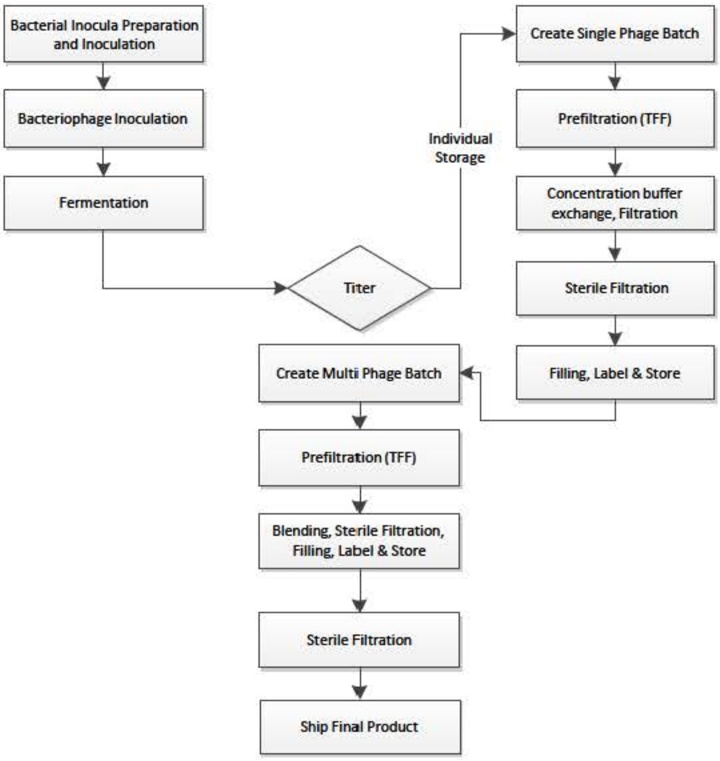
The individual bacteriophages are produced in an aerobic fermentation process in an animal-product free growth medium. For each bacteriophage a specific host strain, either *E. coli* or *Salmonella*, is grown to a target optical density at 600 nanometers and infected with the bacteriophage at a previously determined multiplicity of infection (MOI, the ratio of phage to bacteria) and the combination is incubated with aeration and mixing. The bacteriophages will infect their host bacteria, multiply within them and eventually lyse the host bacteria, generating a bacteriophage lysate. After the fermentation process is complete, the bacteriophage lysates are titered, to determine the concentration of the progeny bacteriophages. Thereafter the bacteriophage lysates are clarified by an initial continuous centrifugation process followed by a filtration process using a Tangential Flow Filtration (TFF) system to remove unbroken host cells and host cell debris. In a second filtration step the bacterial growth medium is exchanged to phosphate buffered saline, a common storage buffer that does not contain any unapproved food additives. In a third filtration step the individual bacteriophage solutions are sterilized through a 0.22 μm filter (Lehnherr and Bartsch 2012). All processing aids used in the manufacturing are of food grade quality or of a quality specified in the 5th Edition of the Food Chemical Codex.

Each individual bacteriophage stock has to meet the specified release parameters before it can be used as one of six components to mix the “*Applied Phage Vegetable S2*” bacteriophage cocktail.

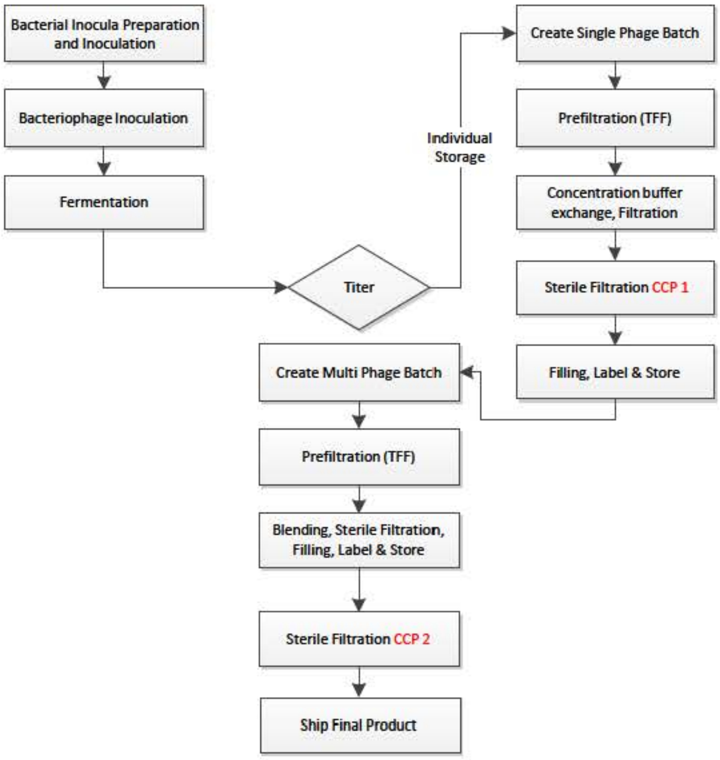
Table 1: Product specification for each batch of an individual bacteriophage.

Parameter	Specification
Bacteriophage titer	>5 x 10^9 PFU/mL
Microbial sterility	no growth
PCR identity	identical to PCR reference profile

II.2.3 Process flow diagram



II.2.4 Critical Control Points



II.2.5 HACCP plan summary

Subject	ISSUE DATE	PRODUCT
CCP HACCP Plan Summary	2.03.2016	*Applied Phage Vegetable S2*
FinkTec GmbH		Page 1 of 1
Oberster Kamp 23 59069 Hamm Germany		

Critical Control Points CCP	Hazard(s)	Critical Limit	Monitoring				Corrective Action(s)	CCP Verification	Records
			what	how	Frequency	who			
CCP 1	bacterial contamination	>10 cfu/g	Total aerobic germ count	ISO 4833	each batch	QC	Redo sterile filtration	positive control	
		>10 cfu/g	Yeast and moulds	NMKL 98	each batch	QC	Redo sterile filtration	positive control	
CCP 2	bacterial contamination	>10 cfu/g	Total aerobic germ count	ISO 4833	each batch	QC	Redo sterile filtration	positive control	
		>10 cfu/g	Yeast and moulds	NMKL 98	each batch	QC	Redo sterile filtration	positive control	
		>10 cfu/g	Enterobacteriaceae	ISO 6888-1	each batch	QC	Redo sterile filtration	positive control	

II.2.6 Raw Materials

The fermentation medium is an animal-product free growth medium. Its components are described here, are food grade, and have an existing regulatory status as regulated GRAS ingredients or additives:

Soy Peptone: Peptones are GRAS affirmed at 21 CFR § 184.1553 for use as processing aids, among other uses, at levels not to exceed good manufacturing practice. Peptones are protein hydrolysates consisting of free amino acids and short peptides in an aqueous salt solution.

Yeast Extract: Yeast extract is a commonly used food ingredient. For example, baker’s yeast extract is GRAS affirmed as a flavoring agent or adjuvant at up to 5% in foods generally 21 CFR § 184.1983.

Sodium Chloride: Sodium chloride “salt” is the prototype in 21 CFR § 182.1 (a) of an ingredient that is so obviously GRAS that FDA has not listed it as GRAS.

Magnesium chloride: Magnesium chloride salt is GRAS affirmed at 21 CFR § 184.1426 for use as a processing aid, among other uses, at levels not to exceed good manufacturing practice. Magnesium chloride is a component of the buffer used for the finalized bacteriophage product.

Monopotassium phosphate: Monopotassium phosphate is a GRAS substance (21 CFR § 582.4521) and an indirect additive (21 CFR 175.105) and it is identified as a currently used fermentation aid (FDA Substances added to Food list). Among other uses, monopotassium phosphate is used as a processing aid at levels not to exceed good manufacturing practice. Monopotassium phosphate is a component of the buffer used for the finalized bacteriophage product.

Disodium phosphate: Disodium phosphate is a GRAS substance (21 CFR § 182.6290) used as a processing aid, among other uses, at levels not to exceed good manufacturing practice. Disodium phosphate is a component of the buffer used for the finalized bacteriophage product.

II.3 Specification of “*Applied Phage Vegetable S2*”

The final product specifications are given in Table 2 below:

Table 1: Product specifications of “Applied Phage Vegetable S2”

Description	**Standardized bacteriophage cocktail based on naturally occurring bacteriophages, stabilized**	
Concentration	Approx. > 1 x 10^9 bacteriophages/mL[1]	
Packaging	Stainless steel KEG barrels, flat fitting	
Storage	Cool and dry (recommended 4-8°C), do not store in direct sun light	
Shelf life	6 months, process immediately after opening	
Appearance	Colorless to light yellowish liquid	
Texture	Liquid	
pH	7.0-7.4	
odor / taste	characteristic	
Microbiological Parameters		
Total plate count	ISO 48833[2]	< 50 CFU/g
Yeast and Mould	NMKL 98[3]	< 100 CFU/g
Staphylococcus	ISO 6888[2]	< 10 CFU/g
Salmonella	NMKL 71[3]	not detectable in 25 g
Enterobacteriacea	ISO 21528[2]	< 100 CFU/g
Sulfite-reducing Clostridia	ISO 15213[2]	< 1000 CFU/g
PCR Verification[4]	Complies	Yes/no (for single phage solutions)

[1] Clokie and Kropinski 2009

[2] http://www.iso.org/iso/catalogue_detail htm?csnumber=23036

[3] http://www.nmkl.org/index.php/en/

[4] Mullis et al. 1987

II.4 Bacteriophage names and classification

Order:	Caudovirales
Family:	Myoviridae
Species:	vB_SalM_MP82 vB_SalM_KAZ99a vB_SalM_RMP11k vB_SalM_RMS3b vB_SalM_TAT2F vB_SalM_DIN2 vB_SalM_MP75
Host bacteria:	*Salmonella enterica* spp.

Order:	Caudovirales
Family:	Siphoviridae
Species:	vB_SalS_FV7M4 vB_SalS_RMP9 vB_SalS_OBO18
Host bacteria:	*Salmonella enterica* spp.

II.5 Original sources of bacteriophages in the preparation

All bacteriophages were isolated from wastewater. They are used in their natural form, neither modified nor genetically engineered.

II.6 Bacteriophage properties

II.6.1 Salmonella host range

The bacteriophages are specific for a wide range of *Salmonella enterica* spp. serovars as shown in Table 3. The data was generated in a titration experiment as shown in Attachment I.

Table 2: *Salmonella* host strains covered by "*Applied Phage Vegetable S2":*

- *S. agona*
- *S. anatum*
- *S. brandenburg*
- *S. choleraesius*
- *S. decatur*
- *S. derby*
- *S. dublin*
- *S. duisburg*
- *S. emek*
- *S. enterica*
- *S. enteritidis*
- *S. gallinarum*
- *S. haifa*
- *S. heidelberg*
- *S. indiana*
- *S. infantis*
- *S. java*
- *S. kiambu*
- *S. livingstone*
- *S. london*
- *S. miami*
- *S. minnesota*
- *S. montevideo*
- *S. muenchen*
- *S. newport*
- *S. panama*
- *S. parathyphi A*
- *S. paratyphi B*
- *S. paratyphi C*
- *S. pullorum*
- *S. rubislaw*
- *S. saintpaul*
- *S. sendai*
- *S. senftenberg*
- *S. stanley*
- *S. stanleyville*
- *S. thompson*
- *S. typhimurium*
- *S. tyhpisuis*
- *S. virchow*
- *S. wien*

II.6.2 Type

Eight of the bacteriophages belong to the structural family of Myoviridae, three bacteriophages to the structural family of Siphoviridae. All bacteriophages are strictly lytic as determined by the analysis of their genomes (see Attachment II).

II.6.3 Complete gene sequences of all the bacteriophage genes

The genomes of all bacteriophages were determined using Next-Generation-Sequencing (Illumina technology). They were analyzed using standard bioinformatical methods. The complete and annotated genomic sequences of all eleven bacteriophages are provided in Attachment III. The analyses of these genomes confirmed not only the lytic nature of all bacteriophages but also demonstrated that no virulence genes (Attachment IV) no toxin genes (Attachment V), no antibiotic resistance markers, no genes coding for proteins with allergenic properties (Attachment VI) nor any other detrimental genes were present.

II.7 Host

II.7.1 Pathogenicity profile

Six bacteriophages, namely vB_SalM_ELB17, vB_SalM_KAZ99a, vB_SalM_RMS3b, vB_SalS_RMP9, vB_SalM_MP75 and vB_SalS_FV7M4 are grown on the *E. coli* K12 derivative MG1655 (ATCC 47076) (Guyer et al. 1981). Two bacteriophages, namely vB_SalM_MP82, vB_SalM_RMP11k are grown on the non-human pathogenic strain *Salmonella bongori* (ATCC 43975) and three bacteriophages, namely vB_SalM_TAT2F, vB_SalM_DIN2 and vB_SalS_OBO18 are grown on the non-human pathogenic strain *Salmonella paratyphi* B var. Java (ATCC BAA-1584) (Boyd et al. 1993).

E. coli K12 is not considered a human, animal or plant pathogen, nor is it toxicogenic (Environmental Protection Agency (1997a). *E. coli K12* has a history of safe use in the production of specialty chemicals and human drugs and was exempted from EPA review under TSCA § 725.420 (Toxic Substance Control Act) (Environmental Protection Agency (1997b). In addition, *E. coli* K1 derivatives have been used repeatedly in the production of GRAS notified food additives like α-cyclodextrin, GRAS Notice 000155, L-leucin, GRAS Notice 000308 and Lycopene, GRAS Notice 000299.

The two non-human pathogenic *Salmonella enterica* strains are known to produce no enterotoxins that could compromise the final product and have been considered safe for the production of salmonella-specific bacteriophages (GRAS Notice 000435).

II.7.2 Endotoxins (LPS)

Endotoxins are a class of lipopolysaccharides (LPS) that are located in the outer membrane of gram-negative bacteria like *Salmonella* and *E. coli*. Endotoxins can lead to sepsis (toxic shock syndrome) when they reach the human blood stream (*Pathophysiology of Shock, Sepsis, and Organ Failure* 2012). However, LPS is found everywhere in the environment and in large quantities in human food and in even higher concentrations in the human intestine (Im et al. 2012). For example, milk contains 10^5 to 10^6 EU/mL (Gehring et al. 2008) or beef up to 7.5 x 10^4 EU/g (Jay et al. 1979). Consequently, no regulations for the presence of LPS in the human diet exist. During the destruction of the *Salmonella* or *E. coli* host by the bacteriophages in the fermentation process, up to 10^8 EU/mL LPS is released into the growth medium. However, most of the endotoxin is removed during the purification process described above, to a residual level of approximately 1 x 10^4 EU/mL, in the final "*Applied Phage Vegetable S2*" product. As the concentrated product is further diluted with water to reach the application concentration, the use of "*Applied Phage Vegetable S2*" will not significantly contribute to the LPS concentration naturally found in food.

II.8 Stability

Based on studies assessing the stability of the bacteriophage concentration and bacterial sterility, the shelf life of "*Applied Phage Vegetable S2*" is six months when stored at 2 – 10 °C (35.6 – 50 °F) in a dark, UV-protected area.

II.9 Intended Use

II.9.1 Description of Use

The bacteriophage cocktail, formulated as "*Applied Phage Vegetable S2*", is intended for use as an antimicrobial to control *Salmonella enteric*a spp. that may be present on fresh and processed fruits or fresh and processed vegetables. The phage preparation is applied at processing plant ambient temperature as a spray, using existing approved spray systems in fruit and vegetable processing facilities. The envisioned use is consistent with Good Manufacturing Practices and the expected efficacious dose lies between 1 x 10^5 to 1 x 10^7 plaque forming units per gram of treated fruit or vegetable, depending on the exact application.

II.9.2 Efficacy of Use

The "*Applied Phage Vegetable S2*" preparation has been shown to be effective in reducing the number of *Salmonella* counts in two model system assays for lettuce and apple. Briefly, lettuce leaves or apple cubes of consistent dimensions were first inoculated with 10^3 or 10^4 cells of a *Salmonella* test strain per cm^2 of product surface. Following a brief period to allow for adherence of the test bacteria to the substrate, the lettuce leaves or apple cubes were treated with "*Applied Phage Vegetable S2*" to a final concentration of 2.5 x 10^6 PFU/cm^2 or 1 x 10^7 PFU/cm^2, respectively.

After incubation, the surface bacteria were counted. The results of the studies indicate that the phage preparation can reduce the count of a *Salmonella* test strain by approximately 99.98% from lettuce (Attachment VII) and 80.1 % from apple cubes (Attachment VIII).

III. Dietary Exposure

The expected dietary exposure to *Salmonella*-specific phages as a result of the application of the phage preparation is insignificant and below the level of toxicological concern. Calculation of incremental exposure to the commercial preparation or incremental Estimated Dietary Intake (EDI) was done according to the following:

Assuming the following:

•According to the USDA, the average availability in 2021 was 376.8 pounds of vegetables and pulses and 265.1 pounds of fruits and tree nuts, per capita (https://www.ers.usda.gov/data-products/food-availability-per-capita-data-system/food-availability-documentation/).

•All vegetables and fruits consumed in the US are treated with the phage preparation (highly conservative; see below)

•Phage particle weight = 2×10^{-16} grams (Taylor, Epstein, and Lauffer 1955)(Giddings, Yang, and Myers 1977)(Mazzone, Engler, and Bahr 1980).

•a realistic but high concentration of 1×10^{7} PFU per gram of vegetable or fruit would be used.

NB: The calculations are extremely conservative for the following reason:

1. EDI assumes that all phages applied adhere to the product but the application is by spray and the runoff of the phage preparation is estimated to exceed 90%.
2. That all available vegetables and fruits were consumed (no loss adjustments)
3. All fruits and vegetables are treated with the GRAS substance (Applied Phage Vegetable S2)
4. We do not attempt to correct the available fruit and tree nut availability, by removing the tree nut availability (tree nuts are not covered by this notice).

EDI Calculation

1. Weight of the phage in gram X Concentration of the phage applied per gram of treated product = gram phage per gram of treated product

2. Average fruit and vegetable availability in the US in (g)/person/year

3. Weight of phage/gram of treated product X (Avg. fruit and vegetable availability in the US (g)/person/year / 365 days/year) = Incremental EDI as grams of phage maximally consumed/person/day.

Following the above formula, we obtain:

1. Gram phage/ gram of treated product-= 2×10^{-16} g X 1×10^{7} phage/gram of treated product = 2×10^{-9} grams or 0.002 µg

2. 641.9 lbs X 1000 / 2.2 = 2.92×10^{5} g/year

3. Incremental EDI = (0.002 µg/g of treated product X 2.92×10^{5} grams of fruits and vegetable per year) / 365 days/year =

1.60 µg/person/day

Because the highly conservative, calculated incremental exposure to phages in consumed fruits and vegetables treated with phage preparation is less than 0.5 ppb in the total diet, no toxicological safety studies were done in accordance with FDA guidance in “Guidance for Industry: Summary Table of Recommended Toxicological Testing for Additives Used in Food” June 2006 (https://www.fda.gov/Food/GuidanceRegulation/GuidanceDocumentsRegulatoryInformation/default.htm) and “Guidance for Industry: Preparation of Food Contact Notifications for Food Contact Substances: Toxicology Recommendations”: (http://www.fda.gov/Food/GuidanceRegulation/GuidanceDocumentsRegulatoryInformation/ucm081825.htm#iva).

We further note that the incremental EDI above also implicitly assumes that every gram of fruit and vegetables consumed is treated, which is not the case. Specifically, the use as a spray treatment implies that only the surface of the fruits and vegetables are exposed to the product. None of the interior tissues is intended to come into contact with the phage preparation. Thus, it is quite clear that the presence of the phage preparation is at “de minimus” levels on fruits and vegetables that would be consumed; and it is more likely that consumers will be exposed to phage from the environment rather than as a result of the use of the phage preparation.

Further, all other materials present in the phage preparation are either GRAS ingredients or approved food additives and thus present no risk to consumers of the treated fruits and vegetables.

Phage genome sequences:

358 pages have been removed in accordance with confidentiality laws.

IV. Self-Limiting Levels of Use

None

V. Experience Based on Common Use in Food Before 1958

None and not applicable. Bacteriophages have not been used in foods before 1958. However, it is noted that bacteriophages are ubiquitous and are a normal component of our environment and food supply.

VI. Basis of Determination GRAS: Scientific Procedures

VI.1 Background on *Salmonella*

Foodborne illnesses caused by pathogenic *Salmonella* are a serious health burden worldwide. In the US alone the center for Disease Control estimates that *Salmonella* causes about 1.2 million illnesses, 23,000 hospitalizations, and 450 deaths every year, and that food is the source for about 1 million of these illnesses (CDC Salmonella). While food producers and food processors implemented strict monitoring programs, they do not always have access to active means to reduce the levels of *Salmonella* in food.

The bacteriophage cocktail, formulated as "*Applied Phage Vegetable S2*", offers a means to improve this situation. The application of "*Applied Phage Vegetable S2*" will reduce or eliminate contaminating *Salmonella enterica* spp. from fruits and vegetables. As shown for example in the accompanying studies where the application of "*Applied Phage Vegetable S2*" to lettuce leaves or to apple cubes led to a reduction of the *Salmonella* count by 99.98% and 80.1%, respectively (see Attachments VII, VIII). As a consequence, the treated fruits and vegetables would be safer and the number of foodborne illnesses could be reduced.

VI.2 Bacteriophages are omnipresent in the environment.

