

***Francisella tularensis* subsp. *tularensis*,
Strain SCHU S4, Gateway® Clone Set,
Recombinant in *Escherichia coli*, Plate 12**

Catalog No. NR-19469

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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-19469 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 12, NR-19469."

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.

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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 12 (ZFTKV)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
7803	A01	NT06FT0991	hypothetical protein	805	CAG45507.1	3.78882
7805	A02	NT06FT1591	transcriptional activator, putative, Baf family subfamily	805	CAG46025.1	3.801242
7807	A03	NT06FT1626	possible hydrolase	805	CAG46050.1	4.180124
7809	A04	NT06FT0231	cation ABC transporter, permease protein, putative	808	CAG44840.1	3.77599
7811	A05	NT06FT0351	undecaprenyl diphosphate synthase	808	CAG44950.1	3.808168
7813	A06	NT06FT0842	possible FusE-MFP/HlyD family membrane fusion protein	808	CAG45380.1	3.783416
7816	A07	NT06FT0123	transcriptional activator, putative, Baf family subfamily	811	CAG44745.1	4.166461
7817	A08	NT06FT1086	exodeoxyribonuclease III	811	CAG45592.1	3.790382
7819	A09	NT06FT1154	tRNA pseudouridine synthase A	811	CAG45654.1	4.175092
7821	A10	NT06FT0270	cell wall surface anchor family protein	814	CAG44876.1	4.185504
7823	A11	NT06FT0326	TPR Domain domain protein	814	N/A	3.511057
7825	A12	NT06FT0616	conserved hypothetical protein	814	CAG45186.1	3.765356
7827	B01	NT06FT0785	3-deoxy-8-phosphooctulonate synthase	814	CAG45334.1	3.789926
7831	B02	NT06FT1646	ABC transporter, permease protein, putative	814	CAG46067.1	4.190418
7837	B03	NT06FT0525	biotin--acetyl-CoA-carboxylase ligase	817	CAG45110.1	4.203182
7840	B04	NT06FT0886	enoyl-(acyl-carrier-protein) reductase	817	CAG45415.1	4.182375
7841	B05	NT06FT1589	pantoate--beta-alanine ligase	820	CAG46023.1	3.779268
7843	B06	NT06FT0517	dimethyladenosine transferase	823	CAG45102.1	4.143378
7845	B07	NT06FT0811	glucose 1-dehydrogenase	823	CAG45356.1	4.176185
7847	B08	NT06FT0937	L-aspartate-beta-decarboxylase	823	N/A	3.780073
7852	B09	NT06FT2070	unnamed protein product; Some similarities with unknown protein. Putative transmembrane protein	823	CAG46422.1	4.173755
7857	B10	NT06FT0841	fusaric acid resistance protein, putative	826	CAG45379.1	4.175545
7861	B11	NT06FT1678	capsular polysaccharide biosynthesis protein Cap5N	826	CAG46095.1	3.782082
7863	B12	NT06FT1864	hypothetical protein	826	CAG46254.1	3.77845
7866	C01	NT06FT0352	phosphatidate cytidyltransferase	829	CAG44951.1	3.477684
7867	C02	NT06FT1588	3-methyl-2-oxobutanoate hydroxymethyltransferase	829	CAG46022.1	4.131484

