

***Francisella tularensis* subsp. *tularensis*, Strain SCHU S4, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 16**

Catalog No. NR-19473

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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-19473 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 16, NR-19473."

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 16 (ZFTKZ)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
8693	A01	NT06FT0029	probable transporter, putative	1225	CAG44659.1	4.614694
8695	A02	NT06FT0706	monooxygenase, FAD-binding	1225	CAG45265.1	4.812245
8697	A03	NT06FT1122	Mechanosensitive ion channel family, putative	1225	CAG45625.1	4.321633
8701	A04	NT06FT0309	cytochrome d ubiquinol oxidase, subunit II	1228	CAG44911.1	4.57899
8703	A05	NT06FT0488	drug resistance transporter, Bcr/CflA family, putative	1228	CAG45075.1	4.165309
8705	A06	NT06FT1325	aspartate aminotransferase	1228	CAG45798.1	4.535831
8707	A07	NT06FT0800	2-amino-3-ketobutyrate coenzyme A ligase	1231	CAG45347.1	4.506093
8709	A08	NT06FT1401	cell cycle protein mesJ, putative	1231	CAG45864.1	4.597076
8711	A09	NT06FT1546	IgID	1231	CAG45989.1	4.306255
8713	A10	NT06FT1733	Tyrosine-specific transport protein	1231	CAG46143.1	4.269699
8715	A11	NT06FT1976	IgID	1231	CAG46344.1	4.220959
8717	A12	NT06FT2004	Tyrosine-specific transport protein	1231	CAG46365.1	4.562145
8721	B01	NT06FT1453	sodium:solute symporter family protein, putative	1234	CAG45910.1	4.341167
8723	B02	NT06FT0127	nucleoside permease NupC, putative	1237	CAG44749.1	4.607922
8725	B03	NT06FT0141	major facilitator family transporter, putative	1237	CAG44760.1	4.573161
8729	B04	NT06FT1348	oxidoreductase, FAD-binding family protein, putative	1240	CAG45816.1	3.808871
8731	B05	NT06FT1944	tyrosine-specific transport protein	1240	CAG46321.1	4.490323
8733	B06	NT06FT0006	major facilitator family transporter, putative	1243	CAG44639.1	4.563958
8735	B07	NT06FT1138	sodium:galactoside symporter family protein, putative	1243	CAG45639.1	4.770716
8737	B08	NT06FT0916	conserved hypothetical protein	1246	CAG45440.1	4.739968
8741	B09	NT06FT1925	3,4-dihydroxy-2-butanone-4-phosphate synthase/GTP cyclohydrolase II	1246	CAG46306.1	4.554575
8743	B10	NT06FT0539	probable phospholipase D/ transphosphatidylase, putative	1252	CAG45123.1	4.398562
8745	B11	NT06FT1573	3-oxoacyl-(acyl-carrier-protein) synthase II	1255	CAG46010.1	4.611155

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
8747	B12	NT06FT0647	aminotransferase, class-V	1258	CAG45211.1	3.81717
8749	C01	NT06FT1505	Peptidase M16 inactive domain family	1258	CAG45955.1	4.563593
8751	C02	NT06FT0490	multidrug transporter, putative	1261	CAG45077.1	4.53291
8753	C03	NT06FT0767	proton/peptide symporter family protein, putative	1261	CAG45319.1	4.522601
8755	C04	NT06FT1054	sugar transporter, putative	1261	CAG45564.1	4.475813
8757	C05	NT06FT1132	cobalamin synthesis protein, putative	1261	CAG45633.1	4.561459
8759	C06	NT06FT0896	WbcW protein	1264	CAG45425.1	4.304589
8761	C07	NT06FT1285	pilC protein	1264	CAG45767.1	4.61788
8765	C08	NT06FT1674	O-antigen polymerase	1264	CAG46091.1	4.745253
8767	C09	NT06FT0019	adenylosuccinate lyase	1267	CAG44648.1	4.588792
8769	C10	NT06FT0593	ribonucleoside-diphosphate reductase, beta subunit, putative	1267	CAG45165.1	4.519337
8771	C11	NT06FT0814	glycerol-3-phosphate transporter	1267	CAG45358.1	4.573007
8777	C12	NT06FT1387	monooxygenase family protein, putative	1270	CAG45850.1	4.244094
8779	D01	NT06FT1400	D-3-phosphoglycerate dehydrogenase	1270	CAG45863.1	4.483465
8781	D02	NT06FT0794	major facilitator family transporter	1273	CAG45341.1	4.553024
8783	D03	NT06FT0968	transporter, NadC/P/Pho87 family, putative	1273	CAG45486.1	4.320503
8787	D04	NT06FT1111	2-amino-3-ketobutyrate coenzyme A ligase, putative	1276	CAG45613.1	4.582288
8789	D05	NT06FT2063	major facilitator family transporter, putative	1276	CAG46416.1	4.402821
8791	D06	NT06FT0124	phosphopentomutase	1279	CAG44746.1	4.581704
8793	D07	NT06FT0186	glutamyl-tRNA reductase	1285	CAG44800.1	4.234241
8795	D08	NT06FT0200	DNA uptake/competence protein, putative	1285	N/A	4.242802
8797	D09	NT06FT0499	UDP-N-acetylmuramoylalanine--D-glutamate ligase	1285	CAG45084.1	4.551751
8801	D10	NT06FT0030	diaminopimelate decarboxylase, putative	1288	CAG44660.1	4.501553
8803	D11	NT06FT0037	NADH dehydrogenase I, D subunit	1288	CAG44667.1	4.160714
8805	D12	NT06FT0699	ATP-dependent Clp protease, ATP-binding subunit ClpX	1288	CAG45258.1	4.522516
8807	E01	NT06FT0942	OmpA family domain protein	1288	CAG45464.1	4.571429
8809	E02	NT06FT1413	serine hydroxymethyltransferase	1288	CAG45874.1	4.239907
8812	E03	NT06FT1504	Insulinase family (Peptidase family M16)	1288	CAG45954.1	4.771739
8817	E04	NT06FT0725	membrane protein, putative	1294	CAG45279.1	4.360896
8821	E05	NT06FT1517	Membrane protein involved in the export of O-antigen and teichoic acid, putative	1294	CAG45965.1	4.047913
8823	E06	NT06FT0031	probable transporter, putative	1297	CAG44661.1	4.383963
8825	E07	NT06FT0208	cell division protein FtsA	1297	CAG44820.1	4.268311
8827	E08	NT06FT0446	lipoprotein releasing system transmembrane protein, putative	1297	CAG45037.1	3.276793
8829	E09	NT06FT0798	Serine transporter, putative	1297	CAG45345.1	4.272167
8831	E10	NT06FT1170	ndh, putative	1297	CAG45667.1	4.307633
8833	E11	NT06FT1414	conserved hypothetical protein	1297	CAG45875.1	4.468774
8837	E12	NT06FT0057	histidyl-tRNA synthetase	1300	CAG44685.1	4.326923
8841	F01	NT06FT1411	membrane protein, putative	1306	CAG45872.1	4.375957