Large numbers of bacteriophages have been found in virtually every aquatic or terrestrial habitat where bacteria exist (Gómez and Buckling 2011)(Marston and Sallee 2003)(Clokie et al. 2011). The gut of mammals and humans is an especially rich source of bacteriophages (Dalmasso, Hill, and Ross 2014), many of which have been consumed via various foods (Kennedy, Oblinger, and Bitton 1984)(Atterbury et al. 2003)(Hsu, Shieh, and Sobsey 2002)(Suárez and Reinheimer 2002)(Kiliç et al. 1996). This abundance of bacteriophages in the environment and the continuous exposure of humans to them could explain the absence of any adverse effects in various safety studies in humans and animals (Carlton et al. 2005)(Chibani-Chennoufi et al. 2004)(Bruttin and Brüssow 2005) as well as in long term applications in human medicine (Weber-Dabrowska, Mulczyk, and Górski 2003)(Kutter et al. 2010)(Kutateladze 2015).

VI.3 Lytic bacteriophages are GRAS

The biology of bacteriophages has been exhaustively studied in the 100 years since their discovery. Two major bacteriophage classes have been described, lytic and temperate. Temperate bacteriophages do not necessarily kill their host bacterium. They have the ability to passively invade a host and thereby are transferring their own genes from one host bacterium to the next, in a process called lysogenic conversion (Brüssow et al. 2004)(Fortier and Sekulovic 2013). As some temperate bacteriophages may carry toxin genes (Davis et al. 2000)(Beutin et al. 2004)(Smith et al. 2012), they are not suited to be components of a bacteriophage cocktail produced and applied on an industrial scale. Lytic bacteriophages, on the other hand, lack the genes responsible for lysogenic conversion and an infection by a lytic bacteriophage always leads to the death of the bacterial host. Thus, lytic bacteriophages are safe for practical applications as they do not disseminate toxin genes. With the aid of comparative genomics, it is nowadays possible to clearly distinguish lytic from temperate bacteriophages and thus select only the former for a phage preparation like "*Applied Phage Vegetable S2*". Using in silico analyses the genomic information can also be used to show that lytic phages do not contain genes encoding for antibiotic resistance markers or allergens.

VI.4 Substantial equivalence to previously approved bacteriophage products.

Since the USFDA in 1996 approved a *Listeria*-specific bacteriophage preparation as food additive 21 CFR 172.785), several other products based on lytic bacteriophages, targeting various bacterial pathogens, have been designated GRAS and/or have been cleared for food safety usage by a number of regulatory agencies:

- Listex™ is a bacteriophage preparation containing a single *Listeria monocytogenes* lytic bacteriophage, P100, used for biocontrol of *Listeria* in susceptible foodstuffs, that is GRAS (GRAS Notice No. 000218)
- Listex™ is also listed by the USDA FSIS for use as processing aid for use on ready-to-eat meat products (FSIS Directive 8120.1)
- Listex™ is also approved as a processing aid for susceptible foodstuffs in many countries, including Canada, by Health Canada and FSANZ, Australia and New Zealand. The Dutch Ministry of Health has issued a formal statement, confirming that Listex™ can be used as a processing aid. Additionally, Listex™ has been approved for use in Switzerland in cheese-making and also as processing aid in keeping with European legislation on food safety.
- Listex™ is listed by the Organic Materials Review Institute (OMRI). This means that Listex™ may be used in the certified organic production of food, food processing and handling according to the USDA National Organic Program Rule.
- ListShield™ is a bacteriophage preparation containing six lytic *Listeria monocytogenes*-specific bacteriophages, that is FDA-cleared as a food additive (21 CFRF§172.785)
- ListShield™ is also listed by the USDA FSIS for use as processing aid with no labeling requirements when applied to various ready-to-eat meats

and poultry products (FSIS Directive 7120.1).

- ListShield^{TM} is GRAS for direct application to fish and shellfish (including smoked varieties; e.g. smoked salmon), fresh and processed fruits, fresh and processed vegetables, and dairy products (including cheese) (GRAS notice No. 000528)
- ListShield^{TM} is also EPA-registered for use on non-food surfaces in food processing plants to prevent or significantly reduce contamination of *Listeria monocytogenes* (EPA registration #74234-1).
- ListShield^{TM} is Health Canada approved for use on ready-to-eat meat and poultry, smoked salmon, fresh cut apples and long leaf lettuce (iLONO).
- ListShield^{TM} is National Food Service of Israel approved as a food processing aid for the treatment of ready-to-eat meat and poultry products (Ref: 70275202).
- EcoShield^{TM} is a bacteriophage preparation containing three lytic bacteriophages specific against *E. coli* O157:H7, that is FDA-cleared through a “Food Contact Notification” for use on red meat parts and trim, intended to be ground (FCN no. 1018).
- EcoShield^{TM} is also listed by the USDA FSIS as safe and suitable for use in the production of red meat parts and trim prior to grinding as processing aid with no labeling requirements (FSIS Directive 7120.1).
- EcoShield^{TM} is Health Canada approved for use on red meat parts and trim prior to grinding (iLONO)
- EcoShield^{TM} is National Food Service of Israel approved as food processing aid for the treatment of meat immediately before grinding (Ref: 70275202).
- AgriPhage^{TM} is a bacteriophage preparation targeting *Xanthomonas campestris* pv. *vesicatoria* and *Pseudomonas syringae* pv. *tomato* that is EPA-registered for use on tomatoes and peppers. AgriPhage^{TM} can be applied directly as foliar spray and can be used as a curative on symptomatic plants or preventively prior to visual signs of damage (EPA Reg. No. 67986-1).
- AgriPhage^{TM} has been amended to now include organic usage on tomato and pepper plants as governed by the USDA National Organic Program (NOP).
- AgriPhage-CMM^{TM} is a bacteriophage preparation targeting *Clavibacter michiganensis* pv. *michiganensis*, that is EPA-registered for use on tomatoes. AgriPhage-CMM^{TM} can be applied directly as a foliar spray and can be used as a curative on symptomatic plants or preventively prior to visual signs of damage (EPA Reg. No. 67986-6).
- The Canadian Pest Management Regulatory Agency (PMRA) has approved bio-pesticide AgriPhage-CMM^{TM} for bacterial stem canker in

tomato caused by *Clavibacter michiganensis* pv. *michiganensis* (30301)

- Finalyse™ is a bacteriophage preparation targeting *E. coli* O157:H7, that received USDA Food Safety and Inspection Services approval for commercialization and application as a spray mist or wash on live animals prior to slaughter to decrease pathogen transfer to meat.
- Armament™ is a bacteriophage preparation targeting *Salmonella*, that received USDA Food Safety and Inspection Services approval for the commercialization and application as a spray mist or wash on the feathers of live poultry prior to slaughter to decrease pathogen transfer to meat.
- Salmonelex™ is a bacteriophage preparation containing two specific bacteriophages, S16 and FO1a, for use as antibicrobial to control *Salmonella* serovars in ceartain pork and poultry products at levels up to 10^8 PFU/g of food, that was designated as GRAS (GRAS Notice No. 000468).
- SalmoFresh™ is a bacteriophage preparation for controlling the foodborne bacterial pathogen *Salmonella enterica*, that is GRAS for direct application onto poultry, fish and shellfish and fresh and processed fruits and vegetables (GRAS Notice No. 000435).
- SalmoFresh™ is also FSIS-listed as safe and suitable as antimicrobial for use in the production of poultry products as a processing aid with no labeling requirements (FSIS Directive 7120.1).
- SalmoFresh™ is Health Canada approved as a processing aid for use on fish, shellfish and fresh and processed fruits and vegetables or on ready-to-eat poultry products prior to slicing and on raw poultry prior to grinding or after grinding (iLONO).
- SalmoFresh™ is National Food Service of Israel approved as a food processing aid for the treatment of fish, shellfish, fresh and processed fruits and vegetables and poultry immediately before or after grinding and on ready- to-eat products before slicing (Ref: 70275202).
- Secure Shield E1, a bacteriophage preparation that specifically targets shiga toxin-producing *E. coli* O157:H7 as well as non-O157:H7 shiga toxin producing *E. coli*. that is GRAS for the application on beef carcasses (GRAS Notice No. 000724).
- A preparation containing the bacterial monophages, BP-63 and LVR16-A, specific to *Salmonella* for use as an antimicrobial processing aid (GRAS Notice No. 000752).
- A preparation containing two bacterial phages specific to *E. coli* O157 for use as an antimicrobial on beef carcasses, subprimals, beef cuts and trimmings (GRAS Notice No. 000757).
- A preparation containing three bacterial phages specific to several *E. coli* serotypes for use as an antimicrobial processing aid to control specific *E. coli* serotypes on poultry, red meats, fruits, vegetables, eggs, fish, and

shellfish applied to food surfaces (GRAS Notice No. 000827).

- A preparation containing bacterial phages specific to shiga-toxin producing *E. coli* for use as an antimicrobial to control *E. coli* on food when applied to ground and whole meat and poultry, including whole carcasses, primals and subprimals, trimmings and organs; ready-to-eat meats and poultry; fresh and processed fruits; fresh and processed vegetables; dairy products (including cheese); and fish and other seafood (GRAS Notice No. 000834).
- A preparation containing three bacterial phages specific to *Salmonella* intended for use as an antimicrobial on food to control *Salmonella* (GRAS Notice No. 000888).
- A preparation containing three bacteriophages specific to *Salmonella enterica* serovars for use as antimicrobial on intact poultry, intact red meat, eggs, fruits, vegetables, fish (excluding catfish) and shellfish (GRAS Notice No. 000917).
- A preparation containing three to eight bacteriophages specific to *Campylobacter jejuni*, intended for use as an antimicrobial on raw and ground poultry, and raw red meat products (GRAS Notice No. 000966).

Several regulatory agencies are represented in the preceding list, each of which separately determined that different bacteriophage preparations are safe. The bacteriophage cocktail "*Applied Phage Vegetable S2*" is substantially equivalent to the above-mentioned bacteriophage products and should therefore also be considered GRAS.

VI.5 Raw material Safety.

All the raw materials used in the fermentation and manufacture of the GRAS substances are food grade and are permitted in the manufacture of food (see section II.2.6).

VI.6 Summary and basis for GRAS.

“*Applied Phage Vegetable S2*” is a bacteriophage cocktail specific against *Salmonella enterica* spp. To reach such a broad coverage, a panel of elven lytic bacteriophages was compiled and characterized in detail. All the evidence presented above as well as evidence collected from the scientific literature indicates that the individual lytic bacteriophages, their composition in a cocktail and the bacterial fermentation process used to produce them, are safe. Humans are exposed to large numbers of bacteriophages on a daily basis and consume them naturally through food and water, without any noticeable effects. The treatment of vegetables and fruits with “*Applied Phage Vegetable S2*” would not significantly increase this natural consumption of bacteriophages. However, the desired reduction of pathogenic bacteria present on the products would make them safer for human consumption. Based on these findings and also the significant equivalence of “*Applied Phage Vegetable S2*” to other GRAS- approved products, the scientists of the FINK TEC GmbH came to the conclusion that “*Applied Phage Vegetable S2*” should be considered GRAS.

VII. References

Atterbury, Robert J, Phillippa L Connerton, Christine E R Dodd, Catherine E D Rees, and Ian F Connerton. 2003. "Isolation and Characterization of Campylobacter Bacteriophages from Retail Poultry." *Applied and Environmental Microbiology* 69 (8): 4511–18. http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=169066&tool=pmcentrez&re ndertype=abstract.

Beutin, L, G Krause, S Zimmermann, S Kaulfuss, and K Gleier. 2004. "Characterisation of Shiga Toxin-Producing Escherichia Coli Strains Isolated from Human Patients in Germany over a 3-Year Period." *Journal of Clinical Microbiology* 42 (3): 1099. https://doi.org/10.1128/JCM.42.3.1099.

Boyd, E F, F S Wang, P Beltran, S A Plock, K Nelson, and R K Selander. 1993. "Salmonella Reference Collection B (SARB): Strains of 37 Serovars of Subspecies I." *Journal of General Microbiology* 139 Pt 6 (June): 1125–32. https://doi.org/10.1099/00221287-139-6-1125.

Brüssow, Harald, Carlos Canchaya, Wolf-dietrich Hardt, and Harald Bru. 2004. "Phages and the Evolution of Bacterial Pathogens: From Genomic Rearrangements to Lysogenic Conversion." *Microbiology and Molecular Biology Reviews* 68 (3): 560–602. https://doi.org/10.1128/MMBR.68.3.560.

Bruttin, Anne, and Harald Brüssow. 2005. "Human Volunteers Receiving Escherichia Coli Phage T4 Orally: A Safety Test of Phage Therapy." *Antimicrobial Agents and Chemotherapy* 49 (7): 2874–78. https://doi.org/10.1128/AAC.49.7.2874-2878.2005.

Carlton, R M, W H Noordman, B Biswas, E D de Meester, and M J Loessner. 2005. "Bacteriophage P100 for Control of Listeria Monocytogenes in Foods: Genome Sequence, Bioinformatic Analyses, Oral Toxicity Study, and Application." *Regulatory Toxicology and Pharmacology: RTP* 43 (3): 301–12. https://doi.org/10.1016/j.yrtph.2005.08.005.

Chibani-Chennoufi, Sandra, Josette Sidoti, Anne Bruttin, Elizabeth Kutter, Shafiq Sarker, and Harald Brüssow. 2004. "In Vitro and in Vivo Bacteriolytic Activities of Escherichia Coli Phages: Implications for Phage Therapy." *Antimicrobial Agents and Chemotherapy* 48 (7): 2558–69. https://doi.org/10.1128/AAC.48.7.2558-2569.2004.

Clokie, Martha R. J. and Kropinski, Andrew. M, 2009. "Bacteriophages - Methods and Protocols, Volume 1": http://www.springer.com/us/book/9781588296825

Clokie, Martha Rj, Andrew D Millard, Andrey V Letarov, and Shaun Heaphy. 2011. "Phages in Nature." *Bacteriophage* 1 (1): 31–45. https://doi.org/10.4161/bact.1.1.14942.

Dalmasso, Marion, Colin Hill, and R Paul Ross. 2014. "Exploiting Gut Bacteriophages for Human Health." *Trends in Microbiology* 22 (7): 399–405. https://doi.org/10.1016/j.tim.2014.02.010.

Davis, B M, K E Moyer, E F Boyd, and M K Waldor. 2000. "CTX Prophages in Classical

Biotype Vibrio Cholerae: Functional Phage Genes but Dysfunctional Phage Genomes.” *Journal of Bacteriology* 182 (24): 6992–98. http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=94825&tool=pmcentrez&rendertype=abstract.

Fortier, Louis-Charles, and Ognjen Sekulovic. 2013. “Importance of Prophages to Evolution and Virulence of Bacterial Pathogens.” *Virulence* 4 (5): 354–65. https://doi.org/10.4161/viru.24498.

Gehring, Ulrike, Jack Spithoven, Susanne Schmid, Sondhja Bitter, Charlotte Braun-Fahrländer, Jean-Charles Dalphin, Anne Hyvärinen, et al. 2008. “Endotoxin Levels in Cow’s Milk Samples from Farming and Non-Farming Families - the PASTURE Study.” *Environment International* 34 (8): 1132–36. https://doi.org/10.1016/j.envint.2008.04.003.

Giddings, J C, F J Yang, and M N Myers. 1977. “Flow Field-Flow Fractionation: New Method for Separating, Purifying, and Characterizing the Diffusivity of Viruses.” *Journal of Virology* 21 (1): 131–38. http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=353798&tool=pmcentrez&rendertype=abstract.

Gómez, Pedro, and Angus Buckling. 2011. “Bacteria-Phage Antagonistic Coevolution in Soil.” *Science (New York, N.Y.)* 332 (6025): 106–9. https://doi.org/10.1126/science.1198767.

Guyer, M. S., R. R. Reed, J. A. Steitz, and K. B. Low. 1981. “Identification of a Sex-Factor-Affinity Site in E. Coli As .” *Cold Spring Harbor Symposia on Quantitative Biology* 45 (0): 135–40. https://doi.org/10.1101/SQB.1981.045.01.022.

Hsu, F C, Y S Carol Shieh, and M D Sobsey. 2002. “Enteric Bacteriophages as Potential Fecal Indicators in Ground Beef and Poultry Meat.” *Journal of Food Protection* 65 (1): 93–99. http://www.ncbi.nlm.nih.gov/pubmed/11811158.

Im, Eunok, Franz Martin Riegler, Charalabos Pothoulakis, and Sang Hoon Rhee. 2012. “Elevated Lipopolysaccharide in the Colon Evokes Intestinal Inflammation, Aggravated in Immune Modulator-Impaired Mice.” *American Journal of Physiology. Gastrointestinal and Liver Physiology* 303(4):G4907. https://doi.org/10.1152/ajpgi.00120.2012.

Jay, J M, S Margitic, A L Shereda, and H V Covington. 1979. “Determining Endotoxin Content of Ground Beef by the Limulus Amoebocyte Lysate Test as a Rapid Indicator of Microbial Quality.” *Applied and Environmental Microbiology* 38 (5): 885–90. http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=243603&tool=pmcentrez&rendertype=abstract.

Kennedy, J. E., J. L. Oblinger, and G. Bitton. 1984. “Recovery of Coliphages from Chicken, Pork Sausage and Delicatessen Meats.” *J Food Protection* 47: 623–26. http://www.ingentaconnect.com/contentone/iafp/jfp/1984/00000047/00000008/art00009?crawler=true.

Kiliç, A O, S I Pavlova, W G Ma, and L Tao. 1996. “Analysis of Lactobacillus Phages and Bacteriocins in American Dairy Products and Characterization of a Phage Isolated from Yogurt.” *Applied and Environmental Microbiology* 62 (6): 2111–16.

http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=167989&tool=pmcentrez&rendertype=abstract.

Kutateladze, Mzia. 2015. "Experience of the Eliava Institute in Bacteriophage Therapy." *Virologica Sinica* 30 (1): 80–81. https://doi.org/10.1007/s12250-014-3557-0.

Kutter, Elizabeth, Daniel De Vos, Guram Gvasalia, Zemphira Alavidze, Lasha Gogokhia, Sarah Kuhl, and Stephen T Abedon. 2010. "Phage Therapy in Clinical Practice: Treatment of Human Infections." *Current Pharmaceutical Biotechnology* 11 (1): 69–86. http://www.ncbi.nlm.nih.gov/pubmed/20214609.

Lehnherr, H., and R.A Bartsch. 2012. Process and system for the industrial scale purification of bacteriophages intended for bacteriophage therapy, issued December 12, 2012. http://www.google.com.na/patents/EP2195418B1?cl=enCached4.

Marston, Marcia F, and Jennifer L Sallee. 2003. "Genetic Diversity and Temporal Variation in the Cyanophage Community Infecting Marine Synechococcus Species in Rhode Island's Coastal Waters." *Applied and Environmental Microbiology* 69 (8): 4639–47. http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=169111&tool=pmcentrez&re ndertype=abstract.

Mazzone, H. M., W. F. Engler, and G. F. Bahr. 1980. "Mass and Molecular Weight of Bacteriophages T 2 and T 5." *Current Microbiology* 4 (3): 147–49. https://doi.org/10.1007/BF02602818.

Mullis, K. B. and Falona, F. A. (1987) 'Specific Synthesis of DNA in Vitro via a Polymerase-Catalyzed Chain Reaction', M. Enzymology, 155, pp. 335–350.

Pathophysiology of Shock, Sepsis, and Organ Failure. 2012. Springer Science & Business Media. https://books.google.com/books?id=axf2CAAAQBAJ&pgis=1.

Reeves, M. W., G. M. Evins, A. A. Heiba, B. D. Plikaytis, and J. J. Farmer. 1989. "Clonal Nature of Salmonella Typhi and Its Genetic Relatedness to Other Salmonellae as Shown by Multilocus Enzyme Electrophoresis and Proposal of Salmonella Bongori Comb.
Nov." *Journal of Clinical Microbiology* 27 (2): 313–20.

Smith, Darren L, David J Rooks, Paul C M Fogg, Alistair C Darby, Nick R Thomson, Alan J McCarthy, and Heather E Allison. 2012. "Comparative Genomics of Shiga Toxin Encoding Bacteriophages." *BMC Genomics* 13 (1): 311. https://doi.org/10.1186/1471-2164-13-311.

Suárez, Viviana B, and Jorge A Reinheimer. 2002. "Effectiveness of Thermal Treatments and Biocides in the Inactivation of Argentinian Lactococcus Lactis Phages." *Journal of Food Protection* 65 (11): 1756–59. http://www.ncbi.nlm.nih.gov/pubmed/12430698.

Taylor, N W, H T Epstein, and M A Lauffer. 1955. "The Particle Weight, Hydration and Shape of The" 3: 1270–73.

Weber-Dabrowska, B, M Mulczyk, and A Górski. 2003. "Bacteriophages as an Efficient Therapy for Antibiotic-Resistant Septicemia in Man." *Transplantation Proceedings* 35 (4): 1385–86. http://www.ncbi.nlm.nih.gov/pubmed/12826166.