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
7882	C04	NT06FT1229	Iron-regulated protein frpC, putative	838	CAG45714.1	3.078759
7883	C05	NT06FT1509	Udp	838	CAG45959.1	4.198091
7885	C06	NT06FT1847	ABC transporter, ATP-binding protein	838	CAG46241.1	4.177804
7887	C07	NT06FT0501	YdjC-like protein superfamily	841	CAG45086.1	4.155767
7889	C08	NT06FT0629	putrescine ABC transporter, permease protein	841	CAG45197.1	4.131986
7892	C09	NT06FT1326	predicted glutamine amidotransferase	841	CAG45799.1	4.185493
7893	C10	NT06FT1398	prolipoprotein diacylglyceryl transferase	841	CAG45861.1	4.108205
7895	C11	NT06FT0235	-	844	N/A	4.112559
7897	C12	NT06FT1528	hypothetical protein	844	CAG45976.1	4.171801
7899	D01	NT06FT1796	pvdS	844	CAG46197.1	4.169431
7901	D02	NT06FT2051	tryptophan synthase, alpha subunit	844	CAG46405.1	4.17654
7903	D03	NT06FT0305	drug resistance transporter, Bcr/CflA family, putative	847	N/A	4.172373
7905	D04	NT06FT0687	hypothetical protein	847	CAG45245.1	4.165289
7907	D05	NT06FT0743	conserved hypothetical protein	847	CAG45296.1	4.160567
7909	D06	NT06FT0889	Protein of unknown function, putative	847	CAG45418.1	4.152302
7911	D07	NT06FT1180	macrophage infectivity potentiator, putative	847	CAG45676.1	4.14876
7913	D08	NT06FT1226	Iron-regulated protein frpC	847	CAG45711.1	4.101535
7915	D09	NT06FT1418	bax protein, putative	847	CAG45879.1	4.090909
7917	D10	NT06FT0093	dyp-type peroxidase family protein	850	CAG44719.1	4.155294
7919	D11	NT06FT0530	lipoprotein, putative	850	CAG45115.1	4.131765
7922	D12	NT06FT0839	conserved hypothetical protein	850	CAG45376.1	4.184706
7925	E01	NT06FT1126	cardiolipin synthetase, putative	850	N/A	4.168235
7927	E02	NT06FT1193	RNA pseudouridine synthase, RsuA family	850	CAG45689.1	4.16
7929	E03	NT06FT0764	type IV pilus prepilin peptidase PilD	853	CAG45316.1	4.148886
7931	E04	NT06FT0906	cyanophycinase	853	CAG45435.1	4.135991
7933	E05	NT06FT0362	ribosomal protein L2	859	CAG44961.1	4.112922
7936	E06	NT06FT0397	Short-chain dehydrogenase/reductase	859	CAG44993.1	3.790454
7939	E07	NT06FT0971	4-hydroxybenzoate polyprenyl transferase	859	CAG45489.1	4.06752
7941	E08	NT06FT1399	thymidylate synthase	859	CAG45862.1	4.112922
7943	E09	NT06FT1416	competence lipoprotein ComL, putative	859	CAG45877.1	3.179278
7946	E10	NT06FT1791	pyrroline-5-carboxylate reductase	859	CAG46192.1	4.165308
7947	E11	NT06FT1845	septum site-determining protein MinD	859	CAG46239.1	4.161816
7950	E12	NT06FT0299	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	862	CAG44904.1	4.170534
7951	F01	NT06FT0413	Short-chain fatty acids transporter	862	N/A	4.142691
7953	F02	NT06FT0469	bifunctional aspartokinase/homoserine dehydrogenase I	862	N/A	4.136891
7955	F03	NT06FT0510	delta-aminolevulinic acid dehydratase	862	CAG45095.1	4.12761
7957	F04	NT06FT0518	bis(5-nucleosyl)-tetraphosphatase (symmetrical)	862	CAG45103.1	3.448956
7959	F05	NT06FT0573	-	862	N/A	4.136891
7962	F06	NT06FT1427	transcriptional regulator, AraC family	862	CAG45888.1	4.177494
7963	F07	NT06FT1485	SAM (and some other nucleotide) binding motif, putative	862	CAG45935.1	4.074246
7965	F08	NT06FT1644	inorganic polyphosphate/ATP-NAD kinase	862	CAG46065.1	4.12645
7967	F09	NT06FT1783	delta 9 acyl-lipid fatty acid desaturase	862	CAG46185.1	4.098608
7969	F10	NT06FT1208	-	865	N/A	4.164162
7971	F11	NT06FT1233	yitL protein	865	CAG45719.1	4.147977
7973	F12	NT06FT0220	hypothetical protein	868	CAG44832.1	4.147465
7975	G01	NT06FT1158	hypothetical protein	868	CAG45658.1	3.778802

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
7977	G02	NT06FT0272	Universal stress protein	871	CAG44878.1	4.125144
7979	G03	NT06FT0572	iron-sulfur cluster-binding protein	874	N/A	4.159039
7981	G04	NT06FT0644	prephenate dehydratase	877	CAG45208.1	4.101482
7984	G05	NT06FT0690	magnesium and cobalt efflux protein CorC	877	CAG45248.1	3.477765
7985	G06	NT06FT1577	-	877	N/A	4.052452
7987	G07	NT06FT0174	oxidoreductase, 2OG-Fe(II) oxygenase family, putative	880	CAG44788.1	4.020455
7989	G08	NT06FT0295	hypothetical protein	880	CAG44900.1	4.097727
7991	G09	NT06FT0453	shikimate 5-dehydrogenase/quininate 5-dehydrogenase family protein, putative	880	CAG45044.1	4.1125
7993	G10	NT06FT0577	ribosomal protein L11 methyltransferase	880	CAG45151.1	4.118182
7995	G11	NT06FT0763	hypothetical protein	880	CAG45315.1	4.148864
7997	G12	NT06FT1461	probable hydrolase VCA0877 , putative	880	N/A	4.126136
8000	H01	NT06FT0316	protoheme IX farnesyltransferase	883	CAG44918.1	3.788222
8001	H02	NT06FT0434	NY-REN-58 antigen, putative	883	CAG45027.1	4.106455
8003	H03	NT06FT0641	amino acid permease, putative	883	N/A	4.116648
8005	H04	NT06FT1011	methylenetetrahydrofolate dehydrogenase fold	883	CAG45525.1	4.105323
8007	H05	NT06FT1487	UDP-N-acetylenolpyruvoylglucosamine reductase	883	CAG45937.1	4.101925
8009	H06	NT06FT0027	glycerophospholipid-cholesterol acyltransferase, putative	886	CAG44656.1	4.045147
8011	H07	NT06FT0424	phosphatidylserine decarboxylase	886	CAG45017.1	4.002257
8015	H08	NT06FT0188	protein-(glutamine-N5) methyltransferase, release factor-specific	889	CAG44802.1	4.093363
8019	H09	NT06FT1255	peptide methionine sulfoxide reductase	889	CAG45738.1	4.128234
8021	H10	NT06FT0210	UDP-3-O-acyl N-acetylglucosamine deacetylase	892	CAG44822.1	4.11435
8023	H11	NT06FT0388	hypothetical protein	895	CAG44987.1	4.087151
8025	H12	NT06FT0481	carbon-nitrogen hydrolase family protein	895	CAG45068.1	4.069274