

***Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 14**

**Catalog No. NR-19471**

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**Contributor:**

Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

**Manufacturer:**

BEI Resources

**Product Description:**

The *Francisella tularensis* (*F. tularensis*) subsp. *tularensis*, strain SCHU S4, Gateway® clone set consists of 19 plates which contain 1693 sequence validated clones from *F. tularensis* subsp. *tularensis*, strain SCHU S4 cloned in *Escherichia coli* (*E. coli*) DH10B-T1 cells. Each open reading frame was constructed in vector pDONR™221 (Invitrogen™) with a native start codon and no stop codon. The sequence was validated by full length sequencing of each clone with greater than 1X coverage and a mutation rate of less than 0.2%. Detailed information about each clone is shown in Table 1.

Information related to the use of Gateway® Clones can be obtained from [Invitrogen™](#). Recombination was facilitated through an *attB* substrate (*attB*-PCR product or a linearized *attB* expression clone) with an *attP* substrate (pDONR™221) to create an *attL*-containing entry clone. The entry clone contains recombinational cloning sites, *attL1* and *attL2* to facilitate gene transfer into a destination vector, M13 forward and reverse priming sites for sequencing and a kanamycin resistance gene for selection. Please refer to the [Invitrogen™ Gateway® Technology Manual](#) for additional details.

**Material Provided:**

Each inoculated well of the 96-well plate contains approximately 60 µL of *E. coli* culture (strain DH10B-T1) in Luria Bertani (LB) Broth containing 50 µg/mL kanamycin supplemented with 15% glycerol.

**Note:** Production in the 96-well format has increased risk of cross-contamination between adjacent wells. Individual clones should be purified (e.g. single colony isolation and purification using good microbiological practices) and sequence-verified prior to use. BEI Resources cannot confirm or validate any clone not identified on the plate information table.

**Packaging/Storage:**

NR-19471 was packaged aseptically in a 96-well plate. The

product is provided frozen and should be stored at -80°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

**Growth Conditions:**

Media:

LB Broth or Agar containing 50 µg/mL kanamycin.

Incubation:

Temperature: *E. coli*, strain DH10B-T1 clones should be grown at 37°C.

Atmosphere: Aerobic

Propagation:

1. Scrape top of frozen well with a pipette tip and streak onto agar plate.
2. Incubate the plates at 37°C for 18 to 24 hours.

**Citation:**

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: *Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 14, NR-19471."

**Biosafety Level: 1**

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. [Biosafety in Microbiological and Biomedical Laboratories](#), 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see [www.cdc.gov/biosafety/publications/bmb15/index.htm](http://www.cdc.gov/biosafety/publications/bmb15/index.htm).

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**References:**

1. Larsson, P., et. al. "The Complete Genome Sequence of *Francisella tularensis*, the Causative Agent of Tularemia." Nat. Genet. 37 (2005): 153-159. PubMed: 15640799.
2. Pandya, G. A., et. al. "Whole Genome Single Nucleotide Polymorphism Based Phylogeny of *Francisella tularensis* and its Application to the Development of a Strain Typing Assay." BMC Microbiology 9 (2009): 213. PubMed: 19811647.

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**Table 1: *Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Plate 14 (ZFTKX)**