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Robert J. Atterbury, Phillippa L. Connerton, Christine E. R. Dodd, Catherine E. D. Rees,

and Ian F. Connerton*, "Isolation and Characterization of *Campylobacter* Bacteriophages from Retail Poultry"

ALI O. KILIC,,1 SYLVIA I. PAVLOVA,1,2 WEN-GE MA,1 AND LIN TAO1,2*, "Analysis of *Lactobacillus* Phages and Bacteriocins in American Dairy Products and Characterization of a Phage Isolated from Yogurt"

VIII. Links

Leibniz Institute DSMZ – German Collection of Microorganisms and Cultures:
(https://www.dsmz.de/home.html)

USDA FSIS Directive 7120.1:
(https://www.fsis.usda.gov/policy/fsis-directives/7120.1)

Environmental Protection Agency (1997a) Final risk assessment of *Escherichia coli K-12* derivatives:
(http://www.epa.gov/sites/production/files/2015-09/documents/fra004.pdf).

Environmental Protection Agency (1997b) Final decision document: TSCA Section 5(H)(4) Exemption for *Escherichia coli* K-12:
(https://www.gpo.gov/fdsys/pkg/FR-1997-04-11/pdf/97-8669.pdf).

USDA, average food availability in 2021:
https://www.ers.usda.gov/data-products/food-availability-per-capita-data-system/food-availability-documentation/

FDA “Guidance for Industry: Summary Table of Recommended Toxicological Testing for Additives Used in Food” June 2006
(https://www.fda.gov/Food/GuidanceRegulation/GuidanceDocumentsRegulatoryInformation/default.htm)

FDA “Guidance for Industry: Preparation of Food Contact Notifications for Food Contact Substances: Toxicology Recommendations”:
(http://www.fda.gov/Food/GuidanceRegulation/GuidanceDocumentsRegulatoryInformation/ucm081825.htm#iva)

Host spectrum analysis of the "*Applied Phage Meat S2*" component phages based on titration assays on *Salmonella enterica* spp.

Study Number # R018-007_HS

PTC Phage Technology Center GmbH
Siemensstraße 42
D- 59199 Bönen
Tel.: 49 (0) 2383 919 175
Fax: 49 (0) 2383 919 179
Dr. Michael Fink

FINK TEC GmbH
Oberster Kamp 23
D-59069 Hamm
Tel.: 49 (0) 2385 730

1. STUDY TITLE

Host spectrum analysis of the “*Applied Phage Meat S2*” component phages based on titration assays on *Salmonella enterica* spp.

2. STUDY DIRECTOR

Hansjörg Lehnherr, Ph.D.

3. STUDY PERSONNEL

The following personnel contributed to the conduct and reporting of the studies reported herein:

Name:	**Title:**	**Role:**
Hansjörg Lehnherr, Ph.D.	Chief scientist	Study director
Andrea Kroj, Ph.D.	Research scientist	Hands-on-research

4. PERFORMING LABORATORY

PTC Phage Technology Center GmbH
Siemensstraße 42
D- 59199 Bönen
Tel.: 49 (0) 2383 919 174
Fax: 49 (0) 2383 919 179

5. STUDY OBJECTIVE

To determine the coverage of a collection of *Salmonella enterica* spp. strains by the *“Applied Phage Meat S2”* component phages. The host range analyses were based titration assays with the overlay agar method.

6. PHAGES

The phage preparations used for the host spectrum analyses are listed below:

***Table 1**: Phage data*

Phage		**Date/# Ch.-B.**	**Titer [PFU/mL]**
DSM #	Internal #		
DSM 26158	ELB17	10.06.2020	8×10^{8}
DSM 26173	MP82	04.09.2019	4×10^{9}
DSM 33039	KAZ99a	05.08.2020	2.5×10^{8}
DSM 33040	RMP11k	22.04.2020	2×10^{8}
DSM 33043	RMS3b	12.06.2019	2×10^{10}
DSM 33044	TAT2F	01.04.2020	1×10^{9}
DSM 33045	DIN2	01.04.2020	4×10^{8}
DSM 26125	MP75	14.08.2020	7×10^{10}
DSM 104021	FV7M4	08.04.2020	6×10^{9}
DSM 26157	RMP9	04.09.2019	1×10^{10}
DSM33041	OBO18	12.02.2020	3×10^{10}

7. BACTERIAL STRAINS USED FOR HOST RANGE ANALYSES

The following 41 *Salmonella enterica* spp. bacterial serovars were used to determine the host range of the "*Applied Phage Meat S2*" component phages:

S. agona
S. anatum
S. brandenburg
S. choleraesius
S. decatur
S. derby
S. dublin
S. duisburg
S. emek
S. enterica
S. enteritidis
S. gallinarum
S. haifa
S. heidelberg
S. indiana
S. infantis
S. java
S. kiambu
S. livingstone
S. London
S. miami
S. minnesota
S. montevideo
S. muenchen
S. newport
S. panama
S. parathyphi A
S. paratyphi B
S. paratyphi C
S. pullorum
S. rubislaw
S. saintpaul
S. sendai
S. senftenberg
S. stanley
S. stanleyville
S. thompson
S. typhimurium
S. tyhpisuis
S. virchow
S. wien

8. MEDIA AND REAGENTS

All media and reagents were sterilized before usage.

- LB broth Lennox (Roth, Karlsruhe, Germany; catalog # X964.4)
- LB agar Lennox (Roth, Karlsruhe, Germany; catalog # X965.2)
- Agar-Agar, Kobe I (Roth, Karlsruhe, Germany; catalog # 5210.2)
- LB top agar (LB broth with 0.6 % Agar-Agar)

9. GENERAL OUTLINE OF STUDY

- Overnight cultures of the bacterial test strains were grown in LB medium at 37°C. The LB top agar was melted and kept in a water bath at 55°C.

- The phage preparations were serially diluted in LB medium.

- 100 µL of the overnight bacterial culture were mixed with 100 µL of a phage dilution and 4 mL melted, warm top agar. The mixture was vortexed and distributed on LB agar plates.

- After solidification of the agar, the LB agar plates were incubated at 37°C for 16 h.

- The ability of a phage to form single plaques in the bacterial lawn was classified as positive phage-host interaction.

10. RESULTS

1. Raw Data

***Table 2**: Coverage of 41 Salmonella enterica serovars by the “Applied Phage Meat S2” component phages.*

***Salmonella* strains**	**Phages**										
	FV7M4	**MP82**	**RMP9**	**OBO18**	**DIN2**	**TAT2F**	**RMS3b**	**RMP11k**	**MP75**	**KAZ99a**	**ELB17**
S. agona	-	-	-	-	+	-	-	-	-	+	-
S. anatum	-	-	+	-	+	+	-	+	-	-	-
S. brandenburg	-	-	-	-	+	-	-	-	+	-	-
S. choleraesuis	+	+	+	-	+	+	+	+	-	+	-
S. decatur	-	-	+	-	-	+	+	+	-	+	-
S. derby	-	+	+	+	+	+	+	+	+	-	-
S. dublin	+	+	-	+	+	+	+	+	+	+	-
S. duisburg	-	-	+	-	-	+	+	+	+	+	-
S. emek	-	-	-	-	-	-	-	-	+	-	+
S. enterica	-	-	-	+	-	+	+	+	+	+	-
S. enteritidis	-	+	-	+	-	+	+	+	+	+	+
S. gallinarum	-	-	-	+	-	+	-	+	+	+	-
S. haifa	-	-	+	-	-	-	-	-	-	-	+
S. heidelberg	-	+	+	+	+	+	+	+	+	+	+
S. indiana	+	-	+	-	-	+	+	+	+	+	-
S. infantis	+	+	+	-	+	+	+	+	-	+	-
S. java	+	-	+	-	+	+	+	+	+	+	-
S. kiambu	-	-	-	-	+	-	-	-	+	-	-
S. livingstone	-	+	+	-	+	-	+	-	-	+	-
S. london	-	+	-	-	+	-	-	-	-	-	+
S. miami	-	+	-	-	+	+	+	+	+	+	-
S. minnesota	-	-	-	-	+	+	+	+	-	+	-
S. montevideo	-	-	-	-	-	+	-	+	-	-	-
S. muenchen	+	+	+	+	+	+	+	+	+	+	+
S. newport	-	+	-	+	+	+	+	+	-	+	-
S. panama	-	-	+	+	-	+	+	+	+	+	-
S. paratyphi A	-	-	+	-	-	+	+	+	-	+	-
S. paratyphi B	+	+	-	-	-	+	+	+	+	+	+
S. paratyphi C	+	+	+	+	+	+	+	+	+	+	-
S. pullorum	-	-	-	+	+	+	+	+	+	+	-
S. rubislaw	-	+	+	-	-	+	+	+	-	+	-
S. saintpaul	+	-	-	-	+	+	+	+	+	+	+
S. sendai	-	-	-	-	-	-	-	+	-	+	+
S. senftenberg	-	+	-	-	-	-	-	-	-	-	+
S. stanley	-	-	-	-	-	+	+	+	+	+	-
S. stanleyville	-	-	+	-	-	+	+	+	+	+	-
S. thompson	-	+	-	-	+	+	+	+	-	+	-
S. typhimurium	-	+	+	+	-	+	+	+	+	+	+
S. typhisuis	-	+	-	-	+	+	+	+	-	+	-
S. virchow	-	+	-	-	-	+	+	+	-	+	-
S. wien	-	+	-	-	-	+	+	+	-	+	-

***Table 2**: Ranked coverage*

***Salmonella* strains**	**Phages**											**Pos. int./strain**
	RMP11k	**KAZ99a**	**TAT2F**	**RMS3b**	**MP75**	**DIN2**	**MP82**	**RMP9**	**OBO18**	**ELB17**	**FV7M4**	
S. muenchen	+	+	+	+	+	+	+	+	+	+	+	11
S. heidelberg	+	+	+	+	+	+	+	+	+	+	-	10
S. paratyphi C	+	+	+	+	+	+	+	+	+	-	+	10
S. dublin	+	+	+	+	+	+	+	-	+	-	+	9
S. typhimurium	+	+	+	+	+	-	+	+	+	+	-	9
S. choleraesuis	+	+	+	+	-	+	+	+	-	-	+	8
S. derby	+	-	+	+	+	+	+	+	+	-	-	8
S. enteritidis	+	+	+	+	+	-	+	-	+	+	-	8
S. infantis	+	+	+	+	-	+	+	+	-	-	+	8
S. java	+	+	+	+	+	+	-	+	-	-	+	8
S. paratyphi B	+	+	+	+	+	-	+	-	-	+	+	8
S. saintpaul	+	+	+	+	+	+	-	-	-	+	+	8
S. indiana	+	+	+	+	+	-	-	+	-	-	+	7
S. miami	+	+	+	+	+	+	+	-	-	-	-	7
S. panama	+	+	+	+	+	-	-	+	+	-	-	7
S. newport	+	+	+	+	-	+	+	-	+	-	-	7
S. pullorum	+	+	+	+	+	+	-	-	+	-	-	7
S. duisburg	+	+	+	+	+	-	-	+	-	-	-	6
S. enterica	+	+	+	+	+	-	-	-	+	-	-	6
S. rubislaw	+	+	+	+	-	-	+	+	-	-	-	6
S. stanleyville	+	+	+	+	+	-	-	+	-	-	-	6
S. thompson	+	+	+	+	-	+	+	-	-	-	-	6
S. typhisuis	+	+	+	+	-	+	+	-	-	-	-	6
S. decatur	+	+	+	+	-	-	-	+	-	-	-	5
S. gallinarum	+	+	+	-	+	-	-	-	+	-	-	5
S. livingstone	-	+	-	+	-	+	+	+	-	-	-	5
S. minnesota	+	+	+	+	-	+	-	-	-	-	-	5
S. paratyphi A	+	+	+	+	-	-	-	+	-	-	-	5
S. stanley	+	+	+	+	+	-	-	-	-	-	-	5
S. virchow	+	+	+	+	-	-	+	-	-	-	-	5
S. wien	+	+	+	+	-	-	+	-	-	-	-	5
S. anatum	+	-	+	-	-	+	-	+	-	-	-	4
S. london	-	-	-	-	-	+	+	-	-	+	-	3
S. sendai	+	+	-	-	-	-	-	-	-	+	-	3
S. agona	-	+	-	-	-	+	-	-	-	-	-	2
S. brandenburg	-	-	-	-	+	+	-	-	-	-	-	2
S. emek	-	-	-	-	+	-	-	-	-	+	-	2
S. haifa	-	-	-	-	-	-	-	+	-	+	-	2
S. kiambu	-	-	-	-	+	+	-	-	-	-	-	2
S. montevideo	+	-	+	-	-	-	-	-	-	-	-	2
S. senftenberg	-	-	-	-	-	-	+	-	-	+	-	2
Pos. int./phage	33	32	32	30	22	21	20	18	12	11	9	

Abbreviations:		
	Pos. int./phage	Positive interactions per phage
	Pos. int./strain	Positive interactions per strain

2. Interpretation of the results

All 41 *Salmonella enterica* serovars tested were sensitive to at least two genetically independent component phages of the *"Applied Phage Meat S2"* bacteriophage product. The most sensitive serovar, *S. muenchen*, in fact was supporting the growth of all eleven component phages. Four component phages, namely RMP11k, KAZ99a, TAT2F and RMS3b showed a very broad host range with over 30/41 positive interactions. Since the individual host ranges varied, the different component phages complement each other, increasing the total coverage, which is important for the composition of an efficient phage product like *"Applied Phage Meat S2"*. This information will be used to choose six out of eleven component phages in order to produce an *"Applied Phage Meat S2"* product with an optimal range of activity, adjusted to the serovars present in an individual meat production facility.

11. SUMMARY CONCLUSION OF THE STUDY

For the present study a set 41 of *Salmonella enterica* spp. serovars with relevance in the area of meat production was collected. All these serovars where covered by at least two of the eleven component phages of *"Applied Phage Meat S2"*. By a combination of component phages with complementary host preferences it is possible to generate an *"Applied Phage Meat S2"* product with a broad range of activity.

12. SIGNATURES

[redacted]

Andrea Kroj, Ph.D.
Research scientist

10.02.2021
Date

[redacted]

Hansjörg Lehnherr, Ph.D.
Study director

10.02.2021
Date

Attachment II

Bioninformatic analyses of Salmonella phages.

> The genomes of all bacteriophages were determined using Next Generation Sequencing (Illumina technology). They were analyzed using standard bioinformatics methods with the help of a commercially available software package “Geneious” version 4.8 (Biomatters Ltd, New Zealand), as well as the search engines BLASTN, BLASTX and BLASTP provided online by NCBI (Bethesda, USA) together with the “Genbank” database containing all genomic information available up to date.

[*Confidential Business Information*:

[redacted]

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Home Services Instructions Output

VirulenceFinder-2.0 Server - Results

Organism(s): *Escherichia coli*

Virulence genes for Escherichia coli

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

Shiga-toxin genes

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

extended output

Results as text | Results tsv | Hits in genome seqs | Virulence factor seqs

Input Files: *ELB17.txt*

CITATIONS

For publication of results, please cite:

- Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
  Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM.
  J. Clin. Micobiol. 2014. 52(5): 1501-1510.
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Contact: Vibeke Dybdahl Hammer, Telephone: +45 3588 6420, E-mail: vdha@food.dtu.dk
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VirulenceFinder-2.0 Server - Results

Organism(s): *Escherichia coli*

Virulence genes for Escherichia coli

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

Shiga-toxin genes

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

extended output

Results as text Results tsv Hits in genome seqs Virulence factor seqs

Input Files: *MP82.txt*

CITATIONS

For publication of results, please cite:

- Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
  Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM.
  J. Clin. Micobiol. 2014. 52(5): 1501-1510.
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VirulenceFinder-2.0 Server - Results

Organism(s): *Escherichia coli*

Virulence genes for Escherichia coli

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

Shiga-toxin genes

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

extended output

Results as text Results tsv Hits in genome seqs Virulence factor seqs

Input Files: *KAZ99a.txt*

CITATIONS

For publication of results, please cite:

- Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
  Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM.
  J. Clin. Micobiol. 2014. 52(5): 1501-1510.
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VirulenceFinder-2.0 Server - Results

Organism(s): *Escherichia coli*

Virulence genes for Escherichia coli

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

Shiga-toxin genes

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

extended output

Results as text | Results tsv | Hits in genome seqs | Virulence factor seqs

Input Files: *RMP11k.txt*

CITATIONS

For publication of results, please cite:

- Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
  Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM.
  J. Clin. Micobiol. 2014. 52(5): 1501-1510.
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Contact: Vibeke Dybdahl Hammer, Telephone: +45 3588 6420, E-mail: vdha@food.dtu.dk
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VirulenceFinder-2.0 Server - Results

Organism(s): *Escherichia coli*

Shiga-toxin genes

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

Virulence genes for Escherichia coli

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

extended output

Results as text | Results tsv | Hits in genome seqs | Virulence factor seqs

Input Files: *RMS3b.txt*

CITATIONS

For publication of results, please cite:

- Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
  Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM.
  J. Clin. Micobiol. 2014. 52(5): 1501-1510.
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VirulenceFinder-2.0 Server - Results

Organism(s): *Escherichia coli*

Virulence genes for Escherichia coli

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

Shiga-toxin genes

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

extended output

Results as text | Results tsv | Hits in genome seqs | Virulence factor seqs

Input Files: *TAT2F.txt*

CITATIONS

For publication of results, please cite:

- Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
  Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM.
  J. Clin. Micobiol. 2014. 52(5): 1501-1510.
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VirulenceFinder-2.0 Server - Results

Organism(s): *Escherichia coli*

Shiga-toxin genes

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

Virulence genes for Escherichia coli

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

extended output

Results as text | Results tsv | Hits in genome seqs | Virulence factor seqs

Input Files: *DIN2.txt*

CITATIONS

For publication of results, please cite:

- Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
  Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM.
  J. Clin. Micobiol. 2014. 52(5): 1501-1510.
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VirulenceFinder-2.0 Server - Results

Organism(s): *Escherichia coli*

Virulence genes for Escherichia coli

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

Shiga-toxin genes

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

extended output

Results as text Results tsv Hits in genome seqs Virulence factor seqs

Input Files: *MP75.txt*

CITATIONS

For publication of results, please cite:

- Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
  Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM.
  J. Clin. Micobiol. 2014. 52(5): 1501-1510.
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VirulenceFinder-2.0 Server - Results

Organism(s): *Escherichia coli*

Virulence genes for Escherichia coli

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

Shiga-toxin genes

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

extended output

Results as text Results tsv Hits in genome seqs Virulence factor seqs

Input Files: *FV7M4.txt*

CITATIONS

For publication of results, please cite:

- Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
  Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM.
  J. Clin. Micobiol. 2014. 52(5): 1501-1510.
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VirulenceFinder-2.0 Server - Results

Organism(s): *Escherichia coli*

Shiga-toxin genes

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

Virulence genes for Escherichia coli

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

extended output

Results as text Results tsv Hits in genome seqs Virulence factor seqs

Input Files: *RMP9.txt*

CITATIONS

For publication of results, please cite:

- Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
  Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM.
  J. Clin. Micobiol. 2014. 52(5): 1501-1510.
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Home Services Instructions Output

VirulenceFinder-2.0 Server - Results

Organism(s): *Escherichia coli*

Virulence genes for Escherichia coli

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

Shiga-toxin genes

Virulence factor	Identity	Query / Template length	Contig	Position in contig	Protein function	Accession number
No hit found						

extended output

Results as text Results tsv Hits in genome seqs Virulence factor seqs

Input Files: *OBO18.txt*

CITATIONS

For publication of results, please cite:

- Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli.
  Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM.
  J. Clin. Micobiol. 2014. 52(5): 1501-1510.
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Contact: Vibeke Dybdahl Hammer, Telephone: +45 3588 6420, E-mail: vdha@food.dtu.dk
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Attachment V: Genome safety of the component phages of the "*Applied Phage Meat S2*" product against *Salmonella enterica* spp.

DSM name	Phage internal name	Presence of the genes for toxins listed in EPA 40 CFR Ch. (7-1-11 Edition) § 725.421-725.422 in the phage genomes					Presence of the *E. coli* toxins listed in the VirulenceFinder database
		protein synthesis inhibitors	neuro-toxins	Oxygen-liable cytolysins	toxins affecting membrane integrity & functions	general cytotoxins	
DSM 33041	OBO18	none	none	none	none	none	none
DSM 26125	FV7M4	none	none	none	none	none	none
DSM 26157	RMP9	none	none	none	none	none	none
DSM 26158	ELB17	none	none	none	none	none	none
DSM 33045	DIN2	none	none	none	none	none	none
DSM 26173	MP82	none	none	none	none	none	none
DSM 104023	MP75	none	none	none	none	none	none
DSM 33043	RMS3b	none	none	none	none	none	none
DSM 33039	KAZ99a	none	none	none	none	none	none
DSM 33040	RMP11k	none	none	none	none	none	none
DSM 33044	TAT2F	none	none	none	none	none	none

Attachment VI

Allergen search procedure

Allergen search was carried out against the database AllergenOnline of the University of Nebraska (version 16 released on January 27, 2016) using the recommended algorithm according to Codex Alimentarius 2003 [1] and the AllergenOnline website [2] as followed:

A sliding window of amino acid sequence 80mers of each phage protein was compared to the allergen database by local alignment search using FASTA (Version 36.3.8c Dec 2015, BL50 Blossum scoring matrix ktup:2 and gap open/ext: 20/10).

According to Codex Alimentarius, IgE cross-reactivity between phage proteins and known allergens was considered a possibility for more than 35% identity in a segment of 80 amino acids (80mer). All tested 80mers of phage proteins had identity to known allergens below 35% (see Table 1). Therefore no IgE cross-reactivity with phage proteins is to be expected according to the standards of the Codex Alimentarius and the AllergenOnline website. Detailed search results for all phages are provided below. Files show 80mer similarities from highest to lower values (see file names in Table 1).