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
8843	F02	NT06FT0039	NADH-quinone oxidoreductase, F subunit	1309	CAG44669.1	4.02903
8845	F03	NT06FT0671	sodium:dicarboxylate symporter family protein, putative	1309	CAG45231.1	4.330787
8847	F04	NT06FT1473	D-galactonate transporter, putative	1309	N/A	4.282659
8849	F05	NT06FT0115	membrane protein, putative	1312	CAG44737.1	3.612043
8853	F06	NT06FT0751	major facilitator family transporter, putative	1315	CAG45304.1	4.652471
8855	F07	NT06FT1515	seryl-tRNA synthetase	1315	CAG45963.1	4.298859
8857	F08	NT06FT1581	sun protein	1315	CAG46016.1	3.088213
8859	F09	NT06FT0227	adenylosuccinate synthetase	1321	CAG44837.1	4.010598
8861	F10	NT06FT0474	threonine synthase	1321	CAG45061.1	4.268736
8863	F11	NT06FT0898	phosphoserine phosphatase	1321	CAG45427.1	4.313399
8866	F12	NT06FT1062	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	1321	CAG45571.1	4.716881
8867	G01	NT06FT1996	peptidase, U32 family	1321	CAG46359.1	4.240727
8869	G02	NT06FT1049	glutamate-1-semialdehyde-2,1-aminomutase	1330	CAG45560.1	4.224812
8873	G03	NT06FT0058	major facilitator family transporter, putative	1333	CAG44686.1	3.303076
8875	G04	NT06FT1710	Na ⁺ /H ⁺ antiporter, putative	1333	CAG46123.1	4.15904
8877	G05	NT06FT1874	sodium/proline symporter BH0660	1336	CAG46263.1	3.632485
8879	G06	NT06FT0061	major facilitator family transporter, putative	1339	CAG44689.1	3.848394
8881	G07	NT06FT1488	UDP-N-glucosamine 1-carboxyvinyltransferase	1339	CAG45938.1	4.299477
8883	G08	NT06FT0646	L-serine ammonia-lyase	1342	CAG45210.1	4.245902
8885	G09	NT06FT0705	GTP-binding protein HflX	1342	CAG45264.1	4.260805
8887	G10	NT06FT0951	tolB protein, putative	1342	CAG45473.1	4.336066
8891	G11	NT06FT1676	UDP-GalNAc dehydrogenase	1345	CAG46093.1	4.246097
8893	G12	NT06FT1872	CBS domain protein	1345	CAG46261.1	3.826022
8895	H01	NT06FT0143	major facilitator family transporter, putative	1348	CAG44762.1	4.275964
8901	H02	NT06FT1110	Amino-acid permease rocE	1348	CAG45612.1	4.393175
8903	H03	NT06FT0130	LysM domain protein	1351	CAG44752.1	4.326425
8905	H04	NT06FT0294	ABC transporter, ATP-binding protein	1351	CAG44899.1	4.03701
8907	H05	NT06FT0697	trigger factor	1351	CAG45256.1	4.142857
8909	H06	NT06FT0717	acetolactate synthase, large subunit, biosynthetic type	1351	N/A	4.107328
8911	H07	NT06FT1937	-	1351	N/A	4.311621
8914	H08	NT06FT0379	preprotein translocase, SecY subunit	1360	CAG44978.1	4.608824
8915	H09	NT06FT0807	deoxyguanosinetriphosphate triphosphohydrolase, putative	1360	CAG45353.1	4.639706
8917	H10	NT06FT1079	ATP-dependent RNA helicase RhlE	1360	CAG45585.1	4.228676
8919	H11	NT06FT0693	tRNA-i(6)A37 thiotransferase enzyme MiaB	1363	CAG45251.1	4.239178
8923	H12	NT06FT0084	phosphoglucosamine mutase	1366	CAG44712.1	3.841142