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
8239	A01	NT06FT1735	DnaJ N-terminal domain:DnaJ C terminal domain	961	CAG46145.1	3.930281
8244	A02	NT06FT0060	ribosomal large subunit pseudouridine synthase C	964	CAG44688.1	4.155602
8245	A03	NT06FT0817	ABC transporter, ATP binding/permease protein	967	CAG45361.1	3.906929
8248	A04	NT06FT1718	hypothetical protein	967	CAG46129.1	4.190279
8251	A05	NT06FT1322	-	973	N/A	3.837616
8253	A06	NT06FT0283	hypothetical protein	976	CAG44888.1	3.83709
8256	A07	NT06FT1047	methionyl-tRNA formyltransferase	976	CAG45558.1	3.07377
8257	A08	NT06FT1061	biotin synthase	976	CAG45570.1	3.868852
8259	A09	NT06FT0103	hypothetical protein	979	CAG44728.1	3.895812
8261	A10	NT06FT1645	glycosyl transferase family protein	979	CAG46066.1	3.506639
8263	A11	NT06FT1858	unnamed protein product	979	CAG46250.1	3.522983
8265	A12	NT06FT1720	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit	982	CAG46131.1	3.49389
8267	B01	NT06FT0538	thioredoxin-disulfide reductase	985	CAG45122.1	3.867005
8269	B02	NT06FT0755	ribose-phosphate pyrophosphokinase	988	CAG45307.1	3.862348
8271	B03	NT06FT0321	ATPase, MoxR family	991	CAG44923.1	3.448032
8273	B04	NT06FT0944	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	991	CAG45466.1	3.429869
8278	B05	NT06FT0581	type I restriction enzyme M protein, putative	994	CAG45155.1	4.131791
8279	B06	NT06FT0596	malate dehydrogenase, NAD-dependent	994	CAG45168.1	3.43662
8282	B07	NT06FT0901	glycosyl transferase, group 2 family protein, putative	994	CAG45430.1	3.768612
8283	B08	NT06FT1598	-	994	N/A	3.466801
8285	B09	NT06FT0099	cyanide-insensitive terminal oxidase, putative	997	CAG44724.1	3.835507
8289	B10	NT06FT0754	predicted deacylase, putative	1000	CAG45306.1	3.822
8292	B11	NT06FT0895	UDP-glucose 4-epimerase	1000	CAG45424.1	3.758
8294	B12	NT06FT1240	transaldolase	1000	CAG45726.1	3.763
8295	C01	NT06FT1902	multidrug resistance protein, putative	1000	CAG46287.1	2.161
8297	C02	NT06FT0121	tetraacyldisaccharide 4-kinase	1003	CAG44743.1	3.405783

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
8299	C03	NT06FT0139	oligopeptide ABC transporter, ATP-binding protein	1003	CAG44758.1	3.376869
8301	C04	NT06FT0252	major facilitator family transporter, putative	1003	N/A	3.433699
8303	C05	NT06FT0284	lipopolysaccharide core biosynthesis protein LpsA	1003	CAG44889.1	3.821535
8305	C06	NT06FT0341	hypothetical protein	1003	CAG44941.1	3.448654
8307	C07	NT06FT1260	CcholoIyglycine hydrolase family protein, putative	1003	CAG45742.1	3.463609
8310	C08	NT06FT0892	carbohydrate isomerase, KpsF/GutQ family	1006	CAG45421.1	4.15507
8311	C09	NT06FT1569	3-oxoacyl-(acyl-carrier-protein) synthase III	1006	CAG46006.1	3.464215
8313	C10	NT06FT0140	oligopeptide ABC transporter, ATP-binding protein	1009	CAG44759.1	3.436075
8316	C11	NT06FT1048	glutathione synthase	1009	CAG45559.1	4.140733
8317	C12	NT06FT0212	peptide chain release factor 2	1012	CAG44824.1	3.422925
8319	D01	NT06FT0218	DNA polymerase III, delta subunit	1012	CAG44830.1	3.392292
8321	D02	NT06FT1181	octaprenyl-diphosphate synthase	1012	CAG45677.1	3.358696
8324	D03	NT06FT0562	dihydrouridine synthase	1018	CAG45141.1	3.050098
8325	D04	NT06FT0578	putative TIM-barrel protein, nifR3 family subfamily	1018	CAG45152.1	3.774067
8327	D05	NT06FT0692	PhoH family protein	1018	CAG45250.1	3.799607
8330	D06	NT06FT0732	lipoic acid synthetase	1018	CAG45286.1	4.126719
8335	D07	NT06FT1767	probable periplasmic protein Cj0093 , putative	1018	CAG46171.1	3.802554
8339	D08	NT06FT0845	lipC, putative	1021	CAG45382.1	3.777669
8341	D09	NT06FT1129	lipoprotein, putative	1024	CAG45631.1	3.417969
8343	D10	NT06FT0196	-	1027	N/A	3.377799
8348	D12	NT06FT1830	putative transcriptional regulator, LysR family	1027	CAG46227.1	4.075949
8349	E01	NT06FT1928	lipoprotein, putative	1027	CAG46309.1	3.393379
8351	E02	NT06FT0131	signal recognition particle-docking protein FtsY	1030	CAG44753.1	3.385437
8353	E03	NT06FT0167	fatty acid desaturase, family 1	1030	CAG44781.1	3.025243
8356	E04	NT06FT0246	phosphate transporter family protein	1030	CAG44852.1	4.096117
8357	E05	NT06FT0418	hypothetical protein	1030	CAG45011.1	3.430097
8360	E06	NT06FT1112	hypothetical protein	1030	CAG45614.1	3.398058
8362	E07	NT06FT1438	hypothetical protein	1030	CAG45896.1	3.751456
8363	E08	NT06FT0325	batB protein, putative	1033	N/A	3.399806
8365	E09	NT06FT0988	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	1033	CAG45504.1	3.784124
8368	E10	NT06FT1417	ribosomal large subunit pseudouridine synthase D	1033	CAG45878.1	3.725073
8370	E11	NT06FT0324	batA protein, putative	1036	CAG44926.1	4.096525
8373	E12	NT06FT1564	glyceraldehyde-3-phosphate dehydrogenase, type I	1036	CAG46001.1	3.751931
8376	F01	NT06FT1666	dTDP-glucose 4,6-dehydratase	1036	CAG46083.1	3.087838
8377	F02	NT06FT1318	hypothetical protein	1039	CAG45793.1	4.025987
8379	F03	NT06FT1708	tryptophanyl-tRNA synthetase	1039	CAG46121.1	4.310876
8381	F04	NT06FT1740	mercuric reductase, putative	1039	N/A	4.842156