Table 1. Highest similarity scores between phage protein 80mers and the AllergenOnline database. No similarity equal or higher than 35% has been found.

Phage name	Phage protein showing the highest similarity in 80mer	highest similarity in 80mer	detailed search result on page
ELB17	gp239	27.5%	2-5
MP82	gp42	30%	6-14
KAZ99a	gp73	28.8%	15-16
RMP11k	gp127	27.5%	17
RMS3b	gp78	28.8%	18-19
TAT2F	gp131	27.5%	20
DIN2	gp32	28.7%	21
MP75	gp35 and gp103	25%	22
FV7M4	gp17	26.2%	23
RMP9	gp23	27.5%	24-25
OBO18	gp42	27.5%	26-27

References:

[1] Codex Alimentarius Commission, 2003. Alinorm 03/34: Joint FAO/WHO Food Standard Programme, Codex Alimentarius Commission, Twenty-Fifth Session, Rome, Italy 30 June-5 July, 2003. Appendix III and Appendix IV Section 3.2: *Annex on the assessment of possible allergenicity*, pp. 47-60

[2] http://www.allergenonline.org/

query ID	subject ID	% identity	alignment length	mismatch count	gap open count	query start	query end	subject start	subject end	e-Value	bitScore	% identity 80mer
ELB17_gp239	gi|18093971|emb|CAD20405.1|	30.14	73	51	0	1	73	30	102	0.53	26.2	27.5
ELB17_gp239	gi|2266625|emb|CAB10765.1|	27.85	79	57	0	1	79	29	107	0.42	26.6	27.5
ELB17_gp239	gi|18093971|emb|CAD20405.1|	29.73	74	52	0	7	80	29	102	0.53	26.2	27.5
ELB17_gp239	gi|18093971|emb|CAD20405.1|	29.73	74	52	0	6	79	29	102	0.53	26.2	27.5
ELB17_gp239	gi|18093971|emb|CAD20405.1|	29.73	74	52	0	5	78	29	102	0.53	26.2	27.5
ELB17_gp239	gi|18093971|emb|CAD20405.1|	29.73	74	52	0	4	77	29	102	0.53	26.2	27.5
ELB17_gp239	gi|18093971|emb|CAD20405.1|	29.73	74	52	0	3	76	29	102	0.53	26.2	27.5
ELB17_gp239	gi|18093971|emb|CAD20405.1|	29.73	74	52	0	2	75	29	102	0.53	26.2	27.5
ELB17_gp239	gi|18093971|emb|CAD20405.1|	29.73	74	52	0	1	74	29	102	0.53	26.2	27.5
ELB17_gp239	gi|2266625|emb|CAB10765.1|	27.5	80	58	0	1	80	28	107	0.26	27.2	27.5
ELB17_gp239	gi|18093971|emb|CAD20405.1|	28.77	73	52	0	8	80	29	101	0.53	26.2	26.3
ELB17_gp239	gi|14423124|gb|AAK62278.1|AF325267_1	28.77	73	52	0	1	73	55	127	1.5	24.9	26.3
ELB17_gp239	gi|15886861|emb|CAC85911.1|	28.38	74	53	0	7	80	30	103	1.1	25.5	26.3
ELB17_gp239	gi|15886861|emb|CAC85911.1|	28.38	74	53	0	6	79	30	103	1.1	25.5	26.3
ELB17_gp239	gi|15886861|emb|CAC85911.1|	28.38	74	53	0	5	78	30	103	1.1	25.5	26.3
ELB17_gp239	gi|15886861|emb|CAC85911.1|	28.38	74	53	0	4	77	30	103	1.1	25.5	26.3
ELB17_gp239	gi|15886861|emb|CAC85911.1|	28.38	74	53	0	3	76	30	103	1.1	25.5	26.3
ELB17_gp239	gi|15886861|emb|CAC85911.1|	28.38	74	53	0	2	75	30	103	1.1	25.5	26.3
ELB17_gp239	gi|15886861|emb|CAC85911.1|	28.38	74	53	0	1	74	30	103	1.1	25.5	26.3
ELB17_gp239	gi|14423124|gb|AAK62278.1|AF325267_1	28.38	74	53	0	7	80	54	127	1.5	24.9	26.3
ELB17_gp239	gi|14423124|gb|AAK62278.1|AF325267_1	28.38	74	53	0	6	79	54	127	1.5	24.9	26.3
ELB17_gp239	gi|14423124|gb|AAK62278.1|AF325267_1	28.38	74	53	0	5	78	54	127	1.5	24.9	26.3
ELB17_gp239	gi|14423124|gb|AAK62278.1|AF325267_1	28.38	74	53	0	4	77	54	127	1.5	24.9	26.3
ELB17_gp239	gi|14423124|gb|AAK62278.1|AF325267_1	28.38	74	53	0	3	76	54	127	1.5	24.9	26.3
ELB17_gp239	gi|14423124|gb|AAK62278.1|AF325267_1	28.38	74	53	0	2	75	54	127	1.5	24.9	26.3
ELB17_gp239	gi|14423124|gb|AAK62278.1|AF325267_1	28.38	74	53	0	1	74	54	127	1.5	24.9	26.3
ELB17_gp166	gi|442577833|gb|AGC60020.1|	30	70	49	0	11	80	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	30	70	49	0	11	80	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|442577833|gb|AGC60020.1|	30	70	49	0	10	79	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	30	70	49	0	10	79	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|442577833|gb|AGC60020.1|	30	70	49	0	9	78	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	30	70	49	0	9	78	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|442577833|gb|AGC60020.1|	30	70	49	0	8	77	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	30	70	49	0	8	77	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|442577833|gb|AGC60020.1|	30	70	49	0	7	76	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	30	70	49	0	7	76	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|442577833|gb|AGC60020.1|	30	70	49	0	6	75	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	30	70	49	0	6	75	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|442577833|gb|AGC60020.1|	30	70	49	0	5	74	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	30	70	49	0	5	74	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|442577833|gb|AGC60020.1|	30	70	49	0	4	73	169	238	0.0042	34.9	26.3

ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	30	70	49	0	4	73	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|442577833|gb|AGC60020.1|	30	70	49	0	3	72	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	30	70	49	0	3	72	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|442577833|gb|AGC60020.1|	30	70	49	0	2	71	169	238	0.0042	34.9	26.3
ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	26.58	79	58	0	2	80	150	228	0.0016	36.3	26.2
ELB17_gp166	gi|442577833|gb|AGC60020.1|	26.58	79	58	0	2	80	150	228	0.0016	36.3	26.2
ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	26.58	79	58	0	1	79	150	228	0.0016	36.3	26.2
ELB17_gp166	gi|442577833|gb|AGC60020.1|	26.58	79	58	0	1	79	150	228	0.0016	36.3	26.2
ELB17_gp239	gi|2266625|emb|CAB10765.1|	26.92	78	57	0	3	80	28	105	0.33	26.9	26.2
ELB17_gp239	gi|2266625|emb|CAB10765.1|	26.92	78	57	0	2	79	28	105	0.33	26.9	26.2
ELB17_gp82	gi|2114497|gb|AAB58417.1|	25.32	79	59	0	2	80	27	105	0.0039	33.3	25.0
ELB17_gp82	gi|2114497|gb|AAB58417.1|	25.32	79	59	0	1	79	27	105	0.0039	33.3	25.0
ELB17_gp82	gi|2114497|gb|AAB58417.1|	25.32	79	59	0	2	80	29	107	0.0019	34.3	25.0
ELB17_gp82	gi|2114497|gb|AAB58417.1|	25.32	79	59	0	1	79	29	107	0.0019	34.3	25.0
ELB17_gp32	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	26.67	75	55	0	6	80	75	149	2	24.5	25.0
ELB17_gp32	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	26.67	75	55	0	5	79	75	149	2	24.5	25.0
ELB17_gp32	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	26.67	75	55	0	4	78	75	149	2	24.5	25.0
ELB17_gp32	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	26.67	75	55	0	3	77	75	149	2	24.5	25.0
ELB17_gp32	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	26.67	75	55	0	2	76	75	149	2	24.5	25.0
ELB17_gp32	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	26.67	75	55	0	1	75	75	149	2	24.5	25.0
ELB17_gp239	gi|2266625|emb|CAB10765.1|	27.03	74	54	0	7	80	28	101	1.1	25.2	25.0
ELB17_gp239	gi|2266625|emb|CAB10765.1|	27.03	74	54	0	6	79	28	101	1.1	25.2	25.0
ELB17_gp239	gi|2266625|emb|CAB10765.1|	27.03	74	54	0	5	78	28	101	1.1	25.2	25.0
ELB17_gp239	gi|2266625|emb|CAB10765.1|	27.03	74	54	0	4	77	28	101	1.1	25.2	25.0
ELB17_gp239	gi|15886861|emb|CAC85911.1|	27.4	73	53	0	1	73	31	103	3.6	23.9	25.0
ELB17_gp239	gi|14423124|gb|AAK62278.1|AF325267_1	27.4	73	53	0	8	80	54	126	1.5	24.9	25.0
ELB17_gp82	gi|94468546|gb|ABF18122.1|	27.4	73	53	0	8	80	46	118	0.021	30.9	25.0
ELB17_gp82	gi|94468546|gb|ABF18122.1|	27.4	73	53	0	7	79	46	118	0.021	30.9	25.0
ELB17_gp82	gi|94468546|gb|ABF18122.1|	27.4	73	53	0	6	78	46	118	0.021	30.9	25.0
ELB17_gp82	gi|94468546|gb|ABF18122.1|	27.4	73	53	0	5	77	46	118	0.021	30.9	25.0
ELB17_gp82	gi|94468546|gb|ABF18122.1|	27.4	73	53	0	4	76	46	118	0.021	30.9	25.0
ELB17_gp82	gi|94468546|gb|ABF18122.1|	27.4	73	53	0	3	75	46	118	0.021	30.9	25.0
ELB17_gp82	gi|94468546|gb|ABF18122.1|	27.4	73	53	0	2	74	46	118	0.021	30.9	25.0
ELB17_gp82	gi|94468546|gb|ABF18122.1|	27.4	73	53	0	1	73	46	118	0.021	30.9	25.0
ELB17_gp32	gi|291482310|emb|CBK62695.1|	32.79	61	41	0	20	80	64	124	0.0079	31.3	25.0
ELB17_gp32	gi|291482310|emb|CBK62695.1|	32.79	61	41	0	19	79	64	124	0.0079	31.3	25.0
ELB17_gp32	gi|291482310|emb|CBK62695.1|	32.79	61	41	0	18	78	64	124	0.0079	31.3	25.0
ELB17_gp32	gi|291482310|emb|CBK62695.1|	32.79	61	41	0	17	77	64	124	0.0079	31.3	25.0
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ELB17_gp32	gi|291482310|emb|CBK62695.1|	32.79	61	41	0	15	75	64	124	0.0079	31.3	25.0
ELB17_gp32	gi|291482310|emb|CBK62695.1|	32.79	61	41	0	14	74	64	124	0.0079	31.3	25.0
ELB17_gp32	gi|291482310|emb|CBK62695.1|	32.79	61	41	0	13	73	64	124	0.0079	31.3	25.0
ELB17_gp32	gi|291482310|emb|CBK62695.1|	32.79	61	41	0	12	72	64	124	0.0079	31.3	25.0
ELB17_gp32	gi|291482310|emb|CBK62695.1|	32.79	61	41	0	11	71	64	124	0.0079	31.3	25.0
ELB17_gp32	gi|291482310|emb|CBK62695.1|	32.79	61	41	0	10	70	64	124	0.0079	31.3	25.0
ELB17_gp239	gi|15886861|emb|CAC85911.1|	27.78	72	52	0	1	72	32	103	5.8	23.2	25.0

<table>
<tr><td>ELB17_gp239</td><td>gi|113561|sp|P22285.1|MPA92_POAPR</td><td>41.67</td><td>48</td><td>28</td><td>0</td><td>2</td><td>49</td><td>284</td><td>331</td><td>0.013</td><td>31.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|113561|sp|P22285.1|MPA92_POAPR</td><td>41.67</td><td>48</td><td>28</td><td>0</td><td>1</td><td>48</td><td>284</td><td>331</td><td>0.013</td><td>31.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp166</td><td>gi|42559536|sp|Q9NJA9.1|MYSP_ANISI</td><td>27.78</td><td>72</td><td>52</td><td>0</td><td>7</td><td>78</td><td>157</td><td>228</td><td>0.0033</td><td>35.3</td><td>25.0</td></tr>
<tr><td>ELB17_gp166</td><td>gi|442577833|gb|AGC60020.1|</td><td>27.78</td><td>72</td><td>52</td><td>0</td><td>7</td><td>78</td><td>157</td><td>228</td><td>0.0033</td><td>35.3</td><td>25.0</td></tr>
<tr><td>ELB17_gp166</td><td>gi|442577833|gb|AGC60020.1|</td><td>27.78</td><td>72</td><td>52</td><td>0</td><td>6</td><td>77</td><td>157</td><td>228</td><td>0.0033</td><td>35.3</td><td>25.0</td></tr>
<tr><td>ELB17_gp166</td><td>gi|42559536|sp|Q9NJA9.1|MYSP_ANISI</td><td>27.78</td><td>72</td><td>52</td><td>0</td><td>6</td><td>77</td><td>157</td><td>228</td><td>0.0033</td><td>35.3</td><td>25.0</td></tr>
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<tr><td>ELB17_gp166</td><td>gi|42559536|sp|Q9NJA9.1|MYSP_ANISI</td><td>27.78</td><td>72</td><td>52</td><td>0</td><td>5</td><td>76</td><td>157</td><td>228</td><td>0.0033</td><td>35.3</td><td>25.0</td></tr>
<tr><td>ELB17_gp166</td><td>gi|442577833|gb|AGC60020.1|</td><td>27.78</td><td>72</td><td>52</td><td>0</td><td>4</td><td>75</td><td>157</td><td>228</td><td>0.0033</td><td>35.3</td><td>25.0</td></tr>
<tr><td>ELB17_gp166</td><td>gi|42559536|sp|Q9NJA9.1|MYSP_ANISI</td><td>27.78</td><td>72</td><td>52</td><td>0</td><td>4</td><td>75</td><td>157</td><td>228</td><td>0.0033</td><td>35.3</td><td>25.0</td></tr>
<tr><td>ELB17_gp166</td><td>gi|442577833|gb|AGC60020.1|</td><td>27.78</td><td>72</td><td>52</td><td>0</td><td>3</td><td>74</td><td>157</td><td>228</td><td>0.0033</td><td>35.3</td><td>25.0</td></tr>
<tr><td>ELB17_gp166</td><td>gi|42559536|sp|Q9NJA9.1|MYSP_ANISI</td><td>27.78</td><td>72</td><td>52</td><td>0</td><td>3</td><td>74</td><td>157</td><td>228</td><td>0.0033</td><td>35.3</td><td>25.0</td></tr>
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<tr><td>ELB17_gp239</td><td>gi|4416516|gb|AAD20386.1|</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>24</td><td>80</td><td>19</td><td>75</td><td>0.0058</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|332278195|sp|Q40240.2|MPA5A_LOLPR</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>24</td><td>80</td><td>19</td><td>75</td><td>0.0059</td><td>32.9</td><td>25.0</td></tr>
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<tr><td>ELB17_gp239</td><td>gi|4416516|gb|AAD20386.1|</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>19</td><td>75</td><td>19</td><td>75</td><td>0.0058</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|332278195|sp|Q40240.2|MPA5A_LOLPR</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>19</td><td>75</td><td>19</td><td>75</td><td>0.0059</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|4416516|gb|AAD20386.1|</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>18</td><td>74</td><td>19</td><td>75</td><td>0.0058</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|332278195|sp|Q40240.2|MPA5A_LOLPR</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>18</td><td>74</td><td>19</td><td>75</td><td>0.0059</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|4416516|gb|AAD20386.1|</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>17</td><td>73</td><td>19</td><td>75</td><td>0.0058</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|332278195|sp|Q40240.2|MPA5A_LOLPR</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>17</td><td>73</td><td>19</td><td>75</td><td>0.0059</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|4416516|gb|AAD20386.1|</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>16</td><td>72</td><td>19</td><td>75</td><td>0.0058</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|332278195|sp|Q40240.2|MPA5A_LOLPR</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>16</td><td>72</td><td>19</td><td>75</td><td>0.0059</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|4416516|gb|AAD20386.1|</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>15</td><td>71</td><td>19</td><td>75</td><td>0.0058</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|332278195|sp|Q40240.2|MPA5A_LOLPR</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>15</td><td>71</td><td>19</td><td>75</td><td>0.0059</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|4416516|gb|AAD20386.1|</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>14</td><td>70</td><td>19</td><td>75</td><td>0.0058</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|332278195|sp|Q40240.2|MPA5A_LOLPR</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>14</td><td>70</td><td>19</td><td>75</td><td>0.0059</td><td>32.9</td><td>25.0</td></tr>
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<tr><td>ELB17_gp239</td><td>gi|4416516|gb|AAD20386.1|</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>12</td><td>68</td><td>19</td><td>75</td><td>0.0058</td><td>32.9</td><td>25.0</td></tr>
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<tr><td>ELB17_gp239</td><td>gi|4416516|gb|AAD20386.1|</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>11</td><td>67</td><td>19</td><td>75</td><td>0.0058</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|332278195|sp|Q40240.2|MPA5A_LOLPR</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>11</td><td>67</td><td>19</td><td>75</td><td>0.0059</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|4416516|gb|AAD20386.1|</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>10</td><td>66</td><td>19</td><td>75</td><td>0.0058</td><td>32.9</td><td>25.0</td></tr>
<tr><td>ELB17_gp239</td><td>gi|332278195|sp|Q40240.2|MPA5A_LOLPR</td><td>35.09</td><td>57</td><td>37</td><td>0</td><td>10</td><td>66</td><td>19</td><td>75</td><td>0.0059</td><td>32.9</td><td>25.0</td></tr>
</table>

ELB17_gp239	gi|4416516|gb|AAD20386.1|	35.09	57	37	0	9	65	19	75	0.0058	32.9	25.0
ELB17_gp239	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	35.09	57	37	0	9	65	19	75	0.0059	32.9	25.0
ELB17_gp239	gi|4416516|gb|AAD20386.1|	35.09	57	37	0	8	64	19	75	0.0058	32.9	25.0
ELB17_gp239	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	35.09	57	37	0	8	64	19	75	0.0059	32.9	25.0
ELB17_gp239	gi|4416516|gb|AAD20386.1|	35.09	57	37	0	7	63	19	75	0.0058	32.9	25.0
ELB17_gp239	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	35.09	57	37	0	7	63	19	75	0.0059	32.9	25.0
ELB17_gp239	gi|4416516|gb|AAD20386.1|	35.09	57	37	0	6	62	19	75	0.0058	32.9	25.0
ELB17_gp239	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	35.09	57	37	0	6	62	19	75	0.0059	32.9	25.0
ELB17_gp239	gi|4416516|gb|AAD20386.1|	35.09	57	37	0	5	61	19	75	0.0058	32.9	25.0
ELB17_gp239	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	35.09	57	37	0	5	61	19	75	0.0059	32.9	25.0
ELB17_gp239	gi|4416516|gb|AAD20386.1|	35.09	57	37	0	4	60	19	75	0.0058	32.9	25.0
ELB17_gp239	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	35.09	57	37	0	4	60	19	75	0.0059	32.9	25.0
ELB17_gp239	gi|4416516|gb|AAD20386.1|	35.09	57	37	0	3	59	19	75	0.0058	32.9	25.0
ELB17_gp239	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	35.09	57	37	0	3	59	19	75	0.0059	32.9	25.0
ELB17_gp239	gi|4416516|gb|AAD20386.1|	35.09	57	37	0	2	58	19	75	0.0058	32.9	25.0
ELB17_gp239	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	35.09	57	37	0	2	58	19	75	0.0059	32.9	25.0
ELB17_gp239	gi|4416516|gb|AAD20386.1|	35.09	57	37	0	1	57	19	75	0.0058	32.9	25.0
ELB17_gp239	gi|332278195|sp|Q40240.2|MPA5A_LOLPR	35.09	57	37	0	1	57	19	75	0.0059	32.9	25.0
ELB17_gp166	gi|42559536|sp|Q9NJA9.1|MYSP_ANISI	30	70									

