

Francisella tularensis subsp. tularensis, Strain SCHU S4, Gateway® Clone Set, Recombinant in Escherichia coli, Plate 10

Catalog No. NR-19467

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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-19467 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 10, NR-19467."

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/bmbl5/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 10 (ZFTKT)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
7365	A01	NT06FT1353	hypothetical protein	670	CAG45821.1	3.817910448
7367	A02	NT06FT1643	translocator protein, LysE family superfamily	670	CAG46064.1	2.701492537
7369	A03	NT06FT1327	Glycoprotease,	673	CAG45800.1	3.424962853
7371	A04	NT06FT1337	Imp2, putative	673	CAG45808.1	2
7373	A05	NT06FT1876	conserved hypothetical protein	673	CAG46265.1	2.722139673
7376	A06	NT06FT0542	major facilitator family transporter	676	N/A	3.828402367
7379	A08	NT06FT0844	transcriptional regulator, lclR family, putative	676	CAG45381.1	4.218934911
7381	A09	NT06FT0955	MiaB-like tRNA modifying enzyme YliG, TIGR01125	676	N/A	4.221893491
7386	A10	NT06FT1027	PROBABLE PARTITION PROTEIN, putative	676	CAG45540.1	2.795857988
7388	A11	NT06FT1683	adenosine deaminase, putative	676	N/A	2.405325444
7389	A12	NT06FT1993	4-phosphopantetheinyl transferase superfamily family	676	CAG46356.1	4.210059172
7391	B01	NT06FT0036	NADH dehydrogenase I, C subunit	679	CAG44666.1	3.110456554
7393	B02	NT06FT0729	glutaredoxin 2, putative	679	CAG45283.1	4.228276878
7395	B03	NT06FT1007	Fimbrial protein ecpC precursor (Pilin)	679	CAG45521.1	3.42562592
7397	B04	NT06FT2061	conserved hypothetical protein	679	CAG46414.1	4.22533137
7401	B05	NT06FT1287	-	682	N/A	4.215542522
7403	B06	NT06FT1393	DedA family protein	682	CAG45856.1	4.234604106
7405	B07	NT06FT1760	sugar-proton symporter, putative	682	N/A	4.23313783
7407	B08	NT06FT0635	phosphoserine phosphatase precursor, chloroplast [validated], putative	685	CAG45201.1	4.224817518
7409	B09	NT06FT0738	Holliday junction DNA helicase RuvA	685	CAG45291.1	4.24379562
7411	B10	NT06FT1507	membrane protein, putative	685	CAG45957.1	3.832116788
7413	B11	NT06FT0337	NAD(P)H-flavin oxidoreductase, putative	688	CAG44937.1	4.216569767
7415	B12	NT06FT0987	hypothetical protein	688	CAG45502.1	3.841569767
7418	C01	NT06FT1165	membrane protein, putative	688	N/A	3.502906977
7419	C02	NT06FT1499	thiamine pyrophosphokinase	688	CAG45949.1	4.219476744
7421	C03	NT06FT1601	Putative repressor protein of prophage, putative	688	CAG46034.1	3.520348837
7423	C04	NT06FT2043	membrane protein, putative	688	CAG46398.1	3.129360465
7426	C05	NT06FT0185	conserved hypothetical protein	691	CAG44799.1	3.500723589
7427	C06	NT06FT0247	conserved hypothetical protein	691	CAG44853.1	4.2170767