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
8383	F05	NT06FT2003	GTP-binding protein, GTP1/OBG family	1039	CAG46364.1	4.566891
8385	F06	NT06FT0041	NADH dehydrogenase I, H subunit	1045	CAG44671.1	3.524402
8387	F07	NT06FT0166	O-sialoglycoprotein endopeptidase	1045	CAG44780.1	4.860287
8389	F08	NT06FT2053	Thermostable carboxypeptidase 1	1045	N/A	4.044976
8391	F09	NT06FT0903	glycosyl transferase, group 1 family protein domain protein	1048	CAG45432.1	4.799618
8393	F10	NT06FT1135	phenylalanyl-tRNA synthetase, alpha subunit	1048	CAG45636.1	4.265267
8395	F11	NT06FT1804	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	1048	CAG46204.1	3.977099
8397	F12	NT06FT2083	anthranilate phosphoribosyltransferase	1048	N/A	4.778626
8399	G01	NT06FT1385	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	1051	CAG45848.1	4.525214
8401	G02	NT06FT1477	glucokinase	1051	CAG45928.1	4.836346
8405	G03	NT06FT1568	fatty acid/phospholipid synthesis protein PlsX	1054	CAG46005.1	3.533207
8407	G04	NT06FT1908	histidine kinase-related ATPase, putative	1054	CAG46292.1	4.542694
8409	G05	NT06FT0636	INTEGRAL MEMBRANE PROTEIN	1057	CAG45202.1	4.8193
8411	G06	NT06FT1429	multidrug resistance protein, putative	1057	CAG45890.1	4.8193
8413	G07	NT06FT0554	Hypothetical UPF0118 protein, putative	1060	CAG45134.1	2.942453
8415	G08	NT06FT1560	Trehalase	1060	N/A	4.782075
8419	G09	NT06FT0095	twitching motility protein PilT	1063	CAG44721.1	4.738476
8422	G10	NT06FT0672	SIS domain protein	1063	CAG45232.1	4.975541
8423	G11	NT06FT1897	-	1063	N/A	4.467545
8425	G12	NT06FT1723	conserved hypothetical protein	1066	N/A	4.787992
8427	H01	NT06FT0051	uroporphyrinogen decarboxylase	1069	CAG44680.1	4.821328
8429	H02	NT06FT0815	Glycerophosphoryl diester phosphodiesterase	1069	CAG45359.1	4.219832
8431	H03	NT06FT0217	glutamine synthetase	1072	CAG44829.1	4.255597
8437	H04	NT06FT0317	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	1078	CAG44919.1	4.183673
8442	H05	NT06FT0489	conserved hypothetical protein	1078	CAG45076.1	5.103896
8443	H06	NT06FT1012	phosphoribosylformylglycinamide cyclo-ligase	1078	CAG45526.1	2.816327
8445	H07	NT06FT1798	glycosyl hydrolase, family 3	1078	N/A	4.736549
8448	H08	NT06FT1146	Holliday junction DNA helicase RuvB	1081	CAG45646.1	4.502313
8449	H09	NT06FT1673	glycosyltransferase	1081	CAG46090.1	4.004625
8451	H10	NT06FT1913	carbamoyl-phosphate synthase, small subunit	1081	CAG46296.1	3.694727
8453	H11	NT06FT0861	RecF protein, putative	1084	CAG45395.1	4.754613
8455	H12	NT06FT0623	Phosphoserine aminotransferase (PSAT)	1087	CAG45193.1	4.724931