query ID	subject ID	% identity	alignment length	mismatch count	gap open count	query start	query end	subject start	subject end	e-Value	bitScore	% identity 80mer
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	34.78	69	45	0	2	70	425	493	1.8	25.5	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	34.78	69	45	0	1	69	425	493	1.8	25.5	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.8	71	47	0	10	80	423	493	0.35	27.9	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.8	71	47	0	9	79	423	493	0.35	27.9	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.8	71	47	0	8	78	423	493	0.28	28.2	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.8	71	47	0	7	77	423	493	0.22	28.6	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.8	71	47	0	6	76	423	493	0.22	28.6	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.8	71	47	0	5	75	423	493	0.22	28.6	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.8	71	47	0	4	74	423	493	0.44	27.6	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.8	71	47	0	3	73	423	493	0.44	27.6	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.8	71	47	0	2	72	423	493	1.8	25.5	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.8	71	47	0	1	71	423	493	1.8	25.5	30.0
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	34.33	67	44	0	2	68	427	493	2.8	24.9	28.8
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	34.33	67	44	0	1	67	427	493	2.8	24.9	28.8
MP82_gp80	gi|3135499|gb|AAC16526.1|	31.08	74	51	0	7	80	183	256	0.068	29.2	28.7
MP82_gp80	gi|1684720|emb|CAB05372.1|	31.08	74	51	0	7	80	183	256	0.068	29.2	28.7
MP82_gp80	gi|3135501|gb|AAC16527.1|	31.08	74	51	0	7	80	183	256	0.068	29.2	28.7
MP82_gp80	gi|29500897|emb|CAD87529.1|	31.08	74	51	0	7	80	191	264	0.07	29.2	28.7
MP82_gp80	gi|345108717|emb|CCD28287.1|	31.08	74	51	0	7	80	216	289	0.077	29.2	28.7
MP82_gp80	gi|13430402|gb|AAK25823.1|	31.08	74	51	0	7	80	182	255	0.086	28.9	28.7
MP82_gp80	gi|3135503|gb|AAC16528.1|	31.08	74	51	0	7	80	183	256	0.086	28.9	28.7
MP82_gp80	gi|398830|emb|CAA52753.1|	31.08	74	51	0	7	80	219	292	0.098	28.9	28.7
MP82_gp80	gi|3309039|gb|AAC25994.1|	31.08	74	51	0	7	80	219	292	0.098	28.9	28.7
MP82_gp80	gi|3135499|gb|AAC16526.1|	31.08	74	51	0	6	79	183	256	0.068	29.2	28.7
MP82_gp80	gi|1684720|emb|CAB05372.1|	31.08	74	51	0	6	79	183	256	0.068	29.2	28.7
MP82_gp80	gi|3135501|gb|AAC16527.1|	31.08	74	51	0	6	79	183	256	0.068	29.2	28.7
MP82_gp80	gi|29500897|emb|CAD87529.1|	31.08	74	51	0	6	79	191	264	0.07	29.2	28.7
MP82_gp80	gi|345108717|emb|CCD28287.1|	31.08	74	51	0	6	79	216	289	0.077	29.2	28.7
MP82_gp80	gi|13430402|gb|AAK25823.1|	31.08	74	51	0	6	79	182	255	0.086	28.9	28.7
MP82_gp80	gi|3135503|gb|AAC16528.1|	31.08	74	51	0	6	79	183	256	0.086	28.9	28.7
MP82_gp80	gi|398830|emb|CAA52753.1|	31.08	74	51	0	6	79	219	292	0.098	28.9	28.7
MP82_gp80	gi|3309039|gb|AAC25994.1|	31.08	74	51	0	6	79	219	292	0.098	28.9	28.7
MP82_gp80	gi|3135499|gb|AAC16526.1|	31.08	74	51	0	5	78	183	256	0.068	29.2	28.7
MP82_gp80	gi|1684720|emb|CAB05372.1|	31.08	74	51	0	5	78	183	256	0.068	29.2	28.7
MP82_gp80	gi|3135501|gb|AAC16527.1|	31.08	74	51	0	5	78	183	256	0.068	29.2	28.7
MP82_gp80	gi|29500897|emb|CAD87529.1|	31.08	74	51	0	5	78	191	264	0.07	29.2	28.7
MP82_gp80	gi|345108717|emb|CCD28287.1|	31.08	74	51	0	5	78	216	289	0.077	29.2	28.7
MP82_gp80	gi|13430402|gb|AAK25823.1|	31.08	74	51	0	5	78	182	255	0.086	28.9	28.7
MP82_gp80	gi|3135503|gb|AAC16528.1|	31.08	74	51	0	5	78	183	256	0.086	28.9	28.7
MP82_gp80	gi|398830|emb|CAA52753.1|	31.08	74	51	0	5	78	219	292	0.098	28.9	28.7
MP82_gp80	gi|3309039|gb|AAC25994.1|	31.08	74	51	0	5	78	219	292	0.098	28.9	28.7

MP82_gp80	gi|3135499|gb|AAC16526.1|	31.08	74	51	0	4	77	183	256	0.068	29.2	28.7
MP82_gp80	gi|1684720|emb|CAB05372.1|	31.08	74	51	0	4	77	183	256	0.068	29.2	28.7
MP82_gp80	gi|3135501|gb|AAC16527.1|	31.08	74	51	0	4	77	183	256	0.068	29.2	28.7
MP82_gp80	gi|29500897|emb|CAD87529.1|	31.08	74	51	0	4	77	191	264	0.07	29.2	28.7
MP82_gp80	gi|345108717|emb|CCD28287.1|	31.08	74	51	0	4	77	216	289	0.077	29.2	28.7
MP82_gp80	gi|13430402|gb|AAK25823.1|	31.08	74	51	0	4	77	182	255	0.086	28.9	28.7
MP82_gp80	gi|3135503|gb|AAC16528.1|	31.08	74	51	0	4	77	183	256	0.086	28.9	28.7
MP82_gp80	gi|398830|emb|CAA52753.1|	31.08	74	51	0	4	77	219	292	0.098	28.9	28.7
MP82_gp80	gi|3309039|gb|AAC25994.1|	31.08	74	51	0	4	77	219	292	0.098	28.9	28.7
MP82_gp80	gi|3135499|gb|AAC16526.1|	31.08	74	51	0	3	76	183	256	0.068	29.2	28.7
MP82_gp80	gi|1684720|emb|CAB05372.1|	31.08	74	51	0	3	76	183	256	0.068	29.2	28.7
MP82_gp80	gi|3135501|gb|AAC16527.1|	31.08	74	51	0	3	76	183	256	0.068	29.2	28.7
MP82_gp80	gi|29500897|emb|CAD87529.1|	31.08	74	51	0	3	76	191	264	0.07	29.2	28.7
MP82_gp80	gi|345108717|emb|CCD28287.1|	31.08	74	51	0	3	76	216	289	0.077	29.2	28.7
MP82_gp80	gi|13430402|gb|AAK25823.1|	31.08	74	51	0	3	76	182	255	0.086	28.9	28.7
MP82_gp80	gi|3135503|gb|AAC16528.1|	31.08	74	51	0	3	76	183	256	0.086	28.9	28.7
MP82_gp80	gi|398830|emb|CAA52753.1|	31.08	74	51	0	3	76	219	292	0.098	28.9	28.7
MP82_gp80	gi|3309039|gb|AAC25994.1|	31.08	74	51	0	3	76	219	292	0.098	28.9	28.7
MP82_gp80	gi|3135499|gb|AAC16526.1|	31.08	74	51	0	2	75	183	256	0.068	29.2	28.7
MP82_gp80	gi|1684720|emb|CAB05372.1|	31.08	74	51	0	2	75	183	256	0.068	29.2	28.7
MP82_gp80	gi|3135501|gb|AAC16527.1|	31.08	74	51	0	2	75	183	256	0.068	29.2	28.7
MP82_gp80	gi|29500897|emb|CAD87529.1|	31.08	74	51	0	2	75	191	264	0.07	29.2	28.7
MP82_gp80	gi|345108717|emb|CCD28287.1|	31.08	74	51	0	2	75	216	289	0.077	29.2	28.7
MP82_gp80	gi|13430402|gb|AAK25823.1|	31.08	74	51	0	2	75	182	255	0.086	28.9	28.7
MP82_gp80	gi|3135503|gb|AAC16528.1|	31.08	74	51	0	2	75	183	256	0.086	28.9	28.7
MP82_gp80	gi|398830|emb|CAA52753.1|	31.08	74	51	0	2	75	219	292	0.098	28.9	28.7
MP82_gp80	gi|3309039|gb|AAC25994.1|	31.08	74	51	0	2	75	219	292	0.098	28.9	28.7
MP82_gp80	gi|3135499|gb|AAC16526.1|	31.08	74	51	0	1	74	183	256	0.068	29.2	28.7
MP82_gp80	gi|1684720|emb|CAB05372.1|	31.08	74	51	0	1	74	183	256	0.068	29.2	28.7
MP82_gp80	gi|3135501|gb|AAC16527.1|	31.08	74	51	0	1	74	183	256	0.068	29.2	28.7
MP82_gp80	gi|29500897|emb|CAD87529.1|	31.08	74	51	0	1	74	191	264	0.07	29.2	28.7
MP82_gp80	gi|345108717|emb|CCD28287.1|	31.08	74	51	0	1	74	216	289	0.077	29.2	28.7
MP82_gp80	gi|13430402|gb|AAK25823.1|	31.08	74	51	0	1	74	182	255	0.086	28.9	28.7
MP82_gp80	gi|3135503|gb|AAC16528.1|	31.08	74	51	0	1	74	183	256	0.086	28.9	28.7
MP82_gp80	gi|398830|emb|CAA52753.1|	31.08	74	51	0	1	74	219	292	0.098	28.9	28.7
MP82_gp80	gi|3309039|gb|AAC25994.1|	31.08	74	51	0	1	74	219	292	0.098	28.9	28.7
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.33	69	46	0	12	80	423	491	0.7	26.9	28.7
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.33	69	46	0	11	79	423	491	0.7	26.9	28.7
MP82_gp42	gi|5815436|gb|AAD52672.1|AF178772_1	33.82	68	45	0	13	80	423	490	0.7	26.9	28.7
MP82_gp42	gi|267048|sp|P29600.1|SUBS_BACLE	28.21	78	56	0	1	78	56	133	0.0033	33.6	27.5
MP82_gp80	gi|3135499|gb|AAC16526.1|	30.14	73	51	0	1	73	184	256	0.22	27.6	27.5
MP82_gp80	gi|1684720|emb|CAB05372.1|	30.14	73	51	0	1	73	184	256	0.22	27.6	27.5
MP82_gp80	gi|3135501|gb|AAC16527.1|	30.14	73	51	0	1	73	184	256	0.22	27.6	27.5
MP82_gp80	gi|29500897|emb|CAD87529.1|	30.14	73	51	0	1	73	192	264	0.22	27.6	27.5
MP82_gp80	gi|345108717|emb|CCD28287.1|	30.14	73	51	0	1	73	217	289	0.24	27.6	27.5
MP82_gp80	gi|13430402|gb|AAK25823.1|	30.14	73	51	0	1	73	183	255	0.27	27.2	27.5

MP82_gp80	gi|3135503|gb|AAC16528.1|	30.14	73	51	0	1	73	184	256	0.28	27.2	27.5
MP82_gp80	gi|398830|emb|CAA52753.1|	30.14	73	51	0	1	73	220	292	0.31	27.2	27.5
MP82_gp80	gi|3309039|gb|AAC25994.1|	30.14	73	51	0	1	73	220	292	0.31	27.2	27.5
MP82_gp42	gi|267048|sp|P29600.1|SUBS_BACLE	27.85	79	57	0	2	80	55	133	0.0021	34.3	27.5
MP82_gp42	gi|267048|sp|P29600.1|SUBS_BACLE	27.85	79	57	0	1	79	55	133	0.0021	34.3	27.5
MP82_gp80	gi|2398757|emb|CAA50281.1|	29.73	74	52	0	7	80	193	266	0.36	26.9	27.5
MP82_gp80	gi|2398757|emb|CAA50281.1|	29.73	74	52	0	6	79	193	266	0.36	26.9	27.5
MP82_gp80	gi|2398757|emb|CAA50281.1|	29.73	74	52	0	5	78	193	266	0.36	26.9	27.5
MP82_gp80	gi|2398757|emb|CAA50281.1|	29.73	74	52	0	4	77	193	266	0.36	26.9	27.5
MP82_gp80	gi|2398757|emb|CAA50281.1|	29.73	74	52	0	3	76	193	266	0.36	26.9	27.5
MP82_gp80	gi|2398757|emb|CAA50281.1|	29.73	74	52	0	2	75	193	266	0.36	26.9	27.5
MP82_gp80	gi|2398757|emb|CAA50281.1|	29.73	74	52	0	1	74	193	266	0.36	26.9	27.5
MP82_gp68	gi|219806592|dbj|BAH10151.1|	35.48	62	40	0	19	80	181	242	0.0017	34.6	27.5
MP82_gp68	gi|219806592|dbj|BAH10151.1|	35.48	62	40	0	18	79	181	242	0.0017	34.6	27.5
MP82_gp68	gi|219806592|dbj|BAH10151.1|	35.48	62	40	0	17	78	181	242	0.0017	34.6	27.5
MP82_gp68	gi|219806592|dbj|BAH10151.1|	35.48	62	40	0	16	77	181	242	0.0017	34.6	27.5
MP82_gp68	gi|219806592|dbj|BAH10151.1|	35.48	62	40	0	15	76	181	242	0.0017	34.6	27.5
MP82_gp68	gi|219806592|dbj|BAH10151.1|	35.48	62	40	0	14	75	181	242	0.0017	34.6	27.5
MP82_gp68	gi|219806592|dbj|BAH10151.1|	34.43	61	40	0	20	80	181	241	0.0055	32.9	26.3
MP82_gp42	gi|1225905|dbj|BAA05540.1|	28.77	73	52	0	1	73	155	227	0.028	30.9	26.3
MP82_gp80	gi|2398757|emb|CAA50281.1|	28.77	73	52	0	1	73	194	266	1.1	25.2	26.3
MP82_gp42	gi|1225905|dbj|BAA05540.1|	28.38	74	53	0	7	80	154	227	0.022	31.2	26.3
MP82_gp42	gi|1225905|dbj|BAA05540.1|	28.38	74	53	0	6	79	154	227	0.022	31.2	26.3
MP82_gp42	gi|1225905|dbj|BAA05540.1|	28.38	74	53	0	5	78	154	227	0.022	31.2	26.3
MP82_gp42	gi|1225905|dbj|BAA05540.1|	28.38	74	53	0	4	77	154	227	0.022	31.2	26.3
MP82_gp42	gi|1225905|dbj|BAA05540.1|	28.38	74	53	0	3	76	154	227	0.022	31.2	26.3
MP82_gp42	gi|1225905|dbj|BAA05540.1|	28.38	74	53	0	2	75	154	227	0.022	31.2	26.3
MP82_gp42	gi|1225905|dbj|BAA05540.1|	28.38	74	53	0	1	74	154	227	0.022	31.2	26.3
MP82_gp143	gi|27526732|emb|CAD24068.1|	60	35	14	0	46	80	158	192	2.10E-08	51	26.3
MP82_gp143	gi|14575525|emb|CAC42881.1|	60	35	14	0	46	80	158	192	2.10E-08	51	26.3
MP82_gp80	gi|3135499|gb|AAC16526.1|	30	70	49	0	3	72	187	256	1.4	24.9	26.3
MP82_gp80	gi|1684720|emb|CAB05372.1|	30	70	49	0	3	72	187	256	1.4	24.9	26.3
MP82_gp80	gi|3135501|gb|AAC16527.1|	30	70	49	0	3	72	187	256	1.4	24.9	26.3
MP82_gp80	gi|29500897|emb|CAD87529.1|	30	70	49	0	3	72	195	264	1.4	24.9	26.3
MP82_gp80	gi|345108717|emb|CCD28287.1|	30	70	49	0	3	72	220	289	1.6	24.9	26.3
MP82_gp80	gi|398830|emb|CAA52753.1|	30	70	49	0	3	72	223	292	1.6	24.9	26.3
MP82_gp80	gi|3309039|gb|AAC25994.1|	30	70	49	0	3	72	223	292	1.6	24.9	26.3
MP82_gp80	gi|13430402|gb|AAK25823.1|	30	70	49	0	3	72	186	255	1.8	24.5	26.3
MP82_gp80	gi|3135503|gb|AAC16528.1|	30	70	49	0	3	72	187	256	1.8	24.5	26.3
MP82_gp80	gi|3135499|gb|AAC16526.1|	30	70	49	0	2	71	187	256	1.4	24.9	26.3
MP82_gp80	gi|1684720|emb|CAB05372.1|	30	70	49	0	2	71	187	256	1.4	24.9	26.3
MP82_gp80	gi|3135501|gb|AAC16527.1|	30	70	49	0	2	71	187	256	1.4	24.9	26.3
MP82_gp80	gi|29500897|emb|CAD87529.1|	30	70	49	0	2	71	195	264	1.4	24.9	26.3
MP82_gp80	gi|345108717|emb|CCD28287.1|	30	70	49	0	2	71	220	289	1.6	24.9	26.3
MP82_gp80	gi|398830|emb|CAA52753.1|	30	70	49	0	2	71	223	292	1.6	24.9	26.3
MP82_gp80	gi|3309039|gb|AAC25994.1|	30	70	49	0	2	71	223	292	1.6	24.9	26.3

MP82_gp80	gi|13430402|gb|AAK25823.1|	30	70	49	0	2	71	186	255	1.8	24.5	26.3
MP82_gp80	gi|3135503|gb|AAC16528.1|	30	70	49	0	2	71	187	256	1.8	24.5	26.3
MP82_gp80	gi|3135499|gb|AAC16526.1|	30	70	49	0	1	70	187	256	1.4	24.9	26.3
MP82_gp80	gi|1684720|emb|CAB05372.1|	30	70	49	0	1	70	187	256	1.4	24.9	26.3
MP82_gp80	gi|3135501|gb|AAC16527.1|	30	70	49	0	1	70	187	256	1.4	24.9	26.3
MP82_gp80	gi|29500897|emb|CAD87529.1|	30	70	49	0	1	70	195	264	1.4	24.9	26.3
MP82_gp80	gi|345108717|emb|CCD28287.1|	30	70	49	0	1	70	220	289	1.6	24.9	26.3
MP82_gp80	gi|398830|emb|CAA52753.1|	30	70	49	0	1	70	223	292	1.6	24.9	26.3
MP82_gp80	gi|3309039|gb|AAC25994.1|	30	70	49	0	1	70	223	292	1.6	24.9	26.3
MP82_gp80	gi|13430402|gb|AAK25823.1|	30	70	49	0	1	70	186	255	1.8	24.5	26.3
MP82_gp80	gi|3135503|gb|AAC16528.1|	30	70	49	0	1	70	187	256	1.8	24.5	26.3
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	45	80	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	45	80	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	44	79	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	44	79	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	43	78	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	43	78	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	42	77	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	42	77	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	41	76	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	41	76	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	40	75	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	40	75	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	39	74	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	39	74	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	38	73	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	38	73	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	37	72	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	37	72	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	36	71	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	36	71	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	35	70	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	35	70	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	34	69	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	34	69	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	33	68	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	33	68	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	32	67	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	32	67	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	31	66	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	31	66	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	30	65	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	30	65	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	29	64	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	29	64	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	28	63	158	193	1.60E-08	51.3	26.2

MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	28	63	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	27	62	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	27	62	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	26	61	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	26	61	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	25	60	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	25	60	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	24	59	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	24	59	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	23	58	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	23	58	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	22	57	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	22	57	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	21	56	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	21	56	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	20	55	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	20	55	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	19	54	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	19	54	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	18	53	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	18	53	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	17	52	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	17	52	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	16	51	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	16	51	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	15	50	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	15	50	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	14	49	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	14	49	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	13	48	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	13	48	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	12	47	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	12	47	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	11	46	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	11	46	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	10	45	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	10	45	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	9	44	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	9	44	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	8	43	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	8	43	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	7	42	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	7	42	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	6	41	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	6	41	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	5	40	158	193	1.60E-08	51.3	26.2

MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	5	40	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	4	39	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	4	39	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	3	38	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	3	38	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	2	37	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	2	37	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|27526732|emb|CAD24068.1|	58.33	36	15	0	1	36	158	193	1.60E-08	51.3	26.2
MP82_gp143	gi|14575525|emb|CAC42881.1|	58.33	36	15	0	1	36	158	193	1.60E-08	51.3	26.2
MP82_gp68	gi|666431137|gb|KEY78748.1|	26.58	79	58	0	2	80	63	141	0.21	27.6	26.2
MP82_gp68	gi|83300389|sp|O42799.2|ALL7_ASPFU	26.58	79	58	0	2	80	63	141	0.27	27.2	26.2
MP82_gp68	gi|666431137|gb|KEY78748.1|	26.58	79	58	0	1	79	63	141	0.21	27.6	26.2
MP82_gp68	gi|83300389|sp|O42799.2|ALL7_ASPFU	26.58	79	58	0	1	79	63	141	0.27	27.2	26.2
MP82_gp67	gi|3309047|gb|AAC25998.1|	26.58	79	58	0	2	80	16	94	2.9	23.9	26.2
MP82_gp67	gi|3309045|gb|AAC25997.1|	26.58	79	58	0	2	80	16	94	2.9	23.9	26.2
MP82_gp67	gi|3309047|gb|AAC25998.1|	26.58	79	58	0	1	79	16	94	2.9	23.9	26.2
MP82_gp67	gi|3309045|gb|AAC25997.1|	26.58	79	58	0	1	79	16	94	2.9	23.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	22	80	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	21	79	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	20	78	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	19	77	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	18	76	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	17	75	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	16	74	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	15	73	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	14	72	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	13	71	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	12	70	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	11	69	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	10	68	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	9	67	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	8	66	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	7	65	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	6	64	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	5	63	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	4	62	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	3	61	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	2	60	194	252	0.0014	34.9	26.2
MP82_gp80	gi|21725630|emb|CAD38396.1|	35.59	59	38	0	1	59	194	252	0.0014	34.9	26.2
MP82_gp42	gi|267048|sp|P29600.1|SUBS_BACLE	27.27	77	56	0	1	77	57	133	0.01	31.9	26.2
MP82_gp67	gi|3309047|gb|AAC25998.1|	25.32	79	59	0	2	80	12	90	4.6	23.2	25.0
MP82_gp67	gi|3309045|gb|AAC25997.1|	25.32	79	59	0	2	80	12	90	4.7	23.2	25.0
MP82_gp67	gi|3309047|gb|AAC25998.1|	25.32	79	59	0	1	79	12	90	4.6	23.2	25.0
MP82_gp67	gi|3309045|gb|AAC25997.1|	25.32	79	59	0	1	79	12	90	4.7	23.2	25.0
MP82_gp67	gi|3309047|gb|AAC25998.1|	26.67	75	55	0	4	78	16	90	5.8	22.9	25.0
MP82_gp67	gi|3309045|gb|AAC25997.1|	26.67	75	55	0	4	78	16	90	5.9	22.9	25.0