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
7429	C07	NT06FT0485	RNA methyltransferase, TrmH family, group 3	691	CAG45072.1	2.707670043
7433	C08	NT06FT1319	adenylate kinase	691	CAG45794.1	4.228654124
7437	C09	NT06FT2044	O-methyltransferase	691	CAG46399.1	3.421128799
7440	C10	NT06FT0437	MTA/SAH nucleosidase	694	CAG45030.1	2.801152738
7443	C11	NT06FT0533	hypothetical protein	697	CAG45118.1	4.239598278
7447	C12	NT06FT0771	hypothetical protein	697	CAG45322.1	4.226685796
7449	D01	NT06FT0904	pyrimidine 5-nucleotidase	697	CAG45433.1	3.846484935
7451	D02	NT06FT1090	DJ-1/Pfpl family protein	697	CAG45595.1	3.507890961
7453	D03	NT06FT1455	RNA methyltransferase, TrmH family, group 1	697	CAG45912.1	3.803443329
7456	D04	NT06FT1587	conserved hypothetical protein	697	CAG46021.1	3.116212339
7458	D05	NT06FT1811	uracil-DNA glycosylase	697	CAG46211.1	3.109038737
7461	D06	NT06FT0138	oligopeptide ABC transporter, permease protein	700	N/A	4.241428571
7463	D07	NT06FT0633	-	700	N/A	3.431428571
7465	D08	NT06FT0786	uridine kinase	700	CAG45335.1	4.051428571
7467	D09	NT06FT0930	DedA family family	700	CAG45454.1	2.707142857
7469	D10	NT06FT1946	NADH dehydrogenase CC0324	700	CAG46323.1	4.235714286
7471	D11	NT06FT0005	succinate-semialdehyde dehydrogenase	703	N/A	3.122332859
7473	D12	NT06FT0286	carboxylesterase, putative	703	CAG44891.1	4.241820768
7477	E02	NT06FT0395	unnamed protein product	703	N/A	3.823613087
7479	E03	NT06FT0645	Zinc metalloprotease, putative	703	CAG45209.1	3.504978663
7481	E04	NT06FT0893	ribulose-phosphate 3-epimerase	703	CAG45422.1	3.116642959
7484	E05	NT06FT1878	PAP2 superfamily domain protein	703	CAG46267.1	3.509246088
7486	E06	NT06FT1942	conserved hypothetical protein TIGR00044	703	CAG46319.1	3.526315789
7490	E07	NT06FT1352	YdaO	706	CAG45820.1	3.093484419
7491	E08	NT06FT0540	phosphoglycolate phosphatase, putative	709	CAG45124.1	3.528913963
7493	E09	NT06FT0694	O-methyltransferase family protein, putative	709	CAG45252.1	4.234132581
7495	E10	NT06FT1207	type III restriction-modification system, res subunit	709	N/A	3.074753173
7497	E11	NT06FT1377	ribose 5-phosphate isomerase A	709	CAG45841.1	4.207334274
7499	E12	NT06FT0199	DNA internalization-related competence protein ComEC/Rec2	712	N/A	3.841292135
7501	F01	NT06FT1058	dethiobiotin synthetase, putative	712	CAG45567.1	3.831460674
7503	F02	NT06FT1237	transporter, putative	712	CAG45723.1	3.820224719
7505	F03	NT06FT1333	type I restriction enzyme EcoEI specificity protein	712	N/A	3.528089888
7509	F04	NT06FT0816	lipoprotein, putative	715	CAG45360.1	3.816783217
7511	F05	NT06FT0877	drug resistance transporter, Bcr/CflA family protein, putative	715	N/A	3.832167832
7513	F06	NT06FT1634	metallo-beta-lactamase family protein, putative	715	CAG46057.1	4.201398601
7515	F07	NT06FT1910	unnamed protein product; similar to trjQ88LQ9 Pseudomonas putida PP1870 Thiopurine s-methyltransferase, start by similarity, putative	715	CAG46294.1	3.808391608
7517	F08	NT06FT0207	cell division protein FtsQ, putative	718	CAG44819.1	4.227019499
7519	F09	NT06FT1354	major facilitator family transporter, putative	718	N/A	3.816155989
7523	F10	NT06FT0665	beta carbonic anhydrase	721	CAG45225.1	4.226074896
7525	F11	NT06FT0724	membrane protein, putative	721	CAG45278.1	4.20665742
7527	F12	NT06FT0941	-	721	N/A	4.221914008
7530	G01	NT06FT1575	unnamed protein product	721	N/A	3.497919556
7531	G02	NT06FT1788	DNA-binding response regulator	721	CAG46190.1	4.233009709
7533	G03	NT06FT1844	septum site-determining protein MinC	721	CAG46238.1	3.217753121
7535	G04	NT06FT0433	methionine aminopeptidase, type I	724	CAG45026.1	4.216850829

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7540	G05	NT06FT1771	DNA-binding response regulator	724	CAG46176.1	4.214088398
7541	G06	NT06FT2079	Peptide methionine sulfoxide reductase	724	CAG46430.1	4.237569061
7544	G07	NT06FT0610	DNA polymerase III, epsilon subunit	727	CAG45181.1	4.233837689
7545	G08	NT06FT1786	ribonuclease III	727	CAG46188.1	4.213204952
7549	G09	NT06FT0160	ribosomal protein L1	730	CAG44774.1	4.217808219
7552	G10	NT06FT0318	radical SAM domain protein, putative	730	CAG44920.1	3.501369863
7553	G11	NT06FT0447	ABC transporter, ATP-binding protein	730	CAG45038.1	4.184931507
7555	G12	NT06FT0536	permease, putative	730	CAG45120.1	4.217808219
7557	H01	NT06FT1826	ubiquinone biosynthesis O-methyltransferase	730	CAG46223.1	4.209589041
7559	H02	NT06FT0192	Predicted deacylase	733	N/A	4.227830832
7561	H03	NT06FT0250	LamB/YcsF family protein, putative	733	CAG44856.1	3.798090041
7563	H04	NT06FT0827	-	733	N/A	3.804911323
7565	H05	NT06FT0890	hypothetical protein	733	CAG45419.1	4.219645293
7569	H07	NT06FT1071	membrane protein, putative	733	N/A	4.190995907
7573	H08	NT06FT1394	DNA repair protein RecO	733	CAG45857.1	4.207366985
7581	H11	NT06FT1885	hypothetical protein	736	N/A	4.216032609
7583	H12	NT06FT0622	cytidylate kinase	739	CAG45192.1	4.204330176