MP82_gp67	gi|3309047|gb|AAC25998.1|	26.67	75	55	0	3	77	16	90	5.8	22.9	25.0
MP82_gp67	gi|3309045|gb|AAC25997.1|	26.67	75	55	0	3	77	16	90	5.9	22.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	31.75	63	43	0	18	80	142	204	8.30E-05	38.9	25.0
MP82_gp41	gi|168419914|gb|ACA23876.1|	27.4	73	53	0	8	80	171	243	8.6	22.2	25.0
MP82_gp41	gi|168419914|gb|ACA23876.1|	27.4	73	53	0	7	79	171	243	8.6	22.2	25.0
MP82_gp41	gi|168419914|gb|ACA23876.1|	27.4	73	53	0	6	78	171	243	8.6	22.2	25.0
MP82_gp41	gi|168419914|gb|ACA23876.1|	27.4	73	53	0	5	77	171	243	8.6	22.2	25.0
MP82_gp41	gi|168419914|gb|ACA23876.1|	27.4	73	53	0	4	76	171	243	8.6	22.2	25.0
MP82_gp41	gi|168419914|gb|ACA23876.1|	27.4	73	53	0	3	75	171	243	8.6	22.2	25.0
MP82_gp41	gi|168419914|gb|ACA23876.1|	27.4	73	53	0	2	74	171	243	8.6	22.2	25.0
MP82_gp41	gi|168419914|gb|ACA23876.1|	27.4	73	53	0	1	73	171	243	8.6	22.2	25.0
MP82_gp42	gi|1225905|dbj|BAA05540.1|	27.78	72	52	0	9	80	154	225	0.057	29.9	25.0
MP82_gp42	gi|1225905|dbj|BAA05540.1|	27.78	72	52	0	8	79	154	225	0.057	29.9	25.0
MP82_gp42	gi|267048|sp|P29600.1|SUBS_BACLE	27.78	72	52	0	5	76	62	133	0.013	31.6	25.0
MP82_gp42	gi|267048|sp|P29600.1|SUBS_BACLE	27.78	72	52	0	4	75	62	133	0.013	31.6	25.0
MP82_gp42	gi|267048|sp|P29600.1|SUBS_BACLE	27.78	72	52	0	3	74	62	133	0.013	31.6	25.0
MP82_gp42	gi|267048|sp|P29600.1|SUBS_BACLE	27.78	72	52	0	2	73	62	133	0.013	31.6	25.0
MP82_gp42	gi|267048|sp|P29600.1|SUBS_BACLE	27.78	72	52	0	1	72	62	133	0.013	31.6	25.0
MP82_gp143	gi|27526732|emb|CAD24068.1|	60.61	33	13	0	48	80	158	190	1.00E-07	48.6	25.0
MP82_gp143	gi|14575525|emb|CAC42881.1|	60.61	33	13	0	48	80	158	190	1.00E-07	48.6	25.0
MP82_gp68	gi|219806592|dbj|BAH10151.1|	33.9	59	39	0	22	80	181	239	0.018	31.2	25.0
MP82_gp68	gi|219806592|dbj|BAH10151.1|	33.9	59	39	0	21	79	181	239	0.018	31.2	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	22	80	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	22	80	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	22	80	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	22	80	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	21	79	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	21	79	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	21	79	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	21	79	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	20	78	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	20	78	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	20	78	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	20	78	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	19	77	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	19	77	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	19	77	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	19	77	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	18	76	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	18	76	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	18	76	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	18	76	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	17	75	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	17	75	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	17	75	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	17	75	194	252	0.014	31.6	25.0

MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	16	74	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	16	74	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	16	74	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	16	74	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	15	73	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	15	73	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	15	73	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	15	73	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	14	72	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	14	72	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	14	72	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	14	72	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	13	71	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	13	71	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	13	71	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	13	71	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	12	70	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	12	70	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	12	70	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	12	70	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	11	69	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	11	69	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	11	69	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	11	69	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	10	68	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	10	68	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	10	68	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	10	68	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	9	67	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	9	67	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	9	67	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	9	67	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	8	66	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	8	66	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	8	66	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	8	66	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	7	65	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	7	65	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	7	65	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	7	65	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	6	64	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	6	64	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	6	64	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	6	64	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	5	63	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	5	63	194	252	0.0055	32.9	25.0

MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	5	63	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	5	63	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	4	62	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	4	62	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	4	62	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	4	62	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	3	61	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	3	61	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	3	61	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	3	61	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	2	60	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	2	60	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	2	60	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	2	60	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725616|emb|CAD38389.1|	33.9	59	39	0	1	59	194	252	0.0044	33.2	25.0
MP82_gp80	gi|21725632|emb|CAD38397.1|	33.9	59	39	0	1	59	194	252	0.0055	32.9	25.0
MP82_gp80	gi|21725618|emb|CAD38390.1|	33.9	59	39	0	1	59	194	252	0.014	31.6	25.0
MP82_gp80	gi|21725626|emb|CAD38394.1|	33.9	59	39	0	1	59	194	252	0.014	31.6	25.0
MP82_gp42	gi|267048|sp|P29600.1|SUBS_BACLE	28.17	71	51	0	1	71	63	133	0.017	31.2	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	16	80	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	15	79	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	14	78	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	13	77	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	12	76	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	11	75	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	10	74	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	9	73	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	8	72	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	7	71	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	6	70	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	5	69	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	4	68	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	3	67	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	2	66	142	206	4.20E-05	39.9	25.0
MP82_gp143	gi|56550550|dbj|BAD77932.1|	30.77	65	45	0	1	65	142	206	4.20E-05	39.9	25.0

query ID	subject ID	% identity	alignment length	mismatch count	gap open count	query start	query end	subject start	subject end	e-Value	bitScore	% identity 80mer
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	28.75	80	57	0	1	80	38	117	0.33	26.9	28.8
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	28.21	78	56	0	3	80	37	114	0.84	25.6	27.5
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	9	80	46	117	0.67	25.9	27.5
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	8	79	46	117	0.53	26.2	27.5
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	8	79	46	117	0.67	25.9	27.5
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	7	78	46	117	0.53	26.2	27.5
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	7	78	46	117	0.67	25.9	27.5
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	6	77	46	117	0.53	26.2	27.5
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	6	77	46	117	0.67	25.9	27.5
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	5	76	46	117	0.53	26.2	27.5
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	5	76	46	117	0.67	25.9	27.5
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	4	75	46	117	0.53	26.2	27.5
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	4	75	46	117	0.67	25.9	27.5
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	3	74	46	117	0.53	26.2	27.5
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	3	74	46	117	0.67	25.9	27.5
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	2	73	46	117	0.53	26.2	27.5
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	2	73	46	117	0.67	25.9	27.5
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	1	72	46	117	0.53	26.2	27.5
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	1	72	46	117	0.67	25.9	27.5
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	27.85	79	57	0	2	80	37	115	0.53	26.2	27.5
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	27.85	79	57	0	1	79	37	115	0.53	26.2	27.5
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	6	71	52	117	1.1	25.2	26.3
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	6	71	52	117	1.3	24.9	26.3
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	5	70	52	117	1.1	25.2	26.3
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	5	70	52	117	1.3	24.9	26.3
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	4	69	52	117	1.1	25.2	26.3
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	4	69	52	117	1.3	24.9	26.3
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	3	68	52	117	1.1	25.2	26.3
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	3	68	52	117	1.3	24.9	26.3
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	2	67	52	117	1.1	25.2	26.3
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	2	67	52	117	1.3	24.9	26.3
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	1	66	52	117	1.1	25.2	26.3
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	1	66	52	117	1.3	24.9	26.3
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30	70	49	0	11	80	46	115	1.3	24.9	26.3
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30	70	49	0	10	79	46	115	1.3	24.9	26.3
KAZ99a_gp73	gi|25989482|gb|AAM10779.1|	27.27	77	56	0	4	80	37	113	2.7	23.9	26.2
KAZ99a_gp73	gi|33667930|gb|AAQ24542.1|	30.43	69	48	0	12	80	46	114	2.1	24.2	26.2
KAZ99a_gp52	gi|8453086|gb|AAF75225.1|AF20898	26.32	76	56	0	5	80	41	116	0.24	28.2	25.0
KAZ99a_gp52	gi|8453086|gb|AAF75225.1|AF20898	26.32	76	56	0	4	79	41	116	0.24	28.2	25.0
KAZ99a_gp52	gi|8453086|gb|AAF75225.1|AF20898	26.32	76	56	0	3	78	41	116	0.24	28.2	25.0
KAZ99a_gp52	gi|8453086|gb|AAF75225.1|AF20898	25.32	79	59	0	2	80	41	119	0.15	28.9	25.0
KAZ99a_gp52	gi|8453086|gb|AAF75225.1|AF20898	25.32	79	59	0	1	79	41	119	0.15	28.9	25.0

KAZ99a_gp52	gi|8453086|gb|AAF75225.1|AF20898	27.03	74	54	0	7	80	41	114	0.47	27.2	25.0
KAZ99a_gp52	gi|8453086|gb|AAF75225.1|AF20898	27.03	74	54	0	6	79	41	114	0.47	27.2	25.0

query ID	subject ID	% identity	alignment length	mismatch count	gap open count	query start	query end	subject start	subject end	e-Value	bitScore	% identity 80mer
RMP11k_gp127	gi|1545895|emb|CAB02216.1|	27.5	80	58	0	1	80	35	114	0.31	26.3	27.5
RMP11k_gp127	gi|1545895|emb|CAB02216.1|	26.25	80	59	0	1	80	33	112	1.3	24.3	26.3
RMP11k_gp127	gi|1545895|emb|CAB02216.1|	28	75	54	0	1	75	40	114	0.63	25.3	26.3
RMP11k_gp127	gi|1545897|emb|CAB02217.1|	28	75	54	0	1	75	40	114	1	24.6	26.3
RMP11k_gp127	gi|1321731|emb|CAA96548.1|	28	75	54	0	1	75	40	114	1.3	24.3	26.3
RMP11k_gp127	gi|1545897|emb|CAB02217.1|	27.63	76	55	0	5	80	39	114	0.79	24.9	26.2
RMP11k_gp127	gi|1321731|emb|CAA96548.1|	27.63	76	55	0	5	80	39	114	0.99	24.6	26.2
RMP11k_gp127	gi|1545895|emb|CAB02216.1|	27.63	76	55	0	4	79	39	114	0.5	25.6	26.2
RMP11k_gp127	gi|1545897|emb|CAB02217.1|	27.63	76	55	0	4	79	39	114	0.79	24.9	26.2
RMP11k_gp127	gi|1321731|emb|CAA96548.1|	27.63	76	55	0	4	79	39	114	0.99	24.6	26.2
RMP11k_gp127	gi|1545895|emb|CAB02216.1|	27.63	76	55	0	3	78	39	114	0.5	25.6	26.2
RMP11k_gp127	gi|1545897|emb|CAB02217.1|	27.63	76	55	0	3	78	39	114	0.79	24.9	26.2
RMP11k_gp127	gi|1321731|emb|CAA96548.1|	27.63	76	55	0	3	78	39	114	0.99	24.6	26.2
RMP11k_gp127	gi|1545895|emb|CAB02216.1|	27.63	76	55	0	2	77	39	114	0.5	25.6	26.2
RMP11k_gp127	gi|1545897|emb|CAB02217.1|	27.63	76	55	0	2	77	39	114	0.79	24.9	26.2
RMP11k_gp127	gi|1321731|emb|CAA96548.1|	27.63	76	55	0	2	77	39	114	0.99	24.6	26.2
RMP11k_gp127	gi|1545895|emb|CAB02216.1|	27.63	76	55	0	1	76	39	114	0.5	25.6	26.2
RMP11k_gp127	gi|1545897|emb|CAB02217.1|	27.63	76	55	0	1	76	39	114	0.79	24.9	26.2
RMP11k_gp127	gi|1321731|emb|CAA96548.1|	27.63	76	55	0	1	76	39	114	0.99	24.6	26.2
RMP11k_gp127	gi|1545895|emb|CAB02216.1|	26.58	79	58	0	2	80	35	113	1	24.6	26.2
RMP11k_gp51	gi|8453086|gb|AAF75225.1|AF208981_1	26.32	76	56	0	5	80	41	116	0.24	28.2	25.0
RMP11k_gp51	gi|8453086|gb|AAF75225.1|AF208981_1	26.32	76	56	0	4	79	41	116	0.24	28.2	25.0
RMP11k_gp51	gi|8453086|gb|AAF75225.1|AF208981_1	26.32	76	56	0	3	78	41	116	0.24	28.2	25.0
RMP11k_gp51	gi|8453086|gb|AAF75225.1|AF208981_1	25.32	79	59	0	2	80	41	119	0.15	28.9	25.0
RMP11k_gp51	gi|8453086|gb|AAF75225.1|AF208981_1	25.32	79	59	0	1	79	41	119	0.15	28.9	25.0
RMP11k_gp127	gi|1545897|emb|CAB02217.1|	26.67	75	55	0	6	80	39	113	2.5	23.3	25.0
RMP11k_gp127	gi|1321731|emb|CAA96548.1|	26.67	75	55	0	6	80	39	113	3.2	22.9	25.0
RMP11k_gp127	gi|1545897|emb|CAB02217.1|	27.03	74	54	0	7	80	39	112	4	22.6	25.0
RMP11k_gp127	gi|1321731|emb|CAA96548.1|	27.03	74	54	0	7	80	39	112	5	22.2	25.0
RMP11k_gp51	gi|8453086|gb|AAF75225.1|AF208981_1	27.03	74	54	0	7	80	41	114	0.47	27.2	25.0
RMP11k_gp51	gi|8453086|gb|AAF75225.1|AF208981_1	27.03	74	54	0	6	79	41	114	0.47	27.2	25.0

query ID	subject ID	% identity	alignment length	mismatch count	gap open count	query start	query end	subject start	subject end	e-Value	bitScore	% identity 80mer
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	28.75	80	57	0	1	80	38	117	0.33	26.9	28.8
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	28.21	78	56	0	3	80	37	114	0.84	25.6	27.5
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	9	80	46	117	0.67	25.9	27.5
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	8	79	46	117	0.53	26.2	27.5
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	8	79	46	117	0.67	25.9	27.5
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	7	78	46	117	0.53	26.2	27.5
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	7	78	46	117	0.67	25.9	27.5
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	6	77	46	117	0.53	26.2	27.5
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	6	77	46	117	0.67	25.9	27.5
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	5	76	46	117	0.53	26.2	27.5
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	5	76	46	117	0.67	25.9	27.5
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	4	75	46	117	0.53	26.2	27.5
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	4	75	46	117	0.67	25.9	27.5
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	3	74	46	117	0.53	26.2	27.5
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	3	74	46	117	0.67	25.9	27.5
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	2	73	46	117	0.53	26.2	27.5
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	2	73	46	117	0.67	25.9	27.5
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	30.56	72	50	0	1	72	46	117	0.53	26.2	27.5
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30.56	72	50	0	1	72	46	117	0.67	25.9	27.5
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	27.85	79	57	0	2	80	37	115	0.53	26.2	27.5
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	27.85	79	57	0	1	79	37	115	0.53	26.2	27.5
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	6	71	52	117	1.1	25.2	26.3
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	6	71	52	117	1.3	24.9	26.3
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	5	70	52	117	1.1	25.2	26.3
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	5	70	52	117	1.3	24.9	26.3
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	4	69	52	117	1.1	25.2	26.3
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	4	69	52	117	1.3	24.9	26.3
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	3	68	52	117	1.1	25.2	26.3
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	3	68	52	117	1.3	24.9	26.3
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	2	67	52	117	1.1	25.2	26.3
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	2	67	52	117	1.3	24.9	26.3
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	31.82	66	45	0	1	66	52	117	1.1	25.2	26.3
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	31.82	66	45	0	1	66	52	117	1.3	24.9	26.3
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30	70	49	0	11	80	46	115	1.3	24.9	26.3
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30	70	49	0	10	79	46	115	1.3	24.9	26.3
RMS3b_gp78	gi|25989482|gb|AAM10779.1|	27.27	77	56	0	4	80	37	113	2.7	23.9	26.2
RMS3b_gp78	gi|33667930|gb|AAQ24542.1|	30.43	69	48	0	12	80	46	114	2.1	24.2	26.2
RMS3b_gp57	gi|8453086|gb|AAF75225.1|AF208981_	26.32	76	56	0	5	80	41	116	0.24	28.2	25.0
RMS3b_gp57	gi|8453086|gb|AAF75225.1|AF208981_	26.32	76	56	0	4	79	41	116	0.24	28.2	25.0
RMS3b_gp57	gi|8453086|gb|AAF75225.1|AF208981_	26.32	76	56	0	3	78	41	116	0.24	28.2	25.0
RMS3b_gp57	gi|8453086|gb|AAF75225.1|AF208981_	25.32	79	59	0	2	80	41	119	0.15	28.9	25.0

RMS3b_gp57	gi|8453086|gb|AAF75225.1|AF208981_	25.32	79	59	0	1	79	41	119	0.15	28.9	25.0
RMS3b_gp57	gi|8453086|gb|AAF75225.1|AF208981_	27.03	74	54	0	7	80	41	114	0.47	27.2	25.0
RMS3b_gp57	gi|8453086|gb|AAF75225.1|AF208981_	27.03	74	54	0	6	79	41	114	0.47	27.2	25.0

query ID	subject ID	% identity	alignment length	mismatch count	gap open count	query start	query end	subject start	subject end	e-Value	bitScore	% identity 80mer
TAT2F_gp131	gi|1545895|emb|CAB02216.1|	27.5	80	58	0	1	80	35	114	0.31	26.3	27.5
TAT2F_gp131	gi|1545895|emb|CAB02216.1|	26.25	80	59	0	1	80	33	112	1.3	24.3	26.3
TAT2F_gp131	gi|1545895|emb|CAB02216.1|	28	75	54	0	1	75	40	114	0.63	25.3	26.3
TAT2F_gp131	gi|1545897|emb|CAB02217.1|	28	75	54	0	1	75	40	114	1	24.6	26.3
TAT2F_gp131	gi|1321731|emb|CAA96548.1|	28	75	54	0	1	75	40	114	1.3	24.3	26.3
TAT2F_gp131	gi|1545897|emb|CAB02217.1|	27.63	76	55	0	5	80	39	114	0.79	24.9	26.2
TAT2F_gp131	gi|1321731|emb|CAA96548.1|	27.63	76	55	0	5	80	39	114	0.99	24.6	26.2
TAT2F_gp131	gi|1545895|emb|CAB02216.1|	27.63	76	55	0	4	79	39	114	0.5	25.6	26.2
TAT2F_gp131	gi|1545897|emb|CAB02217.1|	27.63	76	55	0	4	79	39	114	0.79	24.9	26.2
TAT2F_gp131	gi|1321731|emb|CAA96548.1|	27.63	76	55	0	4	79	39	114	0.99	24.6	26.2
TAT2F_gp131	gi|1545895|emb|CAB02216.1|	27.63	76	55	0	3	78	39	114	0.5	25.6	26.2
TAT2F_gp131	gi|1545897|emb|CAB02217.1|	27.63	76	55	0	3	78	39	114	0.79	24.9	26.2
TAT2F_gp131	gi|1321731|emb|CAA96548.1|	27.63	76	55	0	3	78	39	114	0.99	24.6	26.2
TAT2F_gp131	gi|1545895|emb|CAB02216.1|	27.63	76	55	0	2	77	39	114	0.5	25.6	26.2
TAT2F_gp131	gi|1545897|emb|CAB02217.1|	27.63	76	55	0	2	77	39	114	0.79	24.9	26.2
TAT2F_gp131	gi|1321731|emb|CAA96548.1|	27.63	76	55	0	2	77	39	114	0.99	24.6	26.2
TAT2F_gp131	gi|1545895|emb|CAB02216.1|	27.63	76	55	0	1	76	39	114	0.5	25.6	26.2
TAT2F_gp131	gi|1545897|emb|CAB02217.1|	27.63	76	55	0	1	76	39	114	0.79	24.9	26.2
TAT2F_gp131	gi|1321731|emb|CAA96548.1|	27.63	76	55	0	1	76	39	114	0.99	24.6	26.2
TAT2F_gp131	gi|1545895|emb|CAB02216.1|	26.58	79	58	0	2	80	35	113	1	24.6	26.2
TAT2F_gp55	gi|8453086|gb|AAF75225.1|AF208981_1	26.32	76	56	0	5	80	41	116	0.24	28.2	25.0
TAT2F_gp55	gi|8453086|gb|AAF75225.1|AF208981_1	26.32	76	56	0	4	79	41	116	0.24	28.2	25.0
TAT2F_gp55	gi|8453086|gb|AAF75225.1|AF208981_1	26.32	76	56	0	3	78	41	116	0.24	28.2	25.0
TAT2F_gp55	gi|8453086|gb|AAF75225.1|AF208981_1	25.32	79	59	0	2	80	41	119	0.15	28.9	25.0
TAT2F_gp55	gi|8453086|gb|AAF75225.1|AF208981_1	25.32	79	59	0	1	79	41	119	0.15	28.9	25.0
TAT2F_gp131	gi|1545897|emb|CAB02217.1|	26.67	75	55	0	6	80	39	113	2.5	23.3	25.0
TAT2F_gp131	gi|1321731|emb|CAA96548.1|	26.67	75	55	0	6	80	39	113	3.2	22.9	25.0
TAT2F_gp131	gi|1545897|emb|CAB02217.1|	27.03	74	54	0	7	80	39	112	4	22.6	25.0
TAT2F_gp131	gi|1321731|emb|CAA96548.1|	27.03	74	54	0	7	80	39	112	5	22.2	25.0
TAT2F_gp55	gi|8453086|gb|AAF75225.1|AF208981_1	27.03	74	54	0	7	80	41	114	0.47	27.2	25.0
TAT2F_gp55	gi|8453086|gb|AAF75225.1|AF208981_1	27.03	74	54	0	6	79	41	114	0.47	27.2	25.0

query ID	subject ID	% identity	alignment length	mismatch count	gap open count	query start	query end	subject start	subject end	e-Value	bitScore	% identity 80mer
DIN2_gp32	gi|455288|gb|AAA33405.1|	30.26	76	53	0	5	80	247	322	0.27	27.6	28.7
DIN2_gp32	gi|455288|gb|AAA33405.1|	30.26	76	53	0	4	79	247	322	0.27	27.6	28.7
DIN2_gp60	gi|410060781|gb|AFV53352.1|	31.43	70	48	0	11	80	30	99	0.28	27.2	27.5
DIN2_gp60	gi|410060781|gb|AFV53352.1|	31.43	70	48	0	10	79	30	99	0.28	27.2	27.5
DIN2_gp60	gi|410060781|gb|AFV53352.1|	31.43	70	48	0	9	78	30	99	0.28	27.2	27.5
DIN2_gp32	gi|455288|gb|AAA33405.1|	29.33	75	53	0	6	80	247	321	0.86	25.9	27.5
DIN2_gp60	gi|410060781|gb|AFV53352.1|	31.88	69	47	0	12	80	30	98	0.28	27.2	27.5
DIN2_gp24	gi|6580762|gb|AAF18269.1|AF066055_1	26.25	80	59	0	1	80	13	92	0.00035	37.9	26.3
DIN2_gp24	gi|6580762|gb|AAF18269.1|AF066055_1	26.58	79	58	0	1	79	14	92	0.00056	37.3	26.2
DIN2_gp32	gi|455288|gb|AAA33405.1|	26.58	79	58	0	2	80	241	319	1.7	24.9	26.2
DIN2_gp32	gi|455288|gb|AAA33405.1|	26.58	79	58	0	1	79	241	319	1.7	24.9	26.2
DIN2_gp30	gi|113561|sp|P22285.1|MPA92_POAPR	35.59	59	38	0	22	80	269	327	0.21	27.9	26.2
DIN2_gp30	gi|113561|sp|P22285.1|MPA92_POAPR	35.59	59	38	0	21	79	269	327	0.21	27.9	26.2
DIN2_gp30	gi|113561|sp|P22285.1|MPA92_POAPR	35.59	59	38	0	20	78	269	327	0.21	27.9	26.2
DIN2_gp30	gi|113561|sp|P22285.1|MPA92_POAPR	35.59	59	38	0	19	77	269	327	0.21	27.9	26.2
DIN2_gp33	gi|60116876|gb|AAX14379.1|	25.32	79	59	0	2	80	237	315	0.83	26.5	25.0
DIN2_gp33	gi|148361511|gb|ABQ59329.1|	25.32	79	59	0	1	79	107	185	0.78	26.2	25.0
DIN2_gp33	gi|60116876|gb|AAX14379.1|	25.32	79	59	0	1	79	237	315	0.83	26.5	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	22	80	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	21	79	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	17	75	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	16	74	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	15	73	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	14	72	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	13	71	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	12	70	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	11	69	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	7	65	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	6	64	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	5	63	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	4	62	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	3	61	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	2	60	275	333	0.042	30.2	25.0
DIN2_gp32	gi|455288|gb|AAA33405.1|	33.9	59	39	0	1	59	275	333	0.042	30.2	25.0

query ID	subject ID	% identity	alignment length	mismatch count	gap open count	query start	query end	subject start	subject end	e-Value	bitScore	% identity 80mer
MP75_gp35	gi|121584258|gb|ABM60783.1|	31.75	63	43	0	1	63	17	79	0.36	26.9	25.0
MP75_gp103	gi|442577833|gb|AGC60020.1|	26.32	76	56	0	1	76	430	505	0.11	30.2	25.0
MP75_gp103	gi|42559536|sp|Q9NJA9.1|MYSP_A	26.32	76	56	0	1	76	430	505	0.11	30.2	25.0
MP75_gp103	gi|42559536|sp|Q9NJA9.1|MYSP_A	27.03	74	54	0	2	75	432	505	0.17	29.6	25.0
MP75_gp103	gi|442577833|gb|AGC60020.1|	27.03	74	54	0	2	75	432	505	0.17	29.6	25.0
MP75_gp103	gi|442577833|gb|AGC60020.1|	27.03	74	54	0	1	74	432	505	0.17	29.6	25.0
MP75_gp103	gi|42559536|sp|Q9NJA9.1|MYSP_A	27.03	74	54	0	1	74	432	505	0.17	29.6	25.0

query ID	subject ID	% identity	alignment length	mismatch count	gap open count	query start	query end	subject start	subject end	e-Value	bitScore	% identity 80mer
FV7M4_gp17	gi|21954740|gb|AAM83103.1|	28	75	54	0	6	80	139	213	0.085	30.6	26.3
FV7M4_gp17	gi|21954740|gb|AAM83103.1|	28	75	54	0	5	79	139	213	0.085	30.6	26.3
FV7M4_gp17	gi|21954740|gb|AAM83103.1|	28	75	54	0	4	78	139	213	0.085	30.6	26.3
FV7M4_gp17	gi|21954740|gb|AAM83103.1|	28	75	54	0	3	77	139	213	0.085	30.6	26.3
FV7M4_gp17	gi|21954740|gb|AAM83103.1|	28	75	54	0	2	76	139	213	0.085	30.6	26.3
FV7M4_gp17	gi|21954740|gb|AAM83103.1|	28	75	54	0	1	75	139	213	0.085	30.6	26.3
FV7M4_gp17	gi|219806602|dbj|BAH10156.1|	26.32	76	56	0	1	76	5	80	0.36	26.9	25.0
FV7M4_gp8	gi|20796733|emb|CAC83047.1|	28.99	69	49	0	1	69	33	101	8.4	21	25.0
FV7M4_gp17	gi|219806602|dbj|BAH10156.1|	25.32	79	59	0	2	80	2	80	0.11	28.6	25.0
FV7M4_gp17	gi|219806602|dbj|BAH10156.1|	25.32	79	59	0	1	79	2	80	0.11	28.6	25.0
FV7M4_gp17	gi|21954740|gb|AAM83103.1|	27.03	74	54	0	1	74	140	213	0.43	28.2	25.0
FV7M4_gp17	gi|21954740|gb|AAM83103.1|	27.4	73	53	0	8	80	139	211	0.14	29.9	25.0
FV7M4_gp17	gi|21954740|gb|AAM83103.1|	27.4	73	53	0	7	79	139	211	0.14	29.9	25.0
FV7M4_gp22	gi|21954740|gb|AAM83103.1|	27.78	72	52	0	9	80	67	138	0.69	27.6	25.0
FV7M4_gp22	gi|21954740|gb|AAM83103.1|	27.78	72	52	0	8	79	67	138	0.69	27.6	25.0
FV7M4_gp22	gi|21954740|gb|AAM83103.1|	27.78	72	52	0	7	78	67	138	0.69	27.6	25.0
FV7M4_gp22	gi|21954740|gb|AAM83103.1|	27.78	72	52	0	6	77	67	138	0.69	27.6	25.0
FV7M4_gp22	gi|21954740|gb|AAM83103.1|	27.78	72	52	0	5	76	67	138	0.69	27.6	25.0
FV7M4_gp22	gi|21954740|gb|AAM83103.1|	27.78	72	52	0	4	75	67	138	0.69	27.6	25.0
FV7M4_gp22	gi|21954740|gb|AAM83103.1|	27.78	72	52	0	3	74	67	138	0.69	27.6	25.0
FV7M4_gp22	gi|21954740|gb|AAM83103.1|	27.78	72	52	0	2	73	67	138	0.69	27.6	25.0
FV7M4_gp22	gi|21954740|gb|AAM83103.1|	27.78	72	52	0	1	72	67	138	0.69	27.6	25.0
FV7M4_gp22	gi|21954740|gb|AAM83103.1|	28.17	71	51	0	10	80	67	137	1.1	26.9	25.0

query ID	subject ID	% identity	alignment length	mismatch count	gap open count	query start	query end	subject start	subject end	e-Value	bitScore	% identity 80mer
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30.56	72	50	0	9	80	415	486	1.8	25.5	27.5
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30.56	72	50	0	8	79	415	486	1.8	25.5	27.5
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30.56	72	50	0	7	78	415	486	1.8	25.5	27.5
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30.56	72	50	0	6	77	415	486	1.8	25.5	27.5
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30.56	72	50	0	5	76	415	486	1.8	25.5	27.5
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30.56	72	50	0	4	75	415	486	1.8	25.5	27.5
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30.56	72	50	0	3	74	415	486	1.8	25.5	27.5
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30.56	72	50	0	2	73	415	486	1.8	25.5	27.5
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30.56	72	50	0	1	72	415	486	0.22	28.6	27.5
RMP9_gp23	gi|78128018|gb|AAY84564.2|	29.58	71	50	0	1	71	416	486	2.2	25.2	26.3
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30	70	49	0	11	80	415	484	1.8	25.5	26.3
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30	70	49	0	10	79	415	484	1.8	25.5	26.3
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30	70	49	0	1	70	417	486	2.8	24.9	26.3
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	18	80	423	485	0.16	29	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	17	79	423	485	0.13	29.3	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	16	78	423	485	0.15	29.1	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	15	77	423	485	0.16	29	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	14	76	423	485	0.1	29.7	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	13	75	423	485	0.13	29.3	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	12	74	423	485	0.1	29.7	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	11	73	423	485	0.094	29.8	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	10	72	423	485	0.099	29.7	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	9	71	423	485	0.099	29.7	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	8	70	423	485	0.086	29.9	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	7	69	423	485	0.086	29.9	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	6	68	423	485	0.068	30.3	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	5	67	423	485	0.1	29.7	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	4	66	423	485	0.13	29.3	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	3	65	423	485	0.14	29.2	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	2	64	423	485	0.15	29.1	26.2
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.33	63	42	0	1	63	423	485	0.17	28.9	26.2
RMP9_gp23	gi|78128018|gb|AAY84564.2|	30.43	69	48	0	1	69	418	486	4.5	24.2	26.2
RMP9_gp54	gi|21514|emb|CAA27588.1|	26.32	76	56	0	5	80	261	336	10	22.5	25.0
RMP9_gp54	gi|158517845|sp|P15476.2|PATB1_SOLTU	26.32	76	56	0	5	80	261	336	10	22.5	25.0
RMP9_gp54	gi|21514|emb|CAA27588.1|	26.32	76	56	0	4	79	261	336	10	22.5	25.0
RMP9_gp54	gi|158517845|sp|P15476.2|PATB1_SOLTU	26.32	76	56	0	4	79	261	336	10	22.5	25.0
RMP9_gp54	gi|21514|emb|CAA27588.1|	26.32	76	56	0	3	78	261	336	10	22.5	25.0
RMP9_gp54	gi|158517845|sp|P15476.2|PATB1_SOLTU	26.32	76	56	0	3	78	261	336	10	22.5	25.0
RMP9_gp54	gi|21514|emb|CAA27588.1|	26.32	76	56	0	2	77	261	336	10	22.5	25.0
RMP9_gp54	gi|158517845|sp|P15476.2|PATB1_SOLTU	26.32	76	56	0	2	77	261	336	10	22.5	25.0
RMP9_gp54	gi|21514|emb|CAA27588.1|	26.32	76	56	0	1	76	261	336	10	22.5	25.0

RMP9_gp54	gi|158517845|sp|P15476.2|PATB1_SOLTU	26.32	76	56	0	1	76	261	336	10	22.5	25.0
RMP9_gp31	gi|78128018|gb|AAY84564.2|	33.9	59	39	0	1	59	427	485	0.35	27.9	25.0

query ID	subject ID	% identity	alignment length	mismatch count	gap open count	query start	query end	subject start	subject end	e-Value	bitScore	% identity 80mer
OBO18_gp42	gi|219806598|dbj|BAH10154.1|	28.95	76	54	0	3	78	116	191	0.28	27.2	27.5
OBO18_gp42	gi|219806602|dbj|BAH10156.1|	28.95	76	54	0	3	78	116	191	0.28	27.2	27.5
OBO18_gp42	gi|125659386|dbj|BAF46896.1|	28.95	76	54	0	3	78	116	191	0.28	27.2	27.5
OBO18_gp42	gi|219806600|dbj|BAH10155.1|	28.95	76	54	0	3	78	116	191	0.28	27.2	27.5
OBO18_gp42	gi|219806573|dbj|BAH10157.1|	28.95	76	54	0	3	78	116	191	0.28	27.2	27.5
OBO18_gp42	gi|219806598|dbj|BAH10154.1|	28.95	76	54	0	2	77	116	191	0.28	27.2	27.5
OBO18_gp42	gi|219806602|dbj|BAH10156.1|	28.95	76	54	0	2	77	116	191	0.28	27.2	27.5
OBO18_gp42	gi|125659386|dbj|BAF46896.1|	28.95	76	54	0	2	77	116	191	0.28	27.2	27.5
OBO18_gp42	gi|219806600|dbj|BAH10155.1|	28.95	76	54	0	2	77	116	191	0.28	27.2	27.5
OBO18_gp42	gi|219806573|dbj|BAH10157.1|	28.95	76	54	0	2	77	116	191	0.28	27.2	27.5
OBO18_gp42	gi|219806598|dbj|BAH10154.1|	28.95	76	54	0	1	76	116	191	0.28	27.2	27.5
OBO18_gp42	gi|219806602|dbj|BAH10156.1|	28.95	76	54	0	1	76	116	191	0.28	27.2	27.5
OBO18_gp42	gi|125659386|dbj|BAF46896.1|	28.95	76	54	0	1	76	116	191	0.28	27.2	27.5
OBO18_gp42	gi|219806600|dbj|BAH10155.1|	28.95	76	54	0	1	76	116	191	0.28	27.2	27.5
OBO18_gp42	gi|219806573|dbj|BAH10157.1|	28.95	76	54	0	1	76	116	191	0.28	27.2	27.5
OBO18_gp42	gi|455288|gb|AAA33405.1|	27.5	80	58	0	1	80	247	326	1.1	25.5	27.5
OBO18_gp42	gi|11991227|gb|AAG42254.1|AF306707_	27.5	80	58	0	1	80	218	297	0.3	27.2	27.5
OBO18_gp42	gi|219806596|dbj|BAH10153.1|	29.58	71	50	0	3	73	116	186	0.72	25.9	26.3
OBO18_gp42	gi|219806596|dbj|BAH10153.1|	29.58	71	50	0	2	72	116	186	0.72	25.9	26.3
OBO18_gp42	gi|219806596|dbj|BAH10153.1|	29.58	71	50	0	1	71	116	186	0.72	25.9	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	15	80	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	15	80	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	14	79	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	14	79	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	13	78	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	13	78	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	12	77	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	12	77	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	11	76	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	11	76	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	10	75	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	10	75	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	9	74	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	9	74	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	8	73	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	8	73	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	7	72	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	7	72	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	6	71	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	6	71	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	5	70	216	281	0.14	28.2	26.3

OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	5	70	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	4	69	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	4	69	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	3	68	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	3	68	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	2	67	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	2	67	241	306	0.15	28.2	26.3
OBO18_gp42	gi|29500897|emb|CAD87529.1|	31.82	66	45	0	1	66	216	281	0.14	28.2	26.3
OBO18_gp42	gi|345108717|emb|CCD28287.1|	31.82	66	45	0	1	66	241	306	0.15	28.2	26.3
OBO18_gp42	gi|156145810|gb|ABU53681.1|	27.63	76	55	0	3	78	116	191	0.9	25.6	26.2
OBO18_gp42	gi|156145810|gb|ABU53681.1|	27.63	76	55	0	2	77	116	191	0.9	25.6	26.2
OBO18_gp42	gi|156145810|gb|ABU53681.1|	27.63	76	55	0	1	76	116	191	0.9	25.6	26.2
OBO18_gp50	gi|8453086|gb|AAF75225.1|AF208981_1	26.92	78	57	0	3	80	137	214	0.19	28.6	26.2
OBO18_gp50	gi|8453086|gb|AAF75225.1|AF208981_1	26.92	78	57	0	2	79	137	214	0.19	28.6	26.2
OBO18_gp50	gi|8453086|gb|AAF75225.1|AF208981_1	26.92	78	57	0	1	78	137	214	0.19	28.6	26.2
OBO18_gp15	gi|85701160|sp|Q00002.2|PDI_ALTAL	26.67	75	55	0	6	80	168	242	1.4	25.5	25.0
OBO18_gp15	gi|85701160|sp|Q00002.2|PDI_ALTAL	26.67	75	55	0	5	79	168	242	1.4	25.5	25.0
OBO18_gp15	gi|85701160|sp|Q00002.2|PDI_ALTAL	26.67	75	55	0	4	78	168	242	1.4	25.5	25.0
OBO18_gp15	gi|85701160|sp|Q00002.2|PDI_ALTAL	26.67	75	55	0	3	77	168	242	1.4	25.5	25.0
OBO18_gp15	gi|85701160|sp|Q00002.2|PDI_ALTAL	26.67	75	55	0	2	76	168	242	1.4	25.5	25.0
OBO18_gp15	gi|85701160|sp|Q00002.2|PDI_ALTAL	26.67	75	55	0	1	75	168	242	1.4	25.5	25.0
OBO18_gp42	gi|29500897|emb|CAD87529.1|	32.79	61	41	0	4	64	221	281	0.57	26.2	25.0
OBO18_gp42	gi|345108717|emb|CCD28287.1|	32.79	61	41	0	4	64	246	306	0.62	26.2	25.0
OBO18_gp42	gi|29500897|emb|CAD87529.1|	32.79	61	41	0	3	63	221	281	0.57	26.2	25.0
OBO18_gp42	gi|345108717|emb|CCD28287.1|	32.79	61	41	0	3	63	246	306	0.62	26.2	25.0
OBO18_gp42	gi|29500897|emb|CAD87529.1|	32.79	61	41	0	2	62	221	281	0.57	26.2	25.0
OBO18_gp42	gi|345108717|emb|CCD28287.1|	32.79	61	41	0	2	62	246	306	0.62	26.2	25.0
OBO18_gp42	gi|29500897|emb|CAD87529.1|	32.79	61	41	0	1	61	221	281	0.57	26.2	25.0
OBO18_gp42	gi|345108717|emb|CCD28287.1|	32.79	61	41	0	1	61	246	306	0.62	26.2	25.0
OBO18_gp42	gi|4468224|emb|CAB38044.1|	28.17	71	51	0	3	73	116	186	4.6	23.2	25.0
OBO18_gp42	gi|4468224|emb|CAB38044.1|	28.17	71	51	0	2	72	116	186	4.6	23.2	25.0
OBO18_gp42	gi|4468224|emb|CAB38044.1|	28.17	71	51	0	1	71	116	186	4.6	23.2	25.0
OBO18_gp42	gi|29500897|emb|CAD87529.1|	30.77	65	45	0	1	65	217	281	0.45	26.6	25.0
OBO18_gp42	gi|345108717|emb|CCD28287.1|	30.77	65	45	0	1	65	242	306	0.49	26.6	25.0

Evaluation of the ability of “*Applied Phage Vegetable S2”* to reduce *Salmonella typhimurium* contaminations on experimentally contaminated lettuce.

Study Number #R020-001

PTC Phage Technology Center GmbH
Siemensstraße 42
D- 59199 Bönen
Tel.: 49 (0) 2383 919 174
Fax: 49 (0) 2383 919 179
Dr. Michael Fink

FINK TEC GmbH
Oberster Kamp 23
D-59069 Hamm
Tel.: 49 (0) 2385 730

1. STUDY TITLE

Evaluation of the ability of *"Applied Phage Vegetable S2"* to reduce *Salmonella typhimurium* contaminations on experimentally contaminated lettuce.

2. STUDY DIRECTOR

Hansjörg Lehnherr, Ph.D.

3. STUDY PERSONNEL

The following personnel contributed to the conduct and reporting of the studies reported herein:

Name:	**Title:**	**Role:**
Hansjörg Lehnherr, Ph.D.	Chief scientist	Study director
Andrea Kroj, Ph.D.	Research scientist	Hands-on-research

4. PERFORMING LABORATORY

PTC Phage Technology Center GmbH
Siemensstraße 42
D- 59199 Bönen
Tel.: 49 (0) 2383 919 174
Fax: 49 (0) 2383 919 179

5. STUDY OBJECTIVE

Determine the bacterial load reduction of a *Salmonella typhimurium* strain on lettuce, resulting from an inoculation with *Applied Phage Vegetable S2*, with an application titer of 2.5×10^6 PFU/cm^2.

6. TEST MATRIX

The lettuce was bought from a supermarket in Meschede, NRW, Germany. Samples were not washed or pre-treated prior to the studies.

7. COCKTAIL LOT AND APPLICATION

Applied Phage Vegetable S2 lot # 12022020
Applied Phage Vegetable S2 titer: 5.0 x 10^9 PFU/mL

The application titer was 2.5 x 10^6 PFU/cm^2.

8. BACTERIAL STRAINS USED TO EVALUATE COCKTAIL EFFICIENCY

Lettuce samples were challenged with 10^3/cm^2 or 10^4/cm^2 cells of the *Salmonella* strain indicated below. The total reduction in *Salmonella* bacterial load was evaluated.

- A chloramphenicol resistant *Salmonella typhimurium* isolate was used for the experiments.

9. MEDIA AND REAGENTS

- LB broth Lennox (Roth, Karlsruhe, Germany; catalog # X964.4)
  with 17 µg/mL chloramphenicol (Roth, Karlsruhe, Germany; catalog # 3886.2)
- LB agar Lennox (Roth, Karlsruhe, Germany; catalog # X965.2)
  with 17 µg/mL chloramphenicol (Roth, Karlsruhe, Germany; catalog # 3886.2)
- PBS (8 g/L NaCl, 0.2 g/L KCl, 1.15 g/L Na_2HPO_4, 0.2 g/L KH_2PO_4; pH 7.5)

10. GENERAL OUTLINE OF STUDY

- Original lettuce leaves were cut into 42 quadratic samples (10.00 cm^2/sample) for each experiment.
- *Applied Phage Vegetable S2* was diluted with PBS buffer to an application titer of 5.0 x 10^8 PFU/mL.
- 20 lettuce samples were homogenously contaminated with 10^3/cm^2 (experiment 1) or 10^4/cm^2 (experiment 2) cells of an overnight culture of the test strain. One sample for each experiment was not treated with bacteria and served as an uncontaminated, untreated control.
- All samples were incubated for 30 min at room temperature.

- 10 contaminated lettuce samples for every contamination level were treated with 50 µL of *Applied Phage Vegetable S2* with an application titer of 2.5 x 10^6 PFU/cm^2 (50 µL of PBS buffer was applied to the remaining 10 samples as the contaminated, untreated controls).
- Incubation period was 4 h at room temperature (21°C).
- To each lettuce piece 5 mL of PBS was added and treated for 5 min in a stomacher.
- The supernatant was plated on LB agar plates containing chloramphenicol.
- LB agar plates were incubated at 37°C overnight and the numbers of viable *Salmonella* cells were determined by counting colonies.

11. RESULTS

1. Raw Data

Table 1*: Salmonella plate counts for experiment 1 (starting concentration 1.5 x* 10^3 *CFU/*cm^2*)*

Treatment (PFU/cm^2 *Applied Phage Vegetable S2*)	**Surface (cm^2)**	**Temperature (°C)**	**Bacteria**	**Number of samples**	**Total CFU/cm^2**
PBS	10.00	21	Yes	10	450 300 1900 450 600 650 750 1250 1500 150
2.5 x 10^6	10.00	21	Yes	10	0 0 0 0 1 8 2 0 2 3
lettuce control	10.00	21	No	1	0

***Table 2**: Salmonella plate counts for experiment 2 (starting concentration 7.5 x 10^4 CFU/cm^2)*

Treatment (PFU/cm^2 *Applied Phage Vegetable S2*)	Surface (cm^2)	Temperature (°C)	Bacteria	Number of samples	Total CFU/cm^2
PBS	10.00	21	Yes	10	40000 55600 33600 62400 11800 44000 21400 52800 2650 31200
2.5 x 10^6	10.00	21	Yes	10	2 3 5 9 2 8 23 2 5 3
lettuce control	10.00	21	No	1	0

2. Tabular presentation of results

***Table 3**: Reduction of* Salmonella *counts on lettuce samples treated with Applied Phage Vegetable S2 21°C.*

CFU/cm^2	Treatment (PFU/cm^2 *Applied Phage Vegetable S2*)	Replicates	Mean recovery CFU/cm^2	% Reduction	Significance
1.5 x 10^3	PBS	n = 10	800	99.80	Yes**
1.5 x 10^3	2.5 x 10^6	n = 10	2		
7.5 x 10^4	PBS	n = 10	35545	99.98	Yes***
7.5 x 10^4	2.5 x 10^6	n = 10	6		

** highly significant with $p < 0.01$

*** highest significance with $p < 0.001$

3. Graphical presentation of results:

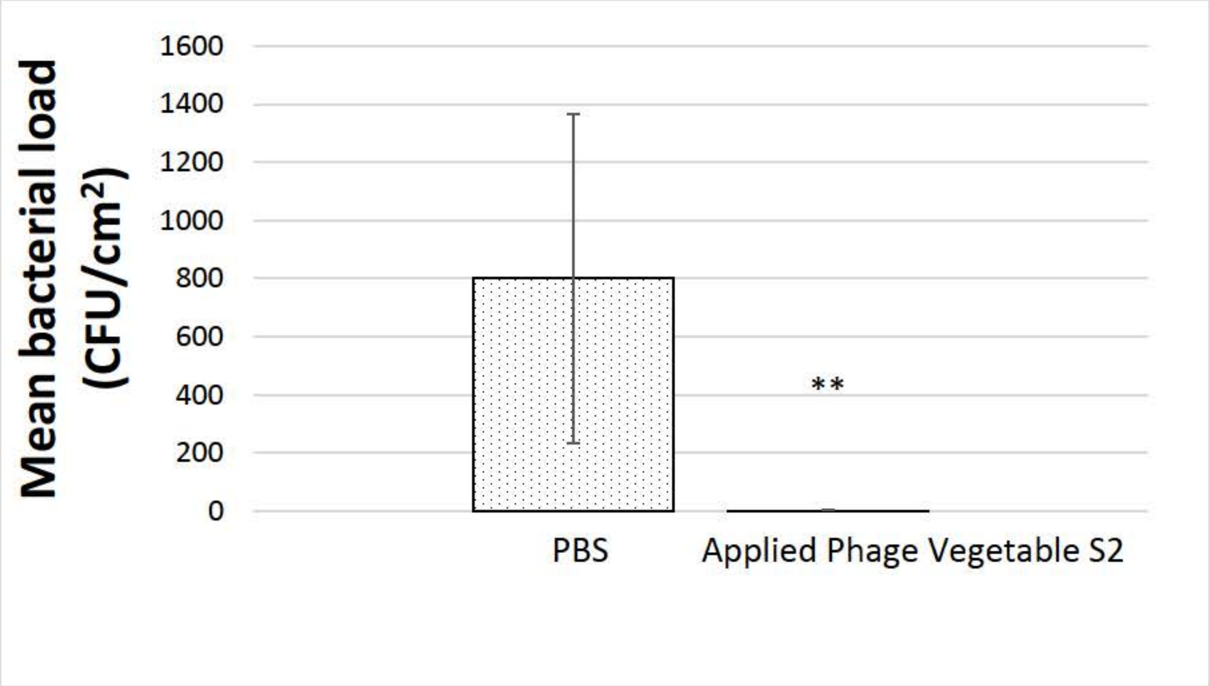

***Figure 1**: Reduction of Salmonella counts on lettuce samples treated with Applied Phage Vegetable S2. Starting contamination 1.5 x 10^3 CFU/cm². Error bars indicate the standard deviation. ** highly significant with $p < 0.01$.*

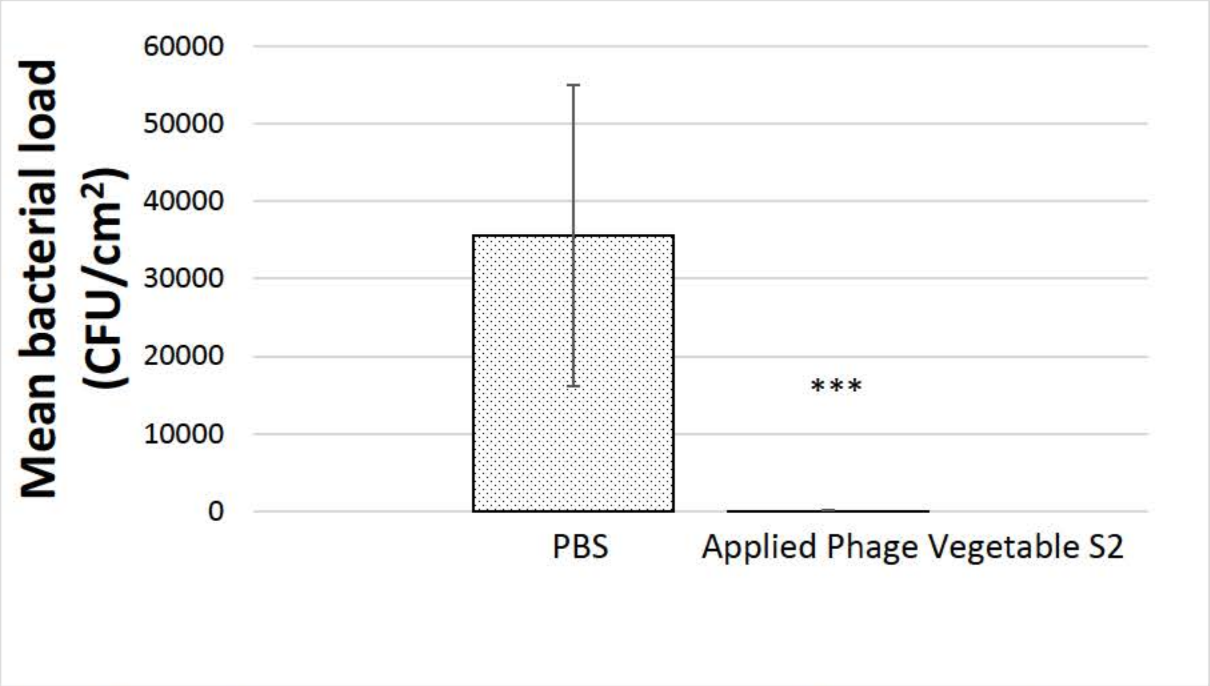

***Figure 2**: Reduction of Salmonella counts on lettuce samples treated with Applied Phage Vegetable S2. Starting contamination 7.5 x 10^4 CFU/cm². Error bars indicate the standard deviation. *** highest significant with $p < 0.001$.*

4. Statistical analysis

Statistical analysis was performed using Office 2013 Excel for Windows (Microsoft Corporation, Redmond, WA).

The efficacy of the *Applied Phage Vegetable S2* treatment in reducing the number of viable *Salmonella typhimurium* on experimentally contaminated lettuce samples was evaluated by comparing the data obtained for PBS treated control samples and for *Applied Phage Vegetable S2* treated samples.

Table 4*: Analysis of Applied Phage Vegetable S2 induced Salmonella reduction on lettuce samples by independent samples t-test.*

Experiment	**T-test**	**Adjusted p value**	**Significance level**	**Significance**	**Summary**
1	PBS vs. *Applied Phage Vegetable S2*	0,0016	$\alpha = 0.01$	Yes	**
2	PBS vs. *Applied Phage Vegetable S2*	0,00026	$\alpha = 0.001$	Yes	***

Applying 2.5 x 10^6 PFU/cm² *Applied Phage Vegetable S2* to lettuce samples (A = 10.00 cm²) reduced the number of viable *Salmonella* by 99.80 % and 99.98 % after 4 h of incubation at 21°C. The observed reduction was highly and highest statistically relevant.

12. SUMMARY CONCLUSION OF THE STUDY

Applied Phage Vegetable S2 can significantly reduce viable *Salmonella typhimurium* levels on experimentally contaminated lettuce samples by 99.98 % in 4 h contact time at 21°C, when used at 2.5 x 10^6 PFU/cm^2.

13. SIGNATURES

[redacted]

Andrea Kroj, Ph.D.
Research scientist

27.03.2020
Date

[redacted]

Hansjörg Lehnherr, Ph.D.
Study director

27.03.2020
Date

Evaluation of the ability of “*Applied Phage Vegetable S2”* to reduce *Salmonella typhimurium* contaminations on experimentally contaminated apple.

Study Number #R021-006

PTC Phage Technology Center GmbH
Siemensstraße 42
D- 59199 Bönen
Tel.: 49 (0) 2383 919 174
Fax: 49 (0) 2383 919 179
Dr. Michael Fink

FINK TEC GmbH
Oberster Kamp 23
D-59069 Hamm
Tel.: 49 (0) 2385 730

1. STUDY TITLE

Evaluation of the ability of *"Applied Phage Vegetable S2"* to reduce *Salmonella typhimurium* contaminations on experimentally contaminated apple.

2. STUDY DIRECTOR

Hansjörg Lehnherr, Ph.D.

3. STUDY PERSONNEL

The following personnel contributed to the conduct and reporting of the studies reported herein:

Name:	**Title:**	**Role:**
Hansjörg Lehnherr, Ph.D.	Chief scientist	Study director
Andrea Kroj, Ph.D.	Research scientist	Hands-on-research

4. PERFORMING LABORATORY

PTC Phage Technology Center GmbH
Siemensstraße 42
D- 59199 Bönen
Tel.: 49 (0) 2383 919 174
Fax: 49 (0) 2383 919 179

5. STUDY OBJECTIVE

Determine the bacterial load reduction of a *Salmonella typhimurium* strain on apple, resulting from an inoculation with *Applied Phage Vegetable S2*, with an application titer of 1.0×10^7 PFU/cm^2.

6. TEST MATRIX

The apples were bought from a supermarket in Meschede, NRW, Germany. Samples were not washed or pre-treated prior to the studies.

7. COCKTAIL LOT AND APPLICATION

Applied Phage Meat S2 lot # 15032021
Applied Phage Meat S2 titer: 5.0 x 10^9 PFU/mL.

The application titer was 1.0 x 10^7 PFU/cm^2.

8. BACTERIAL STRAINS USED TO EVALUATE COCKTAIL EFFICIENCY

Each apple sample was challenged with 1 x 10^4/cm^2 cells of the *Salmonella* strain indicated below. The total reduction in *Salmonella* bacterial load was evaluated.

- A chloramphenicol resistant *Salmonella typhimurium* isolate was used for the experiments.

9. MEDIA AND REAGENTS

- LB broth Lennox (Roth, Karlsruhe, Germany; catalog # X964.4) with 34 µg/mL chloramphenicol (Roth, Karlsruhe, Germany; catalog # 3886.2)
- LB agar Lennox (Roth, Karlsruhe, Germany; catalog # X965.2) with 34 µg/mL chloramphenicol (Roth, Karlsruhe, Germany; catalog # 3886.2)
- PBS (8 g/L NaCl, 0.2 g/L KCl, 1.15 g/L Na_2HPO_4, 0.2 g/L KH_2PO_4; pH 7.5)

10. GENERAL OUTLINE OF STUDY

- Original apples were cut into 21 quadratic samples (10.0 cm^2/sample).
- *Applied Phage Vegetable S2* was diluted with PBS buffer to an application titer of 2 x 10^9 PFU/mL.
- 20 apple samples were homogenously contaminated with 1 x 10^4/cm^2 cells of an overnight culture of the test strain. One sample was not treated with bacteria and served as the uncontaminated, untreated control.
- All samples were incubated for 30 min at room temperature.

- 10 contaminated apple samples were treated with 50 µL of *Applied Phage Vegetable S2* with an application titer of 1 x 10^7 PFU/cm^2 (50 µL of PBS buffer was applied to the remaining 10 samples as the contaminated, untreated controls).
- Incubation period was 4 h at room temperature (21°C).
- To each apple piece 5 mL of PBS was added and treated for 5 min in a stomacher.
- The supernatant was plated on LB agar plates containing chloramphenicol.
- LB agar plates were incubated at 37°C overnight and the numbers of viable *Salmonella* cells were determined by counting colonies.

11. RESULTS

1. Raw Data

Table 1: Salmonella plate counts for Study # R021-006

Treatment (PFU/cm^2 *Applied Phage Vegetable S2*)	**Surface (cm^2)**	**Temperature (°C)**	**Bacteria**	**Number of samples**	**Total CFU/cm^2**
PBS	10.0	21	Yes	10	1145 1590 1085 1195 745 730 670 940 610 680
1.0 x 10^7	10.0	21	Yes	10	30 255 380 45 150 305 310 190 75 95
apple control	10.0	21	No	1	0

2. Tabular presentation of results

***Table 2**: Reduction of Salmonella counts on apple samples treated with Applied Phage Vegetable S2 (1.0 x 10^7 PFU/cm^2) at 21°C.*

Treatment (PFU/mL *Applied Phage Vegetable S2*)	**Temperature (°C)**	**Replicates**	**Mean CFU/cm^2**	**% Reduction**	**Significance**
1.0 x 10^7	21	n = 10	184	80.50 %	Yes***
PBS	21	n = 10	939		

*** highest significant with $p < 0.001$

3. Graphical presentation of results

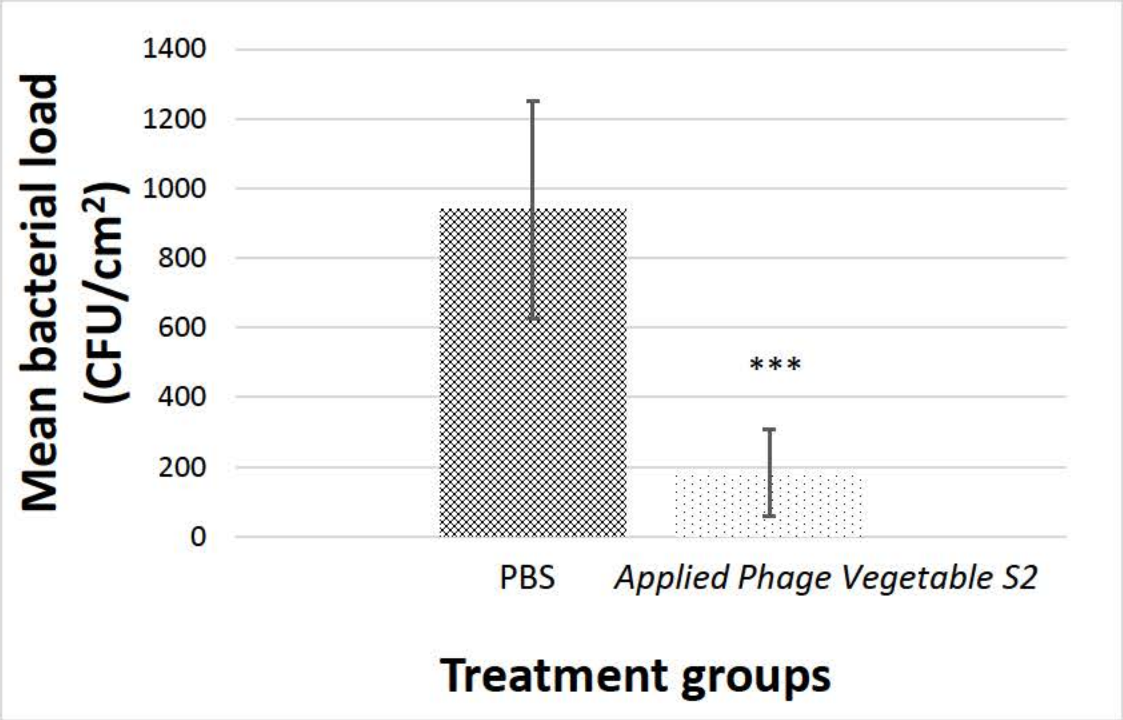

***Figure 1**: Reduction of Salmonella counts on apple samples treated with Applied Phage Vegetable S2. Starting contamination 1.0 x 10^4 CFU/cm^2. Error bars indicate the standard deviation. *** highest significant with p< 0,001.*

4. Statistical analysis

Statistical analysis was performed using Office 2013 Excel for Windows (Microsoft Corporation, Redmond, WA).

The efficacy of the *Applied Phage Vegetable S2* treatment in reducing the number of viable *Salmonella typhimurium* on experimentally contaminated apple samples was evaluated by comparing the data obtained for PBS control samples and for *Applied Phage Vegetable S2* treated samples.

***Table 3**: Analysis of* Applied Phage Vegetable S2 *induced* Salmonella *reduction on apple samples by independent samples t-test.*

T-test	**Adjusted p value**	**Significance level**	**Significance**	**Summary**
PBS vs. *Applied Phage Vegetable S2*	0,00001	$\alpha = 0.001$	Yes	***

Applying 1.0 x 10^7 PFU/cm² *Applied Phage Vegetable S2* to apple samples (A = 10.0 cm²) reduced the number of viable *Salmonella* by 80.5 % after 4 h of incubation at 21°C. The observed reduction was highest statistically significant ($p < 0.001$).

12. SUMMARY CONCLUSION OF THE STUDY

Applied Phage Vegetable S2 can significantly reduce viable *Salmonella typhimurium* levels on experimentally contaminated apple samples by 80.5 % in 4 h contact time at 21°C, when used at 1.0 x 10^7 PFU/cm^2.

13. SIGNATURES

[redacted]

06.08.2021

Andrea Kroj, Ph.D.
Research scientist

Date

[redacted]

06.08.2021

Hansjörg Lehnherr, Ph.D.
Study director